

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2003, 13:55:42 ; Search time 3165.17 Seconds  
(without alignments)  
9377.568 Million cell updates/sec

Title: US-09-700-770-5

Perfect score: 895  
Sequence: 1 ctaactgttactgtaacagc.....aataaattttaaatgtc 895

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 33363688 seqs, 1658189874 residues

Total number of hits satisfying chosen parameters: 66727376

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Pending\_Patents\_NA\_Main:\*

- 1: /cgn2\_6/ptodata/2/pna/PCTUS\_COMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pna/PCTUS\_COMB.seq:old:\*
- 3: /cgn2\_6/ptodata/2/pna/US06\_COMB.seq:\*
- 4: /cgn2\_6/ptodata/2/pna/US07\_COMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pna/US08\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/2/pna/US081\_COMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pna/US082\_COMB.seq:\*
- 8: /cgn2\_6/ptodata/2/pna/US083\_COMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pna/US084\_COMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pna/US085\_COMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pna/US086\_COMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pna/US087\_COMB.seq:\*
- 13: /cgn2\_6/ptodata/2/pna/US088\_COMB.seq:\*
- 14: /cgn2\_6/ptodata/2/pna/US089\_COMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pna/US090\_COMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pna/US091\_COMB.seq:\*
- 17: /cgn2\_6/ptodata/2/pna/US092A\_COMB.seq:\*
- 18: /cgn2\_6/ptodata/2/pna/US092B\_COMB.seq:\*
- 19: /cgn2\_6/ptodata/2/pna/US093A\_COMB.seq:\*
- 20: /cgn2\_6/ptodata/2/pna/US093B\_COMB.seq:\*
- 21: /cgn2\_6/ptodata/2/pna/US094\_COMB.seq:\*
- 22: /cgn2\_6/ptodata/2/pna/US095A\_COMB.seq:\*
- 23: /cgn2\_6/ptodata/2/pna/US095B\_COMB.seq:\*
- 24: /cgn2\_6/ptodata/2/pna/US095C\_COMB.seq:\*
- 25: /cgn2\_6/ptodata/2/pna/US095D\_COMB.seq:\*
- 26: /cgn2\_6/ptodata/2/pna/US096A\_COMB.seq:\*
- 27: /cgn2\_6/ptodata/2/pna/US096B\_COMB.seq:\*
- 28: /cgn2\_6/ptodata/2/pna/US096C\_COMB.seq:\*
- 29: /cgn2\_6/ptodata/2/pna/US096D\_COMB.seq:\*
- 30: /cgn2\_6/ptodata/2/pna/US096E\_COMB.seq:\*
- 31: /cgn2\_6/ptodata/2/pna/US097A\_COMB.seq:\*
- 32: /cgn2\_6/ptodata/2/pna/US097B\_COMB.seq:\*
- 33: /cgn2\_6/ptodata/2/pna/US097C\_COMB.seq:\*
- 34: /cgn2\_6/ptodata/2/pna/US098A\_COMB.seq:\*
- 35: /cgn2\_6/ptodata/2/pna/US098B\_COMB.seq:\*
- 36: /cgn2\_6/ptodata/2/pna/US098C\_COMB.seq:\*
- 37: /cgn2\_6/ptodata/2/pna/US098D\_COMB.seq:\*
- 38: /cgn2\_6/ptodata/2/pna/US099A\_COMB.seq:\*
- 39: /cgn2\_6/ptodata/2/pna/US099C\_COMB.seq:\*
- 40: /cgn2\_6/ptodata/2/pna/US099D\_COMB.seq:\*
- 41: /cgn2\_6/ptodata/2/pna/US099E\_COMB.seq:\*
- 42: /cgn2\_6/ptodata/2/pna/US099F\_COMB.seq:\*
- 43: /cgn2\_6/ptodata/2/pna/US099F\_COMB.seq:\*

44: /cgn2\_6/ptodata/2/pna/US100A\_COMB.seq:\*

45: /cgn2\_6/ptodata/2/pna/US100B\_COMB.seq:\*

46: /cgn2\_6/ptodata/2/pna/US101A\_COMB.seq:\*

47: /cgn2\_6/ptodata/2/pna/US101B\_COMB.seq:\*

48: /cgn2\_6/ptodata/2/pna/US102A\_COMB.seq:\*

49: /cgn2\_6/ptodata/2/pna/US102B\_COMB.seq:\*

50: /cgn2\_6/ptodata/2/pna/US103A\_COMB.seq:\*

51: /cgn2\_6/ptodata/2/pna/US103B\_COMB.seq:\*

52: /cgn2\_6/ptodata/2/pna/US104A\_COMB.seq:\*

53: /cgn2\_6/ptodata/2/pna/US104B\_COMB.seq:\*

54: /cgn2\_6/ptodata/2/pna/US6000\_COMB.seq:\*

55: /cgn2\_6/ptodata/2/pna/US6001\_COMB.seq:\*

56: /cgn2\_6/ptodata/2/pna/US6002\_COMB.seq:\*

57: /cgn2\_6/ptodata/2/pna/US6003\_COMB.seq:\*

58: /cgn2\_6/ptodata/2/pna/US6004\_COMB.seq:\*

59: /cgn2\_6/ptodata/2/pna/US6005\_COMB.seq:\*

60: /cgn2\_6/ptodata/2/pna/US6006\_COMB.seq:\*

61: /cgn2\_6/ptodata/2/pna/US6007\_COMB.seq:\*

62: /cgn2\_6/ptodata/2/pna/US6008\_COMB.seq:\*

63: /cgn2\_6/ptodata/2/pna/US6009\_COMB.seq:\*

64: /cgn2\_6/ptodata/2/pna/US6010\_COMB.seq:\*

65: /cgn2\_6/ptodata/2/pna/US6011\_COMB.seq:\*

66: /cgn2\_6/ptodata/2/pna/US6012\_COMB.seq:\*

67: /cgn2\_6/ptodata/2/pna/US6013\_COMB.seq:\*

68: /cgn2\_6/ptodata/2/pna/US6014\_COMB.seq:\*

69: /cgn2\_6/ptodata/2/pna/US6015\_COMB.seq:\*

70: /cgn2\_6/ptodata/2/pna/US6016\_COMB.seq:\*

71: /cgn2\_6/ptodata/2/pna/US6017\_COMB.seq:\*

72: /cgn2\_6/ptodata/2/pna/US6018\_COMB.seq:\*

73: /cgn2\_6/ptodata/2/pna/US6019\_COMB.seq:\*

74: /cgn2\_6/ptodata/2/pna/US6020\_COMB.seq:\*

75: /cgn2\_6/ptodata/2/pna/US6021\_COMB.seq:\*

76: /cgn2\_6/ptodata/2/pna/US6022\_COMB.seq:\*

77: /cgn2\_6/ptodata/2/pna/US6023A\_COMB.seq:\*

78: /cgn2\_6/ptodata/2/pna/US6023B\_COMB.seq:\*

79: /cgn2\_6/ptodata/2/pna/US6024\_COMB.seq:\*

80: /cgn2\_6/ptodata/2/pna/US6025\_COMB.seq:\*

81: /cgn2\_6/ptodata/2/pna/US6026\_COMB.seq:\*

82: /cgn2\_6/ptodata/2/pna/US6027\_COMB.seq:\*

83: /cgn2\_6/ptodata/2/pna/US6028\_COMB.seq:\*

84: /cgn2\_6/ptodata/2/pna/US6029\_COMB.seq:\*

85: /cgn2\_6/ptodata/2/pna/US6030\_COMB.seq:\*

86: /cgn2\_6/ptodata/2/pna/US6031\_COMB.seq:\*

87: /cgn2\_6/ptodata/2/pna/US6032\_COMB.seq:\*

88: /cgn2\_6/ptodata/2/pna/US6033\_COMB.seq:\*

89: /cgn2\_6/ptodata/2/pna/US6034\_COMB.seq:\*

90: /cgn2\_6/ptodata/2/pna/US6035\_COMB.seq:\*

91: /cgn2\_6/ptodata/2/pna/US6036\_COMB.seq:\*

92: /cgn2\_6/ptodata/2/pna/US6037\_COMB.seq:\*

93: /cgn2\_6/ptodata/2/pna/US6038\_COMB.seq:\*

94: /cgn2\_6/ptodata/2/pna/US6039\_COMB.seq:\*

95: /cgn2\_6/ptodata/2/pna/US6040\_COMB.seq:\*

96: /cgn2\_6/ptodata/2/pna/US6041\_COMB.seq:\*

97: /cgn2\_6/ptodata/2/pna/US6042\_COMB.seq:\*

98: /cgn2\_6/ptodata/2/pna/US6043\_COMB.seq:\*

99: /cgn2\_6/ptodata/2/pna/US6044\_COMB.seq:\*

100: /cgn2\_6/ptodata/2/pna/US6045\_COMB.seq:\*

101: /cgn2\_6/ptodata/2/pna/US6046\_COMB.seq:\*

102: /cgn2\_6/ptodata/2/pna/US6047\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	895	100.0	895	1	PCT-US99-10344-5
2	895	100.0	895	2	PCT-US99-10344-5
3	895	100.0	895	31	US-09-700-770-5
4	895	100.0	895	33	US-09-788-990-2

```

5 895 100.0 895 61 US-60-070-771-1141 Sequence 1141, Ap
6 895 100.0 902 14 US-09-099-824-8 Sequence 96, App1
7 895 100.0 934 75 US-60-209-106-96 Sequence 96, App1
8 895 100.0 1171 33 US-09-788-990-6 Sequence 6, App1
9 895 100.0 1171 48 US-10-237-435-4 Sequence 4, App1
10 895 100.0 1171 52 US-60-317-822-4 Sequence 4, App1
11 895 100.0 1172 58 US-10-412-548-1 Sequence 1, App1
12 895 100.0 1172 98 US-60-431-520-1 Sequence 7, App1
13 895 96.1 869 15 US-09-099-824-7 Sequence 913, App
14 895 96.0 859 31 US-09-705-256A-913 Sequence 913, App
15 895 96.0 859 70 US-60-164-285-913 Sequence 228, App
16 895 95.9 870 63 US-09-720-533-923 Sequence 913, App
17 858 95.9 1148 63 PCR-US01-0983-59 Sequence 59, App1
18 856.4 95.7 1148 2 PCR-US01-03800A-1033 Sequence 1033, Ap
19 856.4 95.7 1148 2 PCR-US01-03800A-1033 Sequence 1033, Ap
20 856.4 95.7 1148 21 US-09-496-914A-8595 Sequence 8595, Ap
21 856.4 95.7 1148 25 US-09-560-875A-8595 Sequence 8595, Ap
22 856.4 95.7 1148 49 US-10-276-774-1033 Sequence 1033, Ap
23 856 95.6 856 1 PCR-US03-17409-27 Sequence 27, App1
24 856 95.6 856 2 PCR-US03-17409-27 Sequence 27, App1
25 852 95.2 870 31 US-09-709-238-164 Sequence 164, App
26 852 95.2 870 40 US-09-941-992-164 Sequence 164, App
27 852 95.2 870 43 US-09-989-279-164 Sequence 164, App
28 852 95.2 870 43 US-09-989-293A-164 Sequence 164, App
29 852 95.2 870 43 US-09-989-328-164 Sequence 164, App
30 852 95.2 870 43 US-09-989-328-164 Sequence 164, App
31 852 95.2 870 43 US-09-989-722-164 Sequence 164, App
32 852 95.2 870 43 US-09-989-722-164 Sequence 164, App
33 852 95.2 870 43 US-09-989-723-164 Sequence 164, App
34 852 95.2 870 43 US-09-989-724-164 Sequence 164, App
35 852 95.2 870 43 US-09-989-725-164 Sequence 164, App
36 852 95.2 870 43 US-09-989-726-164 Sequence 164, App
37 852 95.2 870 43 US-09-989-727-164 Sequence 164, App
38 852 95.2 870 43 US-09-989-728-164 Sequence 164, App
39 852 95.2 870 43 US-09-989-729A-164 Sequence 164, App
40 852 95.2 870 43 US-09-989-730-164 Sequence 164, App
41 852 95.2 870 43 US-09-989-731-164 Sequence 164, App
42 852 95.2 870 43 US-09-989-732-164 Sequence 164, App
43 852 95.2 870 43 US-09-989-733-164 Sequence 164, App
44 852 95.2 870 43 US-09-989-734-164 Sequence 164, App
45 852 95.2 870 43 US-09-989-735-164 Sequence 164, App
46 852 95.2 870 43 US-09-989-862-164 Sequence 164, App

```

## ALIGNMENTS

```

RESULT 1
PCT-US99-10344-5
: Sequence 5, Application PC/TUS9910344
: GENERAL INFORMATION:
: APPLICANT: Yang, Fei
: APPLICANT: Macina, Roberto A.
: TITLE OF INVENTION: Sun, Yongming
: TITLE OF INVENTION: A Novel Method of Diagnosing, Monitoring and Staging
: FILE REFERENCE: DEX-0036
: CURRENT APPLICATION NUMBER: PCT/US99/10344
: EARLIER FILING DATE: 1999-05-12
: EARLIER APPLICATION NUMBER: 60/086,212
: EARLIER FILING DATE: 1998-05-21
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 5
: LENGTH: 895
: TYPE: DNA
: ORGANISM: Homo sapiens
PCT-US99-10344-5

```

```

Query Match 100.0%; Score 895; DB 1; Length 895;
Best Local Similarity 100.0%; Pred. No. 3.6e-256;
Matches 895; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CTAATCTGTACGTACAGACAGACGCTACCTCTGTTCTGCGCCCTCAATATGGA 60

```

```

Db
1 CTAATCTGTACGTACAGACAGACGCTACCTCTGTTCTGCGCCCTCAATATGGA 60
61 ACCTGAGCTGGAGTAAGACATAGACACAGAGTGTGTTCTGACACTAGTCATCC 120
61 ACCGTGGCTGGAGTAAAGCATAGACACAGAGTGTGTTCTGACACTAGTCATCC 120
121 CAGGATATGAGAGCTCCAGAGGAACTTCATATATCTTCAAGCACTACAGCT 180
121 CAGGATATGAGAGCTCCAGAGGAACTTCATATATCTTCAAGCACTACAGCT 180
181 GCACGACAGTGGAGTAAGATCTATCTCTCCCTCCCTGTTGTCCTACTATG 240
181 GCACGACAGTGGAGTAAGATCTATCTCTCCCTCCCTGTTGTCCTACTATG 240
241 CTGATGTTCATGTCTCTTACAGAGCTGATTCAGAGGTTGCGCACAGGACGA 300
241 CTGATGTTCATGTCTCTTACAGAGCTGATTCAGAGGTTGCGCACAGGACGA 300
301 GGCAGAGCTTGTAGAGATGCTCAGAGGAAAGGCGCAAGATGTGATCAAGATTGG 360
301 GGCAGAGCTTGTAGAGATGCTCAGAGGAAAGGCGCAAGATGTGATCAAGATTGG 360
361 TTCTGTAGAGCCCGAGAGAAATTCATGACAGTGTCTGAGGTCGCAAGAGAGTGC 420
361 TTCTGTAGAGCCCGAGAGAAATTCATGACAGTGTCTGAGGTCGCAAGAGAGTGC 420
421 CCCGTGATATCTTCAAGAGGCAATGTGAAGAAACAGACACCAAGGACCAAGAG 480
421 CCCGTGATATCTTCAAGAGGCAATGTGAAGAAACAGACACCAAGGACCAAGAG 480
481 CCAACAGACATTCAGAGGCTGCAAGATTTCTCAACATGTACGTAAGAACTTT 540
481 CCAACAGACATTCAGAGGCTGCAAGATTTCTCAACATGTACGTAAGAACTTT 540
541 GCTCTGCTTTGTAGAGCTCTAGAGGCGCCACTTTCATTAACATTCAGCAAGA 600
541 GCTCTGCTTTGTAGAGCTCTAGAGGCGCCACTTTCATTAACATTCAGCAAGA 600
601 AGACAGTACAGACCTTACAGACACTCTCTCCACACTCTCCACTGACCTACCC 660
601 AGACAGTACAGACCTTACAGACACTCTCTCCACACTCTCCACTGACCTACCC 660
661 ACCCTTAATTCATTCAGAGTGTCTCAAAAAGCATGTTTCAAGATCATTTGTTGG 720
661 ACCCTTAATTCATTCAGAGTGTCTCAAAAAGCATGTTTCAAGATCATTTGTTGG 720
721 CTTCTCTAGTGTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
721 CTTCTCTAGTGTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
781 TAGGCTTAATTCAGAGGATTCAGAGGATTCAGAGGATTCAGAGGATTCAGAGG 840
781 TAGGCTTAATTCAGAGGATTCAGAGGATTCAGAGGATTCAGAGGATTCAGAGG 840
841 CTTAATTCAGAGGATTCAGAGGATTCAGAGGATTCAGAGGATTCAGAGGATTC 895
841 CTTAATTCAGAGGATTCAGAGGATTCAGAGGATTCAGAGGATTCAGAGGATTC 895

```

```

RESULT 2
PCT-US99-10344-5
: Sequence 5, Application PC/TUS9910344
: GENERAL INFORMATION:
: APPLICANT: Yang, Fei
: APPLICANT: Macina, Roberto A.
: TITLE OF INVENTION: Sun, Yongming
: TITLE OF INVENTION: A Novel Method of Diagnosing, Monitoring and Staging
: FILE REFERENCE: DEX-0036
: CURRENT APPLICATION NUMBER: PCT/US99/10344
: EARLIER FILING DATE: 1999-05-12
: EARLIER APPLICATION NUMBER: 60/086,212

```



```
; EARLIER FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 895
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US99-10344-5

Query Match      100.0%; Score 895; DB 2; Length 895;
Best Local Similarity 100.0%; Pred. No. 3.6e-256;
Matches 895; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAATCTGTTACGTAACAGCAAGACAGCTCACCTCACTGTTCTCGCCCTCAATGGGA 60
    |||||||
    1 CTAATCTGTTACGTAACAGCAAGACAGCTCACCTCACTGTTCTCGCCCTCAATGGGA 60
Db 1 CTAATCTGTTACGTAACAGCAAGACAGCTCACCTCACTGTTCTCGCCCTCAATGGGA 60

QY 61 ACCTGGCTGGGACTAAAGCATAGACACAGGCTAGTACTGACTGATCC 120
    |||||||
    61 ACCTGGCTGGGACTAAAGCATAGACACAGGCTAGTACTGACTGATCC 120
Db 61 ACCTGGCTGGGACTAAAGCATAGACACAGGCTAGTACTGACTGATCC 120

QY 121 CAGGATCAGAGGCTCCAGAGGACCTTCCATTATTTCTCAAGCACTTACAGCT 180
    |||||||
    121 CAGGATCAGAGGCTCCAGAGGACCTTCCATTATTTCTCAAGCACTTACAGCT 180
Db 121 CAGGATCAGAGGCTCCAGAGGACCTTCCATTATTTCTCAAGCACTTACAGCT 180

QY 181 GCAACGACAGTTGGATGAAAGTTCTATCTCTCCCTCTGTTGCTGCCACTATG 240
    |||||||
    181 GCAACGACAGTTGGATGAAAGTTCTATCTCTCCCTCTGTTGCTGCCACTATG 240
Db 181 GCAACGACAGTTGGATGAAAGTTCTATCTCTCCCTCTGTTGCTGCCACTATG 240

QY 241 CTGATGTCATGCTCTAGACAGCTTAATCCAGGGGTCCGACAGGCTCACAGGACCGA 300
    |||||||
    241 CTGATGTCATGCTCTAGACAGCTTAATCCAGGGGTCCGACAGGCTCACAGGACCGA 300
Db 241 CTGATGTCATGCTCTAGACAGCTTAATCCAGGGGTCCGACAGGCTCACAGGACCGA 300

QY 301 GGCCAGGCTTCTAGAGATGGCTCCAGAGGCGGCAAGATGTGATGCAAGATTGG 360
    |||||||
    301 GGCCAGGCTTCTAGAGATGGCTCCAGAGGCGGCAAGATGTGATGCAAGATTGG 360
Db 301 GGCCAGGCTTCTAGAGATGGCTCCAGAGGCGGCAAGATGTGATGCAAGATTGG 360

QY 361 TTCCTGAGAGCCCGAGAGAAATTCATGACAGTGTCTGGGCTGCCAAGAACAGATGC 420
    |||||||
    361 TTCCTGAGAGCCCGAGAGAAATTCATGACAGTGTCTGGGCTGCCAAGAACAGATGC 420
Db 361 TTCCTGAGAGCCCGAGAGAAATTCATGACAGTGTCTGGGCTGCCAAGAACAGATGC 420

QY 421 CCTGTGATCATTTTCAAGGGCAATGTGAAGAAAACAAGACCAAGGACACAGAAAG 480
    |||||||
    421 CCTGTGATCATTTTCAAGGGCAATGTGAAGAAAACAAGACCAAGGACACAGAAAG 480
Db 421 CCTGTGATCATTTTCAAGGGCAATGTGAAGAAAACAAGACCAAGGACACAGAAAG 480

QY 481 CCAACAAGATTCACAGAGCTGGCCAGCAATTTCTCAACAATGTGCTAAGAGCTTT 540
    |||||||
    481 CCAACAAGATTCACAGAGCTGGCCAGCAATTTCTCAACAATGTGCTAAGAGCTTT 540
Db 481 CCAACAAGATTCACAGAGCTGGCCAGCAATTTCTCAACAATGTGCTAAGAGCTTT 540

QY 541 GCTCTGCTTTGTAGAGAGCTCTGAGCGCCCACTCTTCCAATTAACAATTTCAAGCA 600
    |||||||
    541 GCTCTGCTTTGTAGAGAGCTCTGAGCGCCCACTCTTCCAATTAACAATTTCAAGCA 600
Db 541 GCTCTGCTTTGTAGAGAGCTCTGAGCGCCCACTCTTCCAATTAACAATTTCAAGCA 600

QY 601 AGACAGTGAACACCTTACAGACACTCTTCTCCACCTCACTCCACACTGTACCC 660
    |||||||
    601 AGACAGTGAACACCTTACAGACACTCTTCTCCACCTCACTCCACACTGTACCC 660
Db 601 AGACAGTGAACACCTTACAGACACTCTTCTCCACCTCACTCCACACTGTACCC 660

QY 661 ACCCTTAATCATTTCCAGTGTCTCAAAAAGCATGTTTTCAGATATTTTGTGTTG 720
    |||||||
    661 ACCCTTAATCATTTCCAGTGTCTCAAAAAGCATGTTTTCAGATATTTTGTGTTG 720
Db 661 ACCCTTAATCATTTCCAGTGTCTCAAAAAGCATGTTTTCAGATATTTTGTGTTG 720

QY 721 CTCTCTAGTGTCTTCTCTCTGTCAGTCTTACCTGTGCTCCCTTACCAAGCT 780
    |||||||
    721 CTCTCTAGTGTCTTCTCTCTGTCAGTCTTACCTGTGCTCCCTTACCAAGCT 780
Db 721 CTCTCTAGTGTCTTCTCTCTGTCAGTCTTACCTGTGCTCCCTTACCAAGCT 780

QY 781 TAGGCTTAATTTACCTGAAGAAATTTCCAGAAAGTGTAGCTTCTAGAGTCAATTTAAC 840
    |||||||
    781 TAGGCTTAATTTACCTGAAGAAATTTCCAGAAAGTGTAGCTTCTAGAGTCAATTTAAC 840
Db 781 TAGGCTTAATTTACCTGAAGAAATTTCCAGAAAGTGTAGCTTCTAGAGTCAATTTAAC 840

QY 841 CTTAAATGCAATGAGAAAGTAGCAAAACAGAAAGTCAATTAATTTTAAATGTC 895
    |||||||
    841 CTTAAATGCAATGAGAAAGTAGCAAAACAGAAAGTCAATTAATTTTAAATGTC 895
Db 841 CTTAAATGCAATGAGAAAGTAGCAAAACAGAAAGTCAATTAATTTTAAATGTC 895
```

```
RESULT 3
US-09-700-770-5
; Sequence 5, Application US/09700770
; GENERAL INFORMATION:
; APPLICANT: Yang Fei
; APPLICANT: Macina, Roberto A.
; APPLICANT: Sun, Yongming
; TITLE OF INVENTION: A Novel Method of Diagnosing, Monitoring and Staging Lung Canc
; FILE REFERENCE: dex-0036
; CURRENT APPLICATION NUMBER: US/09/700,770
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 60/086,212
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 895
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-700-770-5

Query Match      100.0%; Score 895; DB 31; Length 895;
Best Local Similarity 100.0%; Pred. No. 3.6e-256;
Matches 895; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CTAATCTGTTACGTAACAGCAAGACAGGCTCACCTGTTCTCGCCCTCAATGGGA 60
    |||||||
    1 CTAATCTGTTACGTAACAGCAAGACAGGCTCACCTGTTCTCGCCCTCAATGGGA 60
Db 1 CTAATCTGTTACGTAACAGCAAGACAGGCTCACCTGTTCTCGCCCTCAATGGGA 60

QY 61 ACCTGGCTGGGACTAAAGCATAGACACAGGCTAGTACTGACTGATCC 120
    |||||||
    61 ACCTGGCTGGGACTAAAGCATAGACACAGGCTAGTACTGACTGATCC 120
Db 61 ACCTGGCTGGGACTAAAGCATAGACACAGGCTAGTACTGACTGATCC 120

QY 121 CAGGATCAGAGGCTCCAGAGGAACTTCCATTATTTCTCAAGCACTTACAGCT 180
    |||||||
    121 CAGGATCAGAGGCTCCAGAGGAACTTCCATTATTTCTCAAGCACTTACAGCT 180
Db 121 CAGGATCAGAGGCTCCAGAGGAACTTCCATTATTTCTCAAGCACTTACAGCT 180

QY 181 GCACCGACAGTTGGATGAAAGTTCTATCTCTCCCTCTGTTGCTGCCACTATG 240
    |||||||
    181 GCACCGACAGTTGGATGAAAGTTCTATCTCTCCCTCTGTTGCTGCCACTATG 240
Db 181 GCACCGACAGTTGGATGAAAGTTCTATCTCTCCCTCTGTTGCTGCCACTATG 240

QY 241 CTGATGTCATGCTCTAGACAGCTTAATCCAGGGGTCCGACAGGCTCACAGGACCGA 300
    |||||||
    241 CTGATGTCATGCTCTAGACAGCTTAATCCAGGGGTCCGACAGGCTCACAGGACCGA 300
Db 241 CTGATGTCATGCTCTAGACAGCTTAATCCAGGGGTCCGACAGGCTCACAGGACCGA 300

QY 301 GGCCAGGCTTCTAGAGATGGCTCCAGAGGCGGCAAGATGTGATGCAAGATTGG 360
    |||||||
    301 GGCCAGGCTTCTAGAGATGGCTCCAGAGGCGGCAAGATGTGATGCAAGATTGG 360
Db 301 GGCCAGGCTTCTAGAGATGGCTCCAGAGGCGGCAAGATGTGATGCAAGATTGG 360

QY 361 TTCCTGAGAGCCCGAGAGAAATTCATGACAGTGTCTGGGCTGCCAAGAACAGATGC 420
    |||||||
    361 TTCCTGAGAGCCCGAGAGAAATTCATGACAGTGTCTGGGCTGCCAAGAACAGATGC 420
Db 361 TTCCTGAGAGCCCGAGAGAAATTCATGACAGTGTCTGGGCTGCCAAGAACAGATGC 420

QY 421 CCTGTGATCATTTTCAAGGGCAATGTGAAGAAAACAAGACCAAGGACACAGAAAG 480
    |||||||
    421 CCTGTGATCATTTTCAAGGGCAATGTGAAGAAAACAAGACCAAGGACACAGAAAG 480
Db 421 CCTGTGATCATTTTCAAGGGCAATGTGAAGAAAACAAGACCAAGGACACAGAAAG 480

QY 481 CCAACAAGATTCACAGAGCTGGCCAGCAATTTCTCAACAATGTGCTAAGAGCTTT 540
    |||||||
    481 CCAACAAGATTCACAGAGCTGGCCAGCAATTTCTCAACAATGTGCTAAGAGCTTT 540
Db 481 CCAACAAGATTCACAGAGCTGGCCAGCAATTTCTCAACAATGTGCTAAGAGCTTT 540

QY 541 GCTCTGCTTTGTAGAGAGCTCTGAGCGCCCACTCTTCCAATTAACAATTTCAAGCA 600
    |||||||
    541 GCTCTGCTTTGTAGAGAGCTCTGAGCGCCCACTCTTCCAATTAACAATTTCAAGCA 600
Db 541 GCTCTGCTTTGTAGAGAGCTCTGAGCGCCCACTCTTCCAATTAACAATTTCAAGCA 600

QY 541 GCTCTGCTTTGTAGAGAGCTCTGAGCGCCCACTCTTCCAATTAACAATTTCAAGCA 600
    |||||||
    541 GCTCTGCTTTGTAGAGAGCTCTGAGCGCCCACTCTTCCAATTAACAATTTCAAGCA 600
Db 541 GCTCTGCTTTGTAGAGAGCTCTGAGCGCCCACTCTTCCAATTAACAATTTCAAGCA 600

QY 601 AGACAGTGAACACCTTACAGACACTCTTCTCCACCTCACTCCACACTGTACCC 660
    |||||||
    601 AGACAGTGAACACCTTACAGACACTCTTCTCCACCTCACTCCACACTGTACCC 660
Db 601 AGACAGTGAACACCTTACAGACACTCTTCTCCACCTCACTCCACACTGTACCC 660

QY 661 ACCCTTAATCATTTCCAGTGTCTCAAAAAGCATGTTTTCAGATCAATTTTGTGTTG 720
    |||||||
    661 ACCCTTAATCATTTCCAGTGTCTCAAAAAGCATGTTTTCAGATCAATTTTGTGTTG 720
Db 661 ACCCTTAATCATTTCCAGTGTCTCAAAAAGCATGTTTTCAGATCAATTTTGTGTTG 720
```



CLONE: 3116250  
US-60-070-771-1141

Query Match 100.0%; Score 895; DB 61; Length 895;  
Best Local Similarity 100.0%; Pred. No. 3,6e-256;  
Matches 895; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 CTAATCTGTTACGTAACGCAAGACAGCGCTACCTACCTGTTCTGCGCCCTCAAAATGGGA 60
DB 1 CTAATCTGTTACGTAACGCAAGACAGCGCTACCTACCTGTTCTGCGCCCTCAAAATGGGA 60
QY 61 ACCGTGGCTGGGATTAAGCATACACACGCGGTGAGTATCCCTGACCTGAGTATCCC 120
DB 61 ACCGTGGCTGGGATTAAGCATACACACGCGGTGAGTATCCCTGACCTGAGTATCCC 120
QY 121 CAGGATCAGAGAGCTCCAGCAGGAGACCTTCATTATATCTTCAGCAACTTACAGCT 180
DB 121 CAGGATCAGAGAGCTCCAGCAGGAGACCTTCATTATATCTTCAGCAACTTACAGCT 180
QY 181 GCACGACAGTTCGATGAAGTCTAATCTCTCCCTCTCTGTTGCTGCCACTAATG 240
DB 181 GCACGACAGTTCGATGAAGTCTAATCTCTCTCCCTCTCTGTTGCTGCCACTAATG 240
QY 241 CTGATGTCCATGATGTTCTAGCAGCTGAATCCAGGGGTGCCAGAGGCCACAGGACGA 300
DB 241 CTGATGTCCATGATGTTCTAGCAGCTGAATCCAGGGGTGCCAGAGGCCACAGGACGA 300
QY 301 GGCCAGGCTTCTAGAGATGCGCTCCAGAGAGGCGCAAGATGTGATGCAAAAGTTGG 360
DB 301 GGCCAGGCTTCTAGAGATGCGCTCCAGAGAGGCGCAAGATGTGATGCAAAAGTTGG 360
QY 361 TTCTGAGAGCCCCGAGAGAAATTCATGACAGTGTCTGGGCTGCCAAAGAGCAGTGC 420
DB 361 TTCTGAGAGCCCCGAGAGAAATTCATGACAGTGTCTGGGCTGCCAAAGAGCAGTGC 420
QY 421 CCCGTGATCATTTTAAAGGCAATGTGAAGAAACAAAGACCAAGGACCAAGAAAG 480
DB 421 CCCGTGATCATTTTAAAGGCAATGTGAAGAAACAAAGACCAAGGACCAAGAAAG 480
QY 481 CCNAACAAGCATTCAGAGACCTGCGAGCAATTTCTCAACAATGTGAGCTAAGAGCTTT 540
DB 481 CCNAACAAGCATTCAGAGACCTGCGAGCAATTTCTCAACAATGTGAGCTAAGAGCTTT 540
QY 541 GCTGTCCTTTGTAGAGCTGTGAGCGCCCACTCTTCCAAATTAACATTTCTAGCCACGA 600
DB 541 GCTGTCCTTTGTAGAGCTGTGAGCGCCCACTCTTCCAAATTAACATTTCTAGCCACGA 600
QY 601 AGACAGTGAACACCTACACAGACACTCTTCTTCCACCTCAGCTCTCCACTGTACCC 660
DB 601 AGACAGTGAACACCTACACAGACACTCTTCTTCCACCTCAGCTCTCCACTGTACCC 660
QY 661 ACCCTTAATCATTCACAGTGTCTCAAAAAGCATGTTTTCAGATCATTTTGTGTTG 720
DB 661 ACCCTTAATCATTCACAGTGTCTCAAAAAGCATGTTTTCAGATCATTTTGTGTTG 720
QY 721 CTCTCTAGTGTCTTCTTCTGTCAGTCTTAAGCTGTGCTCCCTTACCCAGGCT 780
DB 721 CTCTCTAGTGTCTTCTTCTGTCAGTCTTAAGCTGTGCTCCCTTACCCAGGCT 780
QY 781 TAGGTTAATTAACGTAAGAAAGTTCAGAGAAAGTGTAGTCTTACTAGTATGATTAAC 840
DB 781 TAGGTTAATTAACGTAAGAAAGTTCAGAGAAAGTGTAGTCTTACTAGTATGATTAAC 840
QY 841 CTTAATGCAATCAGAGAAAGTGAACAAGAGTCAATTAATATTTTAAATGTC 895
DB 841 CTTAATGCAATCAGAGAAAGTGAACAAGAGTCAATTAATATTTTAAATGTC 895

```

RESULT 6  
US-09-099-824-8  
; Sequence 8, Application us/0909824  
; GENERAL INFORMATION:  
; APPLICANT: BILLING-MEDEL, PATRICIA

```

? APPLICANT: COHEN, MAURICE
? APPLICANT: COLPIETS, TRACEY L.
? APPLICANT: FRIEDMAN, PAULA N.
? APPLICANT: GRANADOS, EDWARD N.
? APPLICANT: KLAAS, MICHAEL R.
? APPLICANT: RUSSELL, JOHN C.
? APPLICANT: STROUPE, STEPHEN D.
? TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
? NUMBER OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
? CORRESPONDENCE ADDRESS:
? ADDRESS: Abbott Laboratories
? STREET: 100 Abbott Park Road
? CITY: Abbott Park
? STATE: IL
? COUNTRY: USA
? ZIP: 60064-3500
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FastSeq for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/099,824
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 60/050,348
? FILING DATE: 20-JUN-1997
? ATTORNEY/AGENT INFORMATION:
? NAME: Becker, Cheryl L.
? REGISTRATION NUMBER: 35,441
? REFERENCE/DOCKET NUMBER: 6123.US.01
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 847/935-1729
? TELEFAX: 847/938-2623
? TELEX:
? INFORMATION FOR SEQ ID NO: 8:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 902 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? US-09-099-824-8

```

Query Match 100.0%; Score 895; DB 15; Length 902;  
Best Local Similarity 100.0%; Pred. No. 3.7e-256;  
Matches 895; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 CTAATCTGTTACGTAACGCAAGACAGCGCTACCTACCTGTTCTGCGCCCTCAAAATGGGA 60
DB 1 CTAATCTGTTACGTAACGCAAGACAGCGCTACCTACCTGTTCTGCGCCCTCAAAATGGGA 60
QY 61 ACCGTGGCTGGGATTAAGCATACACACGCGGTGAGTATCCCTGACCTGAGTATCCC 120
DB 61 ACCGTGGCTGGGATTAAGCATACACACGCGGTGAGTATCCCTGACCTGAGTATCCC 120
QY 121 CAGGATCAGAGAGCTCCAGCAGGAGACCTTCATTATATCTTCAGCAACTTACAGCT 180
DB 121 CAGGATCAGAGAGCTCCAGCAGGAGACCTTCATTATATCTTCAGCAACTTACAGCT 180
QY 181 GCACGACAGTTCGATGAAGTCTAATCTCTCCCTCTCTGTTGCTGCCACTAATG 240
DB 181 GCACGACAGTTCGATGAAGTCTAATCTCTCCCTCTCTGTTGCTGCCACTAATG 240
QY 241 CTGATGTCCATGATGTTCTAGCAGCTGAATCCAGGGGTGCCAGAGGCCACAGGACGA 300
DB 241 CTGATGTCCATGATGTTCTAGCAGCTGAATCCAGGGGTGCCAGAGGCCACAGGACGA 300
QY 301 GGCCAGGCTTCTAGAGATGCGCTCCAGAGAGGCGCAAGATGTGATGCAAAAGTTGG 360
DB 301 GGCCAGGCTTCTAGAGATGCGCTCCAGAGAGGCGCAAGATGTGATGCAAAAGTTGG 360

```

OY	361	TTCCTAGAGCCCCGAGGAAGAAAATTCATGCACGTGTCTGGGCTGCCAAGAAGCAGTGC	420
Dd	361	TTCTCGAGAGCCCCGAGAAAGAAATTCATGCACGTGTCTGGGCTGCCAAGAAGCAGTGC	420
OY	421	CCCTGTGATCAATTCAGGSGCAATGTGAAGAAAAACAAGACACCMAAGGCAACACAAAG	480
Dd	421	CCCTGTGATCAATTCAGGSGCAATGTGAAGAAAAACAAGACACCMAAGGCAACACAAAG	480
OY	481	CCAAACAAGCATTTCCAGAGCTGCGCCGCAATTCTCAAACAAATGTACGTAAAGACTTT	540
Dd	481	CCAAACAAGCATTTCCAGAGCTGCGCCGCAATTCTCAAACAAATGTACGTAAAGACTTT	540
OY	541	GCTTGCCCTTTTAGSAGCTGTGAGGCGCCACTCTTCCAATTAACATTCTCAGCCANA	600
Dd	541	GCTTGCCCTTTTAGSAGCTGTGAGGCGCCACTCTTCCAATTAACATTCTCAGCCANA	600
OY	601	AGACAGTGCACACACTTACCAGACACTCTTCTTCOCACACCTCACCTGCCACTGTACC	660
Dd	601	AGACAGTGCACACACTTACCAGACACTCTTCTTCOCACACCTCACCTGCCACTGTACC	660
OY	661	ACCCCTAAATCAATTCACAGTGTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTGTTG	720
Dd	661	ACCCCTAAATCAATTCACAGTGTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTGTTG	720
OY	721	CTCTCTAGAGTCTCTCTCTCTCTCCTCAGTCTTACCTGTGGCCTTCOCCTTACCCAGGCT	780
Dd	721	CTCTCTAGAGTCTCTCTCTCTCTCCTCAGTCTTACCTGTGGCCTTCOCCTTACCCAGGCT	780
OY	781	TAGGCTTAATTAACCTGAAGAAGATTCACGAAACTGTAGTCTCTACTAGTAGTCATTTAAC	840
Dd	781	TAGGCTTAATTAACCTGAAGAAGATTCACGAAACTGTAGTCTCTACTAGTAGTCATTTAAC	840
OY	841	CTTAATTCACATTCAGGAAGTAGCAACAAGAAATTAATTAATTTTAAATGTG	895
Dd	841	CTTAATTCACATTCAGGAAGTAGCAACAAGAAATTAATTAATTTTAAATGTG	895

```

RESULT 7
US-60-209-106-96
: Sequence 96, Application US/60209106
: GENERAL INFORMATION:
: APPLICANT: Kaser, Matthew R.
: APPLICANT: Bandman, Olga
: TITLE OF INVENTION: GENES EXPRESSED IN THE ALPHA-TREATED VASCULAR ENDOTHELIUM AND SMCs
: TITLE OF INVENTION: MUSCLE CELLS

```

```

:
:
: CURRENT APPLICATION NUMBER: US/60/209,106
:
: CURRENT FILING DATE: 2000-06-02
:
: NUMBER OF SEQ ID NOS: 499
:
: SOFTWARE: PERL Program
:
: SEQ ID NO 96
:
: LENGTH: 934
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
: FEATURE:
:
: NAME/KEY: misc_feature
:
: OTHER INFORMATION: Incyte ID No: 221807.2
:
: US-60-209-106-96

```

Query Match	100.0%;	Score 895;	DB 74;	Length 934;
Best Local Similarity	100.0%;	Pred. No. 3.7e-256;		
Matches 895; Conservative	0;	Mismatches	0;	Gaps 0

QY 1 CTAATCTGTAGCTAACAGCAAGAGGCTACCCACACTCTTTCGCGCCCTCAATGGGA 60  
 Db 22 CTAATCTGTAGCTAACAGCAAGAGGCTACCCACTCTTTCGCGCCCTCAATGGGA 81  
 QY 61 ACGTCGCGCTGGGACTAAAGCATAGACCACAGGCTGATATCTCTGACTAGATACCC 120  
 Db 82 ACGTCGCGCTGGGACTAAAGCATATAGACCACAGGCTGATATCTCTGACTAGATACCC 141  
 QY 121 CAGGATCAGGAGCGCTCAGCAGGGAACCTTCATATATCTTCAAGCAACTTACGCT 180

D	b		142	CAGGAGTACGAGAGCCCTCAGACAGSAACTTCATTAATTCTTCAAGCAACTTACAGCT	201
O	y		181	GAAOCAGCAATTTGCGATGAAGAATTCTAATCTCTCCCTCTCTGTGGTGCCACTAATG	240
D	b		202	GCACCAGCAATTCGATGAAGAAAGTTCTAATCTCTCCCTCTCTGTGGTGCCACTAATG	261
O	y		241	CTAGTGTCAATGGTCTCTTAGCACCTGAAATCCAGGGGTGCGCAGAGGCCACAGSGCCA	300
D	b		262	CTGATGTCCATGGTGTCTTAGCACCTGAAATCCAGGGGTGCGCAGAGGCCACAGSGCCA	321
O	y		301	GGCCAGGCTCTTAGAGATGGCTCCAGGAAGCGGCCAAGATGTGATGCAAAAGATTGG	360
D	b		322	GGCCAGGCTCTTAGAGATGGCTCCAGGAAGCGGCCAAGATGTGATGCAAAAGATTGG	381
O	y		361	TTCCTAGAGCCCCGAGAAAGAAAATTCATGACAGTCTGAGGCTGCGCAAGAAAGCATGC	420
D	b		382	TTCCTAGAGCCCCGAGAAAGAAAATTCATGACAGTCTGAGGCTGCGCAAGAAAGCATGC	441
O	y		421	CCCTGTGATCATTTCAAAGGCAATGTGAAGAAAAACAAGACCCAAAGGACCAACAAGAAAG	480
D	b		442	CCCTGTGATCATTTCAAAGGCAATGTGAAGAAAAACAAGACCCAAAGGACCAACAAGAAAG	501
O	y		481	CCAAACAACATTTCCAGACCTGCGCGCAATTTCTCAACATATGTCAGTAAAGACTTT	540
D	b		502	CCAAACAACATTTCCAGACCTGCGCGCAATTTCTCAACATATGTCAGTAAAGACTTT	561
O	y		541	GCTCTGCCCTTTGAGAGCTGTAGCGCCACTCTTCCAAATAAACATTTCCAGCCACA	600
D	b		562	GCTCTGCCCTTTGAGAGCTGTAGCGCCACTCTTCCAAATAAACATTTCCAGCCACA	621
O	y		601	AGACAGTGAACACACTTACACACACTCTTCTCCACACCTCATCTCCGCTACCC	660
D	b		622	AGACAGTGAACACACTTACACACACTCTTCTCTCCACCTCATCTCCGCTACCC	681
O	y		661	ACCCCTAAATCAATTCAGTGCCTCTCAAAAAGCATTTTTCAAGATCAATTTGTTGTGG	720
D	b		682	ACCCCTAAATCAATTCAGTGCCTCTCAAAAAGCATTTTTCAAGATCAATTTGTTGTGG	741
O	y		721	CTCTCTAGTGTCTTCTCTCTCTCTCAGTCTTACCTGTGGCCCTCCCTTACCCAGGCT	780
D	b		742	CTCTCTAGTGTCTTCTCTCTCTCTCAGTCTTACCTGTGGCCCTCCCTTACCCAGGCT	801
O	y		781	TAGGCTTAATTAACCTGAAGATTCAGAAACTGTAGCTTCTAGTCTAGTGTCAATTAAAC	840
D	b		802	TAGGCTTAATTAACCTGAAGATTCAGAAACTGTAGCTTCTAGTCTAGTGTCAATTAAAC	861
O	y		841	CTTAATATCAATCAGAAAGTAGCAAAAGAAAGCAATAAATATTTTAAATATGTC	895
D	b		862	CTTAATATCAATCAGAAAGTAGCAAAAGAAAGCAATAAATATTTTAAATATGTC	916

```

RESULT 8
US-09-788-990-6
: Sequence 6, Application US/09788990
: GENERAL INFORMATION:
: APPLICANT: Chen, Sel Yu
: APPLICANT: Sun, Yongming
: APPLICANT: Macina, Roberto
: TITLE OF INVENTION: Method of diagnosing,
: TITLE OF INVENTION: Treating Lung Cancer,
: FILE REFERENCE: DEX-0140
: CURRENT APPLICATION NUMBER: US/09/788,990
: CURRENT FILING DATE: 2001-02-20
: PRIOR APPLICATION NUMBER: 60/183,188
: PRIOR FILING DATE: 2000-02-17
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 6
: LENGTH: 1171
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-788-990-6

```



```

Db      802 TAGGCTTAATTAACCTTAAGATTCAGGAAAGTGTAGCTTCTAGCTAGTGCATTTAAAC 861
QY      841 CTTAATGCAATCAGAAAGTAGCAAGAGTCAATAAATTTTAAATGTC 895
Db      862 CTTAATGCAATCAGAAAGTAGCAAGAGTCAATAAATTTTAAATGTC 916

```

## RESULT 10

```

US-60-317-822-4
; Sequence 4, Application US/60317822
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: LONG SURFACTANT MOLECULES
; FILE REFERENCE: PB-0019 P
; CURRENT APPLICATION NUMBER: US/60/317,822
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 1171
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Inocyte ID No: 221807.2
US-60-317-822-4

```

```

Query Match      100.0%; Score 895; DB 86; Length 1171;
Best Local Similarity 100.0%; Pred. No. 4, 2e-256;
Matches 895; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 CTAATCTTTACGTAACGACAGCGTCACTACCTCTTCCGCTCAATGGA 60
Db      22 CTAATCTTTACGTAACGACAGCGTCACTACCTCTTCCGCTCAATGGA 81
QY      61 ACCTGCGCTGGAGTAAGCATAGACACAGGCTGATCTCTGACCTGATCATCC 120
Db      82 ACCTGCGCTGGAGTAAGCATAGACACAGGCTGATCTCTGACCTGATCATCC 141
QY      121 CAGGATCAGAGCCCTCCAGCAGGAACTTCATTAATTTCAAGCAACTTACAGT 180
Db      142 CAGGATCAGAGCCCTCCAGCAGGAACTTCATTAATTTCAAGCAACTTACAGT 201
QY      181 GCACGACAGTTGGATGAAAGTCTAATCTCTCCCTCCTCGTGTGCTGCACTATG 240
Db      202 GCACGACAGTTGGATGAAAGTCTAATCTCTCCCTCCTCGTGTGCTGCACTATG 261
QY      241 CTGATGTCATGCTCTCTAGCAGCCTGAATCCAGGGGTGCGCCAGAGGCCACAGGACGA 300
Db      262 CTGATGTCATGCTCTCTAGCAGCCTGAATCCAGGGGTGCGCCAGAGGCCACAGGACGA 321
QY      301 GGGCAGGCTCTAGGAGATGGCTCCAGGAAAGGCGCCAGAGATGTGAGTCAAAAGATTGG 360
Db      322 GGGCAGGCTCTAGGAGATGGCTCCAGGAAAGGCGCCAGAGATGTGAGTCAAAAGATTGG 381
QY      361 TTCTGAGAGCCCGGAGAAATTCATGACAGTGTGGGTGCGCAAGAAAGAGCATGTC 420
Db      382 TTCTGAGAGCCCGGAGAAATTCATGACAGTGTGGGTGCGCAAGAAAGAGCATGTC 441
QY      421 CCTGTGATCATTTTCAAGGGCAATGTGAAGAAAAACAAGACCAAGAGGACCAACAAG 480
Db      442 CCTGTGATCATTTTCAAGGGCAATGTGAAGAAAAACAAGACCAAGAGGACCAACAAG 501
QY      481 CCAAAAGCAATTCAGAGCTGCGCCAGCAATTTCTAAACATATGCTAGCTAAGAGCTTT 540
Db      502 CCAAAAGCAATTCAGAGCTGCGCCAGCAATTTCTAAACATATGCTAGCTAAGAGCTTT 561
QY      541 GCTCTGCTTTTGTAGAGCTGTGAGCGCCACTCTTCAATTAACATTTCTAGGCCAAGA 600
Db      562 GCTCTGCTTTTGTAGAGCTGTGAGCGCCACTCTTCAATTAACATTTCTAGGCCAAGA 621

```

```

QY      601 AGACAGTACACACACCTTACAGACACTTCTCTCCACCTCACTCTCCACTGTACCC 660
Db      622 AGACAGTACACACACCTTACAGACACTTCTCTCCACCTCACTCTCCACTGTACCC 681
QY      661 ACCCTTAATCATTCAGTGTGCTCAAAAAGCATGTTTTCATAATCATTTTGTGTG 720
Db      682 ACCCTTAATCATTCAGTGTGCTCAAAAAGCATGTTTTCATAATCATTTTGTGTG 741
QY      721 CTCTCTAGTGTCTCTCTCTCTGTCAGTCTTACCTGAGCCCTCCCTTACCCAGCT 780
Db      742 CTCTCTAGTGTCTCTCTCTCTGTCAGTCTTACCTGAGCCCTCCCTTACCCAGCT 801
QY      781 TAGGCTTAATTAACCTGAAAGATTTCCAGAAACTGATCTTCTGCTAGTGTCAATTAAC 840
Db      802 TAGGCTTAATTAACCTGAAAGATTTCCAGAAACTGATCTTCTGCTAGTGTCAATTAAC 861
QY      841 CTTAATGCAATCAGAAAGTAGCAAGAGTCAATAAATTTTAAATGTC 895
Db      862 CTTAATGCAATCAGAAAGTAGCAAGAGTCAATAAATTTTAAATGTC 916

```

## RESULT 11

```

US-10-412-548-1
; Sequence 1, Application US/10412548
; GENERAL INFORMATION:
; APPLICANT: Pharmacia
; TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED GENES INVOLVED IN ANGIOGENESIS, THE
; FILE REFERENCE: 01055/2
; CURRENT APPLICATION NUMBER: US/10/412,548
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/372,173
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1
; LENGTH: 1172
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-412-548-1

```

```

Query Match      100.0%; Score 895; DB 52; Length 1172;
Best Local Similarity 100.0%; Pred. No. 4, 2e-256;
Matches 895; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 CTAATCTTTACGTAACGACAGCGTCACTACCTCTTCCGCTCAATGGA 60
Db      22 CTAATCTTTACGTAACGACAGCGTCACTACCTCTTCCGCTCAATGGA 81
QY      61 ACCTGCGCTGGAGTAAGCATAGACACAGGCTGATTAATCTGACCTGATCATCC 120
Db      82 ACCTGCGCTGGAGTAAGCATAGACACAGGCTGATTAATCTGACCTGATCATCC 141
QY      121 CAGGGATCAGAGCCCTCCAGCAGGGAACCTTCATTAATTTTCAAGCAACTTACAGT 180
Db      142 CAGGGATCAGAGCCCTCCAGCAGGGAACCTTCATTAATTTTCAAGCAACTTACAGT 201
QY      181 GCACGACAGTTGGATGAAAGTCTAATCTCTCCCTCCTCGTGTGCTGCACTATG 240
Db      202 GCACGACAGTTGGATGAAAGTCTAATCTCTCCCTCCTCGTGTGCTGCACTATG 261
QY      241 CTGATGTCATGCTCTCTAGCAGCCTGAATCCAGGGGTGCGCAAGAGGCCACAGGACCGA 300
Db      262 CTGATGTCATGCTCTCTAGCAGCCTGAATCCAGGGGTGCGCAAGAGGCCACAGGACCGA 321
QY      301 GGCAGAGCTTCTAGAGATGGCTCCAGGAAGGCGCCCAAGATGTGAGTGCATAAGATTGG 360
Db      322 GGCAGAGCTTCTAGAGATGGCTCCAGGAAGGCGCCCAAGATGTGAGTGCATAAGATTGG 381
QY      361 TTCTGAGAGCCCGGAGAAATTCATGACAGTGTGGGCTGCGCAAGAGCAGAGTGC 420
Db      382 TTCTGAGAGCCCGGAGAAATTCATGACAGTGTGGGCTGCGCAAGAGCAGAGTGC 441

```

```

QY 421 CCTGTGATCATTTTCAGGGCAATGTGAAGAAAACAAGACCCAAAGGCCACAGCAAG 480
|
|
|
Db 442 CCTGTGATCATTTTCAGGGCAATGTGAAGAAAACAAGACCCAAAGGCCACAGCAAG 501
|
|
|
QY 481 CCAAAACAGCATTTCCAGAGCCCTGCGCAATTTCTGAAACAAATGTAGGCTAAGAACCTTT 540
|
|
|
Db 502 CCAAAACAGCATTTCCAGAGCCCTGCGCAATTTCTGAAACAAATGTAGGCTAAGAACCTTT 561
|
|
|
QY 541 GCTGTGCTTTGTAGAGCTGTGAGGCCCACTCTTCAATTAACATTTCTGAGCCAGA 600
|
|
|
Db 562 GCTGTGCTTTGTAGAGCTGTGAGGCCCACTCTTCAATTAACATTTCTGAGCCAGA 621
|
|
|
QY 601 AGACAGTGAACACCTTACAGACACTCTTCTTCCACCTGACTCTCCACTGTACCC 660
|
|
|
Db 622 AGACAGTGAACACCTTACAGACACTCTTCTTCCACCTGACTCTCCACTGTACCC 681
|
|
|
QY 661 ACCCCAAATTCATTCAGTGTCTCTCAAAAAGCATGTTTTCAAGATCATTTTGTG 720
|
|
|
Db 682 ACCCCAAATTCATTCAGTGTCTCTCAAAAAGCATGTTTTCAAGATCATTTTGTG 741
|
|
|
QY 721 CTCTCTAGTGTCTTCTCTCTGTCAGTCTTAGCCCTGCCCCCTTACCCAGGCT 780
|
|
|
Db 742 CTCTCTAGTGTCTTCTCTCTGTCAGTCTTAGCCCTGCCCCCTTACCCAGGCT 801
|
|
|
QY 781 TAGGCTTAATTTACCTAAAGATTCAGAAACCTGTAGCTTCCAGTGTATTTAAC 840
|
|
|
Db 802 TAGGCTTAATTTACCTAAAGATTCAGAAACCTGTAGCTTCCAGTGTATTTAAC 861
|
|
|
QY 841 CTTAAATGCAATCAGAAAGTAGCAACAGAACTCAATAATTTTAAATGTC 895
|
|
|
Db 862 CTTAAATGCAATCAGAAAGTAGCAACAGAACTCAATAATTTTAAATGTC 916
|
|
|

```

## RESULT 12

```

; Sequence 1, Application US/60431520
; US-60-431-520-1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia
; TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED GENES INVOLVED IN ANGIOGENESIS, THE PRO
; FILE OF INVENTION: ENCODED THERBY, AND METHODS OF USING THE SAME
; FILE REFERENCE: C-01055
; CURRENT APPLICATION NUMBER: US/60/431, 520
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1172
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-60-431-520-1

```

```

Query Match 100.0%; Score 895; DB 98; Length 1172;
Best Local Similarity 100.0%; Pred. No. 4,2e-256;
Matches 895; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 CTAATGTGTACCTAAAGACAGACAGCTCACCTACCTGTTCTGCGCCCTCAATAGGA 60
|
|
|
Db 22 CTAATGTGTACCTAAAGACAGACAGCTCACCTACCTGTTCTGCGCCCTCAATAGGA 81
|
|
|
QY 61 AGCCTGCGCTGGAGCTAAAGCATAGACACAGGCTGAGATCTGATCTGATCATCC 120
|
|
|
Db 82 AGCCTGCGCTGGAGCTAAAGCATAGACACAGGCTGAGATCTGATCTGATCATCC 141
|
|
|
QY 121 CAGGATTCAGAGACCTCCAGCAGAGAACTTCATATATTTCTCAAGCAACTTAAGCT 180
|
|
|
Db 142 CAGGATTCAGAGACCTCCAGCAGAGAACTTCATATATTTCTCAAGCAACTTAAGCT 201
|
|
|
QY 181 GCACGACAGTGGCGATGAAGAGTTCTAATCTCTCCCTCCCTGTTGCTGCACATAG 240
|
|
|
Db 202 GCACGACAGTGGCGATGAAGAGTTCTAATCTCTCCCTCCCTGTTGCTGCACATAG 261
|
|
|
QY 241 CTGATGTCCATGCTCTCTAGACACCTGAATCCAGGGGTGCGAGAGCCACAGGACGA 300
|
|
|

```

```

Db 262 CTGATGTCCATGCTCTCTAGACACCTGAATCCAGGGGTGCGAGAGCCACAGGACCA 321
|
|
|
QY 301 GGGCAGGCTTCTAGAGATGGCTCCAGAAAGGGGCGCAAGAAATGTAGTGAAGATGG 360
|
|
|
Db 322 GGGCAGGCTTCTAGAGATGGCTCCAGAAAGGGGCGCAAGAAATGTAGTGAAGATGG 381
|
|
|
QY 361 TTCTCTAGAGCCCGGAGAAAGAAATTCATGACAGTGTCTGGGCTGCCAAAGAAAGAGTGC 420
|
|
|
Db 382 TTCTCTAGAGCCCGGAGAAAGAAATTCATGACAGTGTCTGGGCTGCCAAAGAAAGAGTGC 441
|
|
|
QY 421 CCTGTGATCATTTTCAGGGCAATGTGAAGAAAACAAGACCCAAAGGCCACAGCAAG 480
|
|
|
Db 442 CCTGTGATCATTTTCAGGGCAATGTGAAGAAAACAAGACCCAAAGGCCACAGCAAG 501
|
|
|
QY 481 CCAAAACAGCATTTCCAGAGCCCTGCGCAATTTCTGAAACAAATGTAGGCTAAGAACCTTT 540
|
|
|
Db 502 CCAAAACAGCATTTCCAGAGCCCTGCGCAATTTCTGAAACAAATGTAGGCTAAGAACCTTT 561
|
|
|
QY 541 GCTGTGCTTTGTAGAGCTGTGAGGCCCACTCTTCAATTAACATTTCTGAGCCAGA 600
|
|
|
Db 562 GCTGTGCTTTGTAGAGCTGTGAGGCCCACTCTTCAATTAACATTTCTGAGCCAGA 621
|
|
|
QY 601 AGACAGTGAACACCTTACAGACACTCTTCTTCCACCTGACTCTCCACTGTACCC 660
|
|
|
Db 622 AGACAGTGAACACCTTACAGACACTCTTCTTCCACCTGACTCTCCACTGTACCC 681
|
|
|
QY 661 ACCCCAAATTCATTCAGTGTCTCTCAAAAAGCATGTTTTCAAGATCATTTTGTG 720
|
|
|
Db 682 ACCCCAAATTCATTCAGTGTCTCTCAAAAAGCATGTTTTCAAGATCATTTTGTG 741
|
|
|
QY 721 CTCTCTAGTGTCTTCTCTCTGTCAGTCTTAGCCCTGCCCCCTTACCCAGGCT 780
|
|
|
Db 742 CTCTCTAGTGTCTTCTCTCTGTCAGTCTTAGCCCTGCCCCCTTACCCAGGCT 801
|
|
|
QY 781 TAGGCTTAATTTACCTAAAGATTCAGAAACCTGTAGCTTCCAGTGTATTTAAC 840
|
|
|
Db 802 TAGGCTTAATTTACCTAAAGATTCAGAAACCTGTAGCTTCCAGTGTATTTAAC 861
|
|
|
QY 841 CTTAAATGCAATCAGAAAGTAGCAACAGAACTCAATAATTTTAAATGTC 895
|
|
|
Db 862 CTTAAATGCAATCAGAAAGTAGCAACAGAACTCAATAATTTTAAATGTC 916
|
|
|

```

## RESULT 13

```

; Sequence 7, Application US/09099824
; US-09-099-824-7
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAUL N.
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLAAS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099, 824
; FILING DATE:

```



CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/050,348  
 FILING DATE: 20-JUN-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Becker, Cheryl L.  
 REGISTRATION NUMBER: 35,441  
 REFERENCE/DOCKET NUMBER: 6123-US-01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 847/935-1729  
 TELEFAX: 847/938-2623  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 861 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-09-099-824-7

Query Match 96.1%; Score 860; DB 15; Length 861;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-245;

Matches 860; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 36 CACCTGTCGCGCCCTCAAAATGGGAACGCTGGCTGGACTTAAGCATAGACCAGGC 95
DB 1 CACCTGTCGCGCCCTCAAAATGGGAACGCTGGCTGGACTTAAGCATAGACCAGGC 60
QY 96 TGAATATCTGACCTGAGTCATCCCGAGGATCAGAGGCTCCAGAGGAACTTCAT 155
DB 61 TGAATATCTGACCTGAGTCATCCCGAGGATCAGAGGCTCCAGAGGAACTTCAT 120
QY 156 TATATCTTCAAGCAACTTACAGCTGCACCCAGCTGGCATGAAAGTTCTAATCTCTC 215
DB 121 TATATCTTCAAGCAACTTACAGCTGCACCCAGCTGGCATGAAAGTTCTAATCTCTC 180
QY 216 CCTCTCTCTGTGTCGCACTAATGTCATGTCATGTCCTAGACCTGAATCCAGG 275
DB 181 CCTCTCTCTGTGTCGCACTAATGTCATGTCATGTCCTAGACCTGAATCCAGG 240
QY 276 GGTGCCGAGAGCCACAGGAGCCAGGCTTCTAGAGATGGCTCCAGAGAGGCG 335
DB 241 GGTGCCGAGAGCCACAGGAGCCAGGCTTCTAGAGATGGCTCCAGAGAGGCG 300
QY 336 CCAAAATGTGATGCAAAAGATGGTCTCAGAGCCCGCGAAGAAATTCATGACAGT 395
DB 301 CCAAAATGTGATGCAAAAGATGGTCTCAGAGCCCGCGAAGAAATTCATGACAGT 360
QY 396 GTCTGGCTGCCAAAGAGAGTGGCTCTGATCATTTCAAGGGAATGTGAAGAAAC 455
DB 361 GTCTGGCTGCCAAAGAGAGTGGCTCTGATCATTTCAAGGGAATGTGAAGAAAC 420
QY 456 AAGACACCAAGGAGCCACAGAAAGCCAAACAGATTCAGAGCTGCCAGCAATTTCT 515
DB 421 AAGACACCAAGGAGCCACAGAAAGCCAAACAGATTCAGAGCTGCCAGCAATTTCT 480
QY 516 CAAACATGTAGTAAAGCTTTGCTGCTGCTTGTAGAGAGCTGAGGCGCCACTCT 575
DB 481 CAAACATGTAGTAAAGCTTTGCTGCTGCTTGTAGAGAGCTGAGGCGCCACTCT 540
QY 576 TCCAAATTAACATTTCTCAGCCAGAGAGAGTGAAGACACTTACAGACACTCTTCTCT 635
DB 541 TCCAAATTAACATTTCTCAGCCAGAGAGAGTGAAGACACTTACAGACACTCTTCTCT 600
QY 636 CCCAGCTCAGCTCCGCACTGATACCCACCCCTAAATCATTCAGAGTCTCTCAAAAAGCAG 695
DB 601 CCCAGCTCAGCTCCGCACTGATACCCACCCCTAAATCATTCAGAGTCTCTCAAAAAGCAG 660
QY 696 TTTTTCAGAGATTTTGTGTTGCTGCTCAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 755
DB 661 TTTTTCAGAGATTTTGTGTTGCTGCTCAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
QY 756 CCTGTGCTCCCTCCCTTACCCAGGCTTAGGCTTAATTAACCTGAAGAATTCAGAGAACTGT 815

```

RESULT 14  
 US-09-703-256A-913

Sequence 913, Application US/09705256A  
 GENERAL INFORMATION:  
 APPLICANT: Ma, Xiao-Jun; Dotson, Stanton B.; Monsanto Company  
 TITLE OF INVENTION: Tumor Associated Molecules (TAMs): Targets for diagnosis, treat  
 FILE REFERENCE: 3214  
 CURRENT APPLICATION NUMBER: US/09/705,256A  
 CURRENT FILING DATE: 1999-05-11  
 PRIOR APPLICATION NUMBER: US 60/164,285  
 NUMBER OF SEQ ID NOS: 8259  
 SEQ ID NO 913  
 LENGTH: 859  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-09-705-256A-913

Query Match 96.0%; Score 859; DB 31; Length 859;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-245;

Matches 859; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 36 CACCTGTCGCGCCCTCAAAATGGGAACGCTGGCTGGACTTAAGCATAGACCAGGC 95
DB 1 CACCTGTCGCGCCCTCAAAATGGGAACGCTGGCTGGACTTAAGCATAGACCAGGC 60
QY 96 TGAATATCTGACCTGAGTCATCCCGAGGATCAGAGGCTCCAGAGGAACTTCAT 155
DB 61 TGAATATCTGACCTGAGTCATCCCGAGGATCAGAGGCTCCAGAGGAACTTCAT 120
QY 156 TATATCTTCAAGCAACTTACAGCTGCACCCAGCTGGCATGAAAGTTCTAATCTCTC 215
DB 121 TATATCTTCAAGCAACTTACAGCTGCACCCAGCTGGCATGAAAGTTCTAATCTCTC 180
QY 216 CCTCTCTCTGTGTCGCACTAATGTCATGTCATGTCCTAGACCTGAATCCAGG 275
DB 181 CCTCTCTCTGTGTCGCACTAATGTCATGTCATGTCCTAGACCTGAATCCAGG 240
QY 276 GGTGCCGAGAGCCACAGGAGCCAGAGCTTCTAGAGATGGCTCCAGAGAGGCGG 335
DB 241 GGTGCCGAGAGCCACAGGAGCCAGAGCTTCTAGAGATGGCTCCAGAGAGGCGG 300
QY 336 CCAAGATGTGATGCAAAAGATGGTCTCAGAGCCCGGAGAAATTTATGACAGT 395
DB 301 CCAAGATGTGATGCAAAAGATGGTCTCAGAGCCCGGAGAAATTTATGACAGT 360
QY 396 GTCTGGCTGCCAAAGAGAGTGGCTCTGATCATTTCAAGGGAATGTGAAGAAAC 455
DB 361 GTCTGGCTGCCAAAGAGAGTGGCTCTGATCATTTCAAGGGAATGTGAAGAAAC 420
QY 456 AAGACACCAAGGAGCCACAGAAAGCCAAACAGATTCAGAGCTGCCAGCAATTTCT 515
DB 421 AAGACACCAAGGAGCCACAGAAAGCCAAACAGATTCAGAGCTGCCAGCAATTTCT 480
QY 516 CAAACATGTAGTAAAGCTTTGCTGCTGCTTGTAGAGAGCTGAGGCGCCACTCT 575
DB 481 CAAACATGTAGTAAAGAGAGTGTGCTGCTTGTAGAGAGCTGAGGCGCCACTCT 540
QY 576 TCCAAATTAACATTTCTCAGCCAGAGAGAGTGAAGACACTTACAGACACTCTTCTCT 635

```





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2003, 13:55:42 ; Search time 1920.32 Seconds

(without alignments)  
9377.568 Million cell updates/sec

Title: US-09-700-770-6

Perfect score: 543  
Sequence: 1 ccggcgctgagggcgaggg.....gttaagagcaaaaaaaaa 543

Scoring table: IDENTITY-NUC

Gapop 10.0 , Gapext 1.0

Searched: 3363688 seqs, 16581889874 residues

Total number of hits satisfying chosen parameters: 66727376

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents.NA.Main:\*  
1: /cgn2\_6/ptodata/2/pna/PCRTUS\_COMB.seq.\*  
2: /cgn2\_6/ptodata/2/pna/PCRTUS\_COMB.seq.\*  
3: /cgn2\_6/ptodata/2/pna/US06\_COMB.seq.\*  
4: /cgn2\_6/ptodata/2/pna/US07\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/pna/US08\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/pna/US081\_COMB.seq.\*  
7: /cgn2\_6/ptodata/2/pna/US082\_COMB.seq.\*  
8: /cgn2\_6/ptodata/2/pna/US083\_COMB.seq.\*  
9: /cgn2\_6/ptodata/2/pna/US084\_COMB.seq.\*  
10: /cgn2\_6/ptodata/2/pna/US085\_COMB.seq.\*  
11: /cgn2\_6/ptodata/2/pna/US086\_COMB.seq.\*  
12: /cgn2\_6/ptodata/2/pna/US087\_COMB.seq.\*  
13: /cgn2\_6/ptodata/2/pna/US088\_COMB.seq.\*  
14: /cgn2\_6/ptodata/2/pna/US089\_COMB.seq.\*  
15: /cgn2\_6/ptodata/2/pna/US090\_COMB.seq.\*  
16: /cgn2\_6/ptodata/2/pna/US091\_COMB.seq.\*  
17: /cgn2\_6/ptodata/2/pna/US092A\_COMB.seq.\*  
18: /cgn2\_6/ptodata/2/pna/US092B\_COMB.seq.\*  
19: /cgn2\_6/ptodata/2/pna/US093A\_COMB.seq.\*  
20: /cgn2\_6/ptodata/2/pna/US093B\_COMB.seq.\*  
21: /cgn2\_6/ptodata/2/pna/US094\_COMB.seq.\*  
22: /cgn2\_6/ptodata/2/pna/US095A\_COMB.seq.\*  
23: /cgn2\_6/ptodata/2/pna/US095B\_COMB.seq.\*  
24: /cgn2\_6/ptodata/2/pna/US095C\_COMB.seq.\*  
25: /cgn2\_6/ptodata/2/pna/US095D\_COMB.seq.\*  
26: /cgn2\_6/ptodata/2/pna/US096A\_COMB.seq.\*  
27: /cgn2\_6/ptodata/2/pna/US096B\_COMB.seq.\*  
28: /cgn2\_6/ptodata/2/pna/US096C\_COMB.seq.\*  
29: /cgn2\_6/ptodata/2/pna/US096D\_COMB.seq.\*  
30: /cgn2\_6/ptodata/2/pna/US096E\_COMB.seq.\*  
31: /cgn2\_6/ptodata/2/pna/US097A\_COMB.seq.\*  
32: /cgn2\_6/ptodata/2/pna/US097B\_COMB.seq.\*  
33: /cgn2\_6/ptodata/2/pna/US097C\_COMB.seq.\*  
34: /cgn2\_6/ptodata/2/pna/US098A\_COMB.seq.\*  
35: /cgn2\_6/ptodata/2/pna/US098B\_COMB.seq.\*  
36: /cgn2\_6/ptodata/2/pna/US098C\_COMB.seq.\*  
37: /cgn2\_6/ptodata/2/pna/US098D\_COMB.seq.\*  
38: /cgn2\_6/ptodata/2/pna/US099A\_COMB.seq.\*  
39: /cgn2\_6/ptodata/2/pna/US099B\_COMB.seq.\*  
40: /cgn2\_6/ptodata/2/pna/US099C\_COMB.seq.\*  
41: /cgn2\_6/ptodata/2/pna/US099E\_COMB.seq.\*  
42: /cgn2\_6/ptodata/2/pna/US099F\_COMB.seq.\*  
43: /cgn2\_6/ptodata/2/pna/US099F\_COMB.seq.\*

44: /cgn2\_6/ptodata/2/pna/US100A\_COMB.seq.\*  
45: /cgn2\_6/ptodata/2/pna/US100B\_COMB.seq.\*  
46: /cgn2\_6/ptodata/2/pna/US101A\_COMB.seq.\*  
47: /cgn2\_6/ptodata/2/pna/US101B\_COMB.seq.\*  
48: /cgn2\_6/ptodata/2/pna/US102A\_COMB.seq.\*  
49: /cgn2\_6/ptodata/2/pna/US102B\_COMB.seq.\*  
50: /cgn2\_6/ptodata/2/pna/US103A\_COMB.seq.\*  
51: /cgn2\_6/ptodata/2/pna/US103B\_COMB.seq.\*  
52: /cgn2\_6/ptodata/2/pna/US104B\_COMB.seq.\*  
53: /cgn2\_6/ptodata/2/pna/US104C\_COMB.seq.\*  
54: /cgn2\_6/ptodata/2/pna/US6000\_COMB.seq.\*  
55: /cgn2\_6/ptodata/2/pna/US6001\_COMB.seq.\*  
56: /cgn2\_6/ptodata/2/pna/US6002\_COMB.seq.\*  
57: /cgn2\_6/ptodata/2/pna/US6003\_COMB.seq.\*  
58: /cgn2\_6/ptodata/2/pna/US6004\_COMB.seq.\*  
59: /cgn2\_6/ptodata/2/pna/US6005\_COMB.seq.\*  
60: /cgn2\_6/ptodata/2/pna/US6006\_COMB.seq.\*  
61: /cgn2\_6/ptodata/2/pna/US6007\_COMB.seq.\*  
62: /cgn2\_6/ptodata/2/pna/US6008\_COMB.seq.\*  
63: /cgn2\_6/ptodata/2/pna/US6009\_COMB.seq.\*  
64: /cgn2\_6/ptodata/2/pna/US6010\_COMB.seq.\*  
65: /cgn2\_6/ptodata/2/pna/US6011\_COMB.seq.\*  
66: /cgn2\_6/ptodata/2/pna/US6012\_COMB.seq.\*  
67: /cgn2\_6/ptodata/2/pna/US6013\_COMB.seq.\*  
68: /cgn2\_6/ptodata/2/pna/US6014\_COMB.seq.\*  
69: /cgn2\_6/ptodata/2/pna/US6015\_COMB.seq.\*  
70: /cgn2\_6/ptodata/2/pna/US6016\_COMB.seq.\*  
71: /cgn2\_6/ptodata/2/pna/US6017\_COMB.seq.\*  
72: /cgn2\_6/ptodata/2/pna/US6018\_COMB.seq.\*  
73: /cgn2\_6/ptodata/2/pna/US6019\_COMB.seq.\*  
74: /cgn2\_6/ptodata/2/pna/US6020\_COMB.seq.\*  
75: /cgn2\_6/ptodata/2/pna/US6021\_COMB.seq.\*  
76: /cgn2\_6/ptodata/2/pna/US6022\_COMB.seq.\*  
77: /cgn2\_6/ptodata/2/pna/US6023\_COMB.seq.\*  
78: /cgn2\_6/ptodata/2/pna/US6023B\_COMB.seq.\*  
79: /cgn2\_6/ptodata/2/pna/US6024\_COMB.seq.\*  
80: /cgn2\_6/ptodata/2/pna/US6025\_COMB.seq.\*  
81: /cgn2\_6/ptodata/2/pna/US6026\_COMB.seq.\*  
82: /cgn2\_6/ptodata/2/pna/US6027\_COMB.seq.\*  
83: /cgn2\_6/ptodata/2/pna/US6028\_COMB.seq.\*  
84: /cgn2\_6/ptodata/2/pna/US6029\_COMB.seq.\*  
85: /cgn2\_6/ptodata/2/pna/US6030\_COMB.seq.\*  
86: /cgn2\_6/ptodata/2/pna/US6031\_COMB.seq.\*  
87: /cgn2\_6/ptodata/2/pna/US6032\_COMB.seq.\*  
88: /cgn2\_6/ptodata/2/pna/US6033\_COMB.seq.\*  
89: /cgn2\_6/ptodata/2/pna/US6034\_COMB.seq.\*  
90: /cgn2\_6/ptodata/2/pna/US6035\_COMB.seq.\*  
91: /cgn2\_6/ptodata/2/pna/US6036\_COMB.seq.\*  
92: /cgn2\_6/ptodata/2/pna/US6037\_COMB.seq.\*  
93: /cgn2\_6/ptodata/2/pna/US6038\_COMB.seq.\*  
94: /cgn2\_6/ptodata/2/pna/US6039\_COMB.seq.\*  
95: /cgn2\_6/ptodata/2/pna/US6040\_COMB.seq.\*  
96: /cgn2\_6/ptodata/2/pna/US6041\_COMB.seq.\*  
97: /cgn2\_6/ptodata/2/pna/US6042\_COMB.seq.\*  
98: /cgn2\_6/ptodata/2/pna/US6043\_COMB.seq.\*  
99: /cgn2\_6/ptodata/2/pna/US6044\_COMB.seq.\*  
100: /cgn2\_6/ptodata/2/pna/US6045\_COMB.seq.\*  
101: /cgn2\_6/ptodata/2/pna/US6046\_COMB.seq.\*  
102: /cgn2\_6/ptodata/2/pna/US6047\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	543	100.0	543	1	PCR-US99-10344-6
2	543	100.0	543	2	PCR-US99-10344-6
3	543	100.0	543	31	US-09-700-770-6
4	543	100.0	543	32	US-09-720-533-199



QY	121	GGGGGGCCCTGTCCTCGACAGCTCCGCTGCTGCTTCTTAAGTGGGGCTCGGCCAAGCCTGTGG	180
Db	121	GGGTGGCCCTGTCTCGACAGCTCCGCTGCTGCTTCTTAAGTGGGGCTCGGCCAAGCCTGTGG	180
QY	181	CCGAGCCGTGTGGCTGCGCTGGAGTGTGGGGCGGAGGACCGGGGCGCCGGACCTGTGGCAAC	240
Db	181	CCGAGCCGTGTGGCTGCGCTGGAGTGTGGGGCGGAGGACCGGGGCGCCGGAGCCTGTGGCAAC	240
QY	241	CCCTTGGGACCCCTCAACCCGCTGAAGCTCTGCTAAGCAGCCTGGGCAATCCCGTGAAC	300
Db	241	CCCTTGGGACCCCTCAACCCGCTGAAGCTCTGCTAAGCAGCCTGGGCAATCCCGTGAAC	300
QY	301	ACCTCATATAGAGGGCCCGAGAGTGTGTGGCTGGACTGGGTGCCCGAGGGCGTGGGGGGCG	360
Db	301	ACCTCATATAGAGGGCCCGAGAGTGTGTGGCTGGACTGGGTGCCCGAGGGCGTGGGGGGCG	360
QY	361	TGAAGGCCCTGAAGGCCCTGTGTGGGGGCCCTGACAGTGTGGCTGTAGGCCGAGACTGGAG	420
Db	361	TGAAGGCCCTGAAGGCCCTGTGTGGGGGCCCTGACAGTGTGGCTGTAGGCCGAGACTGGAG	420
QY	421	CATGTACACCTGAGGACAAAGAGCGTGGCCACCCCGGAGGGCGTGAACACCCCGCGGGGG	480
Db	421	CATGTACACCTGAGGACAAAGAGCGTGGCCACCCCGGAGGGCGTGAACACCCCGCGGGGG	480
QY	481	AGGACCGTCAATCCCTTCCCGCGGCCCTCTCAATTAACGTGTTAAGGCAAAAAAAA	540
Db	481	AGGACCGTCAATCCCTTCCCGCGGCCCTCTCAATTAACGTGTTAAGGCAAAAAAAA	540
QY	541	AAA AAA 543	
Db	541	AAA AAA 543	

```

RESULT 3
US-09-700-770-6
: Sequence 6, Application US/09700770
: GENERAL INFORMATION:
: APPLICANT: Yang Fei
: APPLICANT: Macina, Roberto A.
: APPLICANT: Sun, Yongling
: TITLE OF INVENTION: A Novel Method of Diagnosing, Monitoring and Staging Lung Cancer
: FILE REFERENCE: DEX-0036
: CURRENT APPLICATION NUMBER: US/09/7700,770
: CURRENT FILING DATE: 2000-11-20
: PRIOR APPLICATION NUMBER: 60/086,212
: PRIOR FILING DATE: 1998-05-21
: NUMBER OF SEQ. ID NOS: 9
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 6
: LENGTH: 543
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-700-770-6

```

Query Match	100.0%;	Score 543;	DB 31;	Length 543;
Best Local Similarity	100.0%;	Pred. No. 4.9e-88;		
Matches 543; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY 1 CCGGCGCTGAGAGGGCCGAGAGACCGGGTATAGAACCTGTGGCTTGGCCGGGACGCCG 60

Db 1 CCGGCGCTGAGAGGGCCGAGAGACCGGGTATAGAGAACCTGTGGCTTGGCCGGGACGCCG 60

QY 61 CAGGTTCCCCGCGCGCCCGAGACCCCCGCGGCCATGAGCTGCGCCGCCCTCTCTGGGGCTCT 120

Db 61 CAGGTTCCCCGCGCGCCCGAGACCCCCGCGGCCATGAGCTGCGCCGCCCTCTCTGGGGCTCT 120

QY 121 GCGTGGCCCTGTCTCTGACAGCTCCGCTGCTTCTTCTAGTGGGACTCGGCCAACCCTGTGG 180

Db 121 GCGTGGCCCTGTCTCTGACAGCTCCGCTGCTTCTTCTAGTGGGACTCGGCCAACCCTGTGG 180

QY 181 CCCAGCCTGTGCTGCTGCGTGGAGTGGCGGCGGAGGCCGGGCGCCGAGACCTTGGCCACC 240

Db	1b1	CCGACGCTGTGCTCGTGGCTGGAGTGGGGGGCGGAGGCGCGGGGCGGGGACCGCTGGCCCAACC	24.0
QY	24.1	CCCTGCGGACCCCTCAACCCCGCTGGAAGCTCCTGCTGAGCAGCCTGGGCAATCCCGGTAAACC	30.0
Db	24.1	CCCTGCGGACCCCTCAACCCCGCTGGAAGCTCCTGCTGAGCAGCCTGGGCAATCCCGGTAAACC	30.0
QY	30.1	ACCTATATAGAGGGGCTCCCAAGAAAGTGTGTGGCTGAGCTGGGGTCCCAAGGCCGTGGGGCCG	36.0
Db	30.1	ACCTATATAGAGGGGCTCCCAAGAAAGTGTGTGGCTGAGCTGGGGTCCCAAGGCCGTGGGGCCG	36.0
QY	36.1	TGAAGGCCCTGAAAGGCCCTGCTGGGGGGCCCTGACAGTGTGTTGGCTAAGCCGAGACTGGAG	42.0
Db	36.1	TGAAGGCCCTGAAAGGCCCTGCTGGGGGGCCCTGACAGTGTGTTGGCTAAGCCGAGACTGGAG	42.0
QY	42.1	CATCTACACCTGAGGACAAAGACGCTGCCCCACCCGCGAGGGCTGAAAAACCCCGCGGGGG	48.0
Db	42.1	CATCTACACCTGAGGACAAAGACGCTGCCCCACCCGCGAGGGCTGAAAAACCCCGCGGGGG	48.0
QY	48.1	AGGACCGTCCATCCCTTCCCGGGCCCTCTTCATTAACGTTGTTAAAGCAAAAAAAA	54.0
Db	48.1	AGGACCGTCCATCCCTTCCCGGGCCCTCTTCATTAACGTTGTTAAAGCAAAAAAAA	54.0
QY	54.1	AAA AAA 543	
Db	54.1	AAA AAA 543	

RESULT 4  
US-09-720-533-199

; Sequence 199, Application US/09720533  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INCYTE PHARMACEUTICALS, INC

```

1  APPLICANT: GORGONE, Gina A.
2  APPLICANT: CORLEY, Neil C.
3  APPLICANT: GOGGLER, Karl J.
4  APPLICANT: BAUGHN, Mariah R.
5  APPLICANT: AKERBLOM, Ingrid E.
6  APPLICANT: AD-YOUNG, Jenice
7  APPLICANT: YUE, Henry
8  APPLICANT: PATTERSON, Chandra
9  APPLICANT: REDDY, Roopa
10 APPLICANT: HILLMAN, Jennifer L.
11 APPLICANT: BANDMAN, Olga
12 TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
13
14 FILE REFERENCE: PF-0541 PCT
15
16 CURRENT APPLICATION NUMBER: US/09/720,533
17
18 CURRENT FILING DATE: 2002-08-26
19
20 PRIOR APPLICATION NUMBER: 60/090,762; 60/094,983; 60/102,686; 60/112,129
21
22 PRIOR FILING DATE: 1998-06-26; 1998-07-31; 1998-10-01; 1998-12-11
23
24 NUMBER OF SEQ. ID NOS: 268
25
26 SOFTWARE: PERL Program
27
28 SEQ ID NO 199
29
30 LENGTH: 543
31
32 TYPE: DNA
33
34 ORGANISM: Homo sapiens
35
36 FEATURE:
37
38 NAME/KEY: misc_feature
39
40 OTHER INFORMATION: Incyte Clone No: 3120415
41
42 US-09/720-533-199

```

Query Match	100.0%;	Score 543;	DB 32;	Length 543;
Best Local Similarity	100.0%;	Pred. No. 4.9e-88;		
Matches 543;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

0Y 1 CCGGGGCTGGAGAGGGGAGAGACCGGGTATAAAGACCTGTGGCCCTTGCCTGGGGCAGCCG 60  
 Db 1 CCGGGCTGTGAAGGGGGAGAGACCGGGTATAAAGACCTGTGGCCCTTGCCTGGGGCAGCCG 60  
 0Y 61 CAGGTTCCTCCGGCGCGCCCGAGACCCCGCGCCCATGAAGCTGGCGGCCCTCTCTGGGGCTCT 120  
 Db 61 CAGGTTCCTCCGGCGCGCCCGAGACCCCGCGCCCATGAAGCTGGCGGCCCTCTCTGGGGCTCT 120

```

QY 121 GCGTGGCCCTGTCTCCTCAGCTCCGCTGCTGCTTTCTTAAGGGGCTGCGCAAGCCCTGCG 180
DB 121 GCGTGGCCCTGTCTCCTCAGCTCCGCTGCTGCTTTCTTAAGGGGCTGCGCAAGCCCTGCG 180
QY 181 CCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 181 CCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 241 CCCTCGGCAACCCCAACCCGCTGAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 241 CCCTCGGCAACCCCAACCCGCTGAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 301 ACCTCATAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 301 ACCTCATAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 361 TGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 361 TGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 421 CATCTACCTGAGGAGCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 CATCTACCTGAGGAGCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 AGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 481 AGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 541 AAA 543
DB 541 AAA 543

```

RESULT 5

```

US-60-090-762-130
; Sequence 130, Application US/60090762
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Gorgone, Gina
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: SIGNAL PEPTIDE-CONTAINING MOLECULES
; NUMBER OF SEQUENCES: 445
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/60/090,762
; FILING DATE: Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0541 P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 130:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 543 base pairs
; TYPE: nucleic acid

```

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNG7UT13
; CLONE: 3120415
US-60-090-762-130

```

Query Match 100.0%; Score 543; DB 63; Length 543;  
 Best Local Similarity 100.0%; Pred. No. 4,9e-88;  
 Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 CCGGGGCTGAGGGGGGAGAGGACCGGATTAAGAAAGCTCTGAGCTTCCCGGACCGG 60
DB 1 CCGGGGCTGAGGGGGGAGAGGACCGGATTAAGAAAGCTCTGAGCTTCCCGGACCGG 60
QY 61 CAGGTTCCCGCGCGCCCGGAGCCCGGCGCATGAGTCTGCGCGCCCTCTGGGGCTCT 120
DB 61 CAGGTTCCCGCGCGCCCGGAGCCCGGCGCATGAGTCTGCGCGCCCTCTGGGGCTCT 120
QY 121 GCGTGGCCCTGTCTCCTCAGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 121 GCGTGGCCCTGTCTCCTCAGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 181 CCAGCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 181 CCAGCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 241 CCGTGGGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 241 CCGTGGGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
QY 301 ACCTCATAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 301 ACCTCATAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 361 TGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 361 TGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 421 CATCTACCTGAGGAGCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 CATCTACCTGAGGAGCAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 AGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 481 AGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 541 AAA 543
DB 541 AAA 543

```

RESULT 6

```

US-60-172-360-22042
; Sequence 22042, Application US/60172360
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; FILE REFERENCE: GX-0007 P
; CURRENT APPLICATION NUMBER: US/60/172,360
; NUMBER OF SEQ ID NOS: 199-12-16
; SOFTWARE: PERL Program
; SEQ ID NO 22042
; LENGTH: 589
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 242745.1

```



```

FEATURE:
NAME/KEY: unsure
LOCATION: 17, 568, 574, 576, 582-583
OTHER INFORMATION: a, t, c, g, or other
US-60-172-360-22042

```

```

Query Match
Best Local Similarity 99.8%; Score 542; DB 71; Length 589;
Matches 342; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 CGGCGCTGAGAGGCGAGAGCGGATATAGAGCGCTGAGCTTGGCCGAGCGG 60
DB 30 CGGCGCTGAGAGGCGAGAGCGGATATAGAGCGCTGAGCTTGGCCGAGCGG 89
QY 61 CAGGTTCCCGCGCGCGCGAGCGCGCGCATGAGCTCGCGCGCTTGGGCTCT 120
DB 90 CAGGTTCCCGCGCGCGCGAGCGCGCGCATGAGCTCGCGCGCTTGGGCTCT 149
QY 121 GCGTGCCCTGTCCTGAGCTCGGCTGCTTCTTATGAGGCTGCGGCAAGCTGTG 180
DB 150 GCGTGCCCTGTCCTGAGCTCGGCTGCTTCTTATGAGGCTGCGGCAAGCTGTG 209
QY 181 CCCAGCCTGCTGCTGAGTGGGCGGAGCGCGGCGCGGACCTGCGCAAC 240
DB 210 CCCAGCCTGCTGCTGAGTGGGCGGAGCGCGGCGCGGACCTGCGCAAC 269
QY 241 CCCTGGGACCCCTCAACCCGCTGAGACCTCTGCTGAGCAAGCTGCGCATCCCGTAAAC 300
DB 270 CCCTGGGACCCCTCAACCCGCTGAGACCTCTGCTGAGCAAGCTGCGCATCCCGTAAAC 329
QY 301 ACCTCATAGAGGCTCCGAGAGTGTGTGCTGAGTGGGCTCCGAGCGCGTGGGCGG 360
DB 330 ACCTCATAGAGGCTCCGAGAGTGTGTGCTGAGTGGGCTCCGAGCGCGTGGGCGG 389
QY 361 TGAAGGCTGTAAGGCTGCTGAGGCGGCTGAGCTGTTGGCTAGCGAGACTGGAG 420
DB 390 TGAAGGCTGTAAGGCTGCTGAGGCGGCTGAGCTGTTGGCTAGCGAGACTGGAG 449
QY 421 CATCTACACTGAGGACGACGAGCTGCCACCGCGAGGCGTGAACCCCGCGCGG 480
DB 450 CATCTACACTGAGGACGACGAGCTGCCACCGCGAGGCGTGAACCCCGCGCGG 509
QY 481 AGGACGCTCATCCCTTCCCGCGGCGCTCTCAATTAAGCTGTGTTAAGCAAAAAA 540
DB 510 AGGACGCTCATCCCTTCCCGCGGCGCTCTCAATTAAGCTGTGTTAAGCAAAAAA 569
QY 541 AAA 543
DB 570 AAA 572

```

```

RESULT 7
US-10-237-435-6
Sequence 6, Application US/10237435
GENERAL INFORMATION:
APPLICANT: Walker, Michael G.
APPLICANT: Spiro, Peter A.
APPLICANT: Murty, Lynn E.
TITLE OF INVENTION: LONG SURFACTANT MOLECULES
FILE REFERENCE: PB-0019 US
CURRENT APPLICATION NUMBER: US/10/237,435
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 60/317,822
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PERL Program
SEQ ID NO 6
LENGTH: 561
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: 242745.1

```

US-10-237-435-6

```

Query Match
Best Local Similarity 98.9%; Score 537; DB 48; Length 561;
Matches 537; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 CGGCGCTGAGAGGCGAGAGCGGATATAGAGCGCTGAGCTTGGCCGAGCGG 60
DB 25 CGGCGCTGAGAGGCGAGAGCGGATATAGAGCGCTGAGCTTGGCCGAGCGG 84
QY 61 CAGGTTCCCGCGCGCGCGAGCGCGCGCATGAGCTCGCGCGCTTGGGCTCT 120
DB 85 CAGGTTCCCGCGCGCGCGAGCGCGCGCATGAGCTCGCGCGCTTGGGCTCT 144
QY 121 GCGTGCCCTGTCCTGAGCTCGGCTGCTTCTTATGAGGCTGCGGCAAGCTGTG 180
DB 145 GCGTGCCCTGTCCTGAGCTCGGCTGCTTCTTATGAGGCTGCGGCAAGCTGTG 204
QY 181 CCCAGCCTGCTGCTGAGTGGGCGGAGCGCGGCGCGGACCTGCGCAAC 240
DB 205 CCCAGCCTGCTGCTGAGTGGGCGGAGCGCGGCGCGGACCTGCGCAAC 264
QY 241 CCCTGGGACCCCTCAACCCGCTGAGACCTCTGCTGAGCAAGCTGCGCATCCCGTAAAC 300
DB 265 CCCTGGGACCCCTCAACCCGCTGAGACCTCTGCTGAGCAAGCTGCGCATCCCGTAAAC 324
QY 301 ACCTCATAGAGGCTCCGAGAGTGTGTGCTGAGTGGGCTCCGAGCGCGTGGGCGG 360
DB 325 ACCTCATAGAGGCTCCGAGAGTGTGTGCTGAGTGGGCTCCGAGCGCGTGGGCGG 384
QY 361 TGAAGGCTGTAAGGCTGCTGAGGCGGCTGAGCTGTTGGCTAGCGAGACTGGAG 420
DB 385 TGAAGGCTGTAAGGCTGCTGAGGCGGCTGAGCTGTTGGCTAGCGAGACTGGAG 444
QY 421 CATCTACACTGAGGACGACGAGCTGCCACCGCGAGGCGTGAACCCCGCGCGG 480
DB 445 CATCTACACTGAGGACGACGAGCTGCCACCGCGAGGCGTGAACCCCGCGCGG 504
QY 481 AGGACGCTCATCCCTTCCCGCGGCGCTCTCAATTAAGCTGTGTTAAGCAAAAAA 537
DB 505 AGGACGCTCATCCCTTCCCGCGGCGCTCTCAATTAAGCTGTGTTAAGCAAAAAA 561

```

```

RESULT 8
US-60-317-822-6
Sequence 6, Application US/60317822
GENERAL INFORMATION:
APPLICANT: Walker, Michael G.
APPLICANT: Spiro, Peter A.
TITLE OF INVENTION: LONG SURFACTANT MOLECULES
FILE REFERENCE: PB-0019 P
CURRENT APPLICATION NUMBER: US/60/317,822
CURRENT FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PERL Program
SEQ ID NO 6
LENGTH: 561
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: 242745.1
US-60-317-822-6

```

```

Query Match
Best Local Similarity 98.9%; Score 537; DB 86; Length 561;
Matches 537; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 CGGCGCTGAGAGGCGAGAGCGGATATAGAGCGCTGAGCTTGGCCGAGCGG 60
DB 25 CGGCGCTGAGAGGCGAGAGCGGATATAGAGCGCTGAGCTTGGCCGAGCGG 84
QY 61 CAGGTTCCCGCGCGCGCGAGCGCGCGCATGAGCTCGCGCGCTTGGGCTCT 120

```

Query Match	98.1%	Score 532.6	DB 1	Length 562
Best Local Similarity	99.8%	Pred. No. 3.6e-86		
Matches 532; Conservative	1	Mismatches 0	Indels 0	Gaps 0

```

RESULT 10
PCT-US01-09339-8
: Sequence 8, Application PC/TUS0109339
: GENERAL INFORMATION:
: APPLICANT: Abbott Laboratories
: APPLICANT: Colpilts, Tracey L.
: APPLICANT: Russell, John C.
: TITLE OF INVENTION: DETECTING AND METHODS USEFUL FOR
: FILE REFERENCE: 5972.US.P6
: CURRENT APPLICATION NUMBER: PCT/US01/09339
: PRIOR FILING DATE: 2001-03-22
: PRIOR APPLICATION NUMBER: US 09/467,602
: PRIOR FILING DATE: 1999-12-20
: PRIOR APPLICATION NUMBER: US 09/215,818
: PRIOR FILING DATE: 1998-12-18
: PRIOR APPLICATION NUMBER: US 08/912,276
: PRIOR FILING DATE: 1997-08-17
: PRIOR APPLICATION NUMBER: US 08/697,105
: PRIOR FILING DATE: 1996-08-19
: PRIOR APPLICATION NUMBER: US 08/912,149
: PRIOR FILING DATE: 1997-08-15
: PRIOR APPLICATION NUMBER: US 08/697,106
: PRIOR FILING DATE: 1996-08-19
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 8
: LENGTH: 562
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (17)..(117)
: OTHER INFORMATION: n = a or g or c or t/u, unknown or other at
: OTHER INFORMATION: position 17
PCT-US01-09339-8

```

```
Query Match      98.1%; Score 532.6; DB 2; Length 562;
Best Local Similarity 99.8%; Pred. No. 3.6e-86;
Matches 532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGCGCTGGAGGGGCGAGACCGGGTATAGAACCTCGTGGGCTTCCCGGCGACCG 60
DB 30 CCGGCGCTGGAGGGGCGAGACCGGGTATAGAACCTCGTGGGCTTCCCGGCGACCG 89
QY 61 CAGGTTCCCGCGCGCGCGCGCGCGCGCATGAGCTGCGCGCTCTCGGGGCTCT 120
DB 90 CAGGTTCCCGCGCGCGCGCGCGCGCGCATGAGCTGCGCGCTCTCGGGGCTCT 149
QY 121 GCGTGGCCCTGCTCGAGCTCGCTGCTGCTTCTTATGAGGCTCGGCGCAAGCTGTGG 180
DB 150 GCGTGGCCCTGCTCGAGCTCGCTGCTGCTTCTTATGAGGCTCGGCGCAAGCTGTGG 209
QY 181 CCGAGCGCTGTGCTGCGCTGAGATGCGGCGCGCGCGCGCGCGCGCGCAACC 240
DB 210 CCGAGCGCTGTGCTGCGCTGAGATGCGGCGCGCGCGCGCGCGCGCGCAACC 269
QY 241 CCGTGGCGACCTCTCAACCCGCTGAAGCTCCTGCTGAGACAGCTGGGCAATCCCGTGAAC 300
DB 270 CCGTGGCGACCTCTCAACCCGCTGAAGCTCCTGCTGAGACAGCTGGGCAATCCCGTGAAC 329
QY 301 ACCTCATAGAGAGGCTCCAGAGTGTGTGCTGAGCTGGGTCGCCAGCGCTGGGGCGG 360
DB 330 ACCTCATAGAGAGGCTCCAGAGTGTGTGCTGAGCTGGGTCGCCAGCGCTGGGGCGG 389
QY 361 TGAAGGCGCTGAAAGGCGCTGCTGGGGGCGCTGAGAGTGTGGCTGAGCGGAGACTGGAG 420
DB 390 TGAAGGCGCTGAAAGGCGCTGCTGGGGGCGCTGAGAGTGTGGCTGAGCGGAGACTGGAG 449
QY 421 CATCTACACTGAGAGCAAGAGCTGCGCAACCCGCGAGGGGTGAAGAACCCCGCGCGAGG 480
DB 450 CATCTACACTGAGAGCAAGAGCTGCGCAACCCGCGAGGGGTGAAGAACCCCGCGCGAGG 509
QY 481 AGGACCGTCCATCCCTTCCCGCGCGCGCTCTCAATAAAGCTGGTTAAGAGCA 533
DB 510 AGGACCGTCCATCCCTTCCCGCGCGCGCTCTCAATAAAGCTGGTTAAGAGCA 562

RESULT 11
US-09-016-387-5
; Sequence 5, Application us/09016387
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA A.
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLAAS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAPP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASE OF THE LUNG
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
```

```
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/016.387
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/791.710
;; FILING DATE: 31-JAN-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Becker, Cheryl L.
;; REGISTRATION NUMBER: 35,441
;; REFERENCE/DOCKET NUMBER: 5998.US.P1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 847/935-1729
;; TELEFAX: 847/938-2623
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 562 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY: base_polymorphism
;; LOCATION: 17
;; OTHER INFORMATION: /note= " N' represents an A or G or
;; OTHER INFORMATION: T or C polymorphism at this position"
;; FEATURE:
;; NAME/KEY: base_polymorphism
;; LOCATION: 177
;; OTHER INFORMATION: /note= " Y' represents a C or T
;; OTHER INFORMATION: polymorphism at this position"
;; US-09-016-387-5

Query Match      98.1%; Score 532.6; DB 15; Length 562;
Best Local Similarity 99.8%; Pred. No. 3.6e-86;
Matches 532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGCGCTGGAGGGGCGAGACCGGGTATAGAACCTCGTGGGCTTCCCGGCGACCG 60
DB 30 CCGGCGCTGGAGGGGCGAGACCGGGTATAGAACCTCGTGGGCTTCCCGGCGACCG 89
QY 61 CAGGTTCCCGCGCGCGCGCGCGCGCATGAGCTGCGCGCTCTCGGGGCTCT 120
DB 90 CAGGTTCCCGCGCGCGCGCGCGCGCATGAGCTGCGCGCTCTCGGGGCTCT 149
QY 121 GCGTGGCCCTGCTCGAGCTCGCTGCTGCTTCTTATGAGGCTCGGCGCAAGCTGTGG 180
DB 150 GCGTGGCCCTGCTCGAGCTCGCTGCTGCTTCTTATGAGGCTCGGCGCAAGCTGTGG 209
QY 181 CCGAGCGCTGTGCTGCGCTGAGATGCGGCGCGCGCGCGCGCGCGCGCAACC 240
DB 210 CCGAGCGCTGTGCTGCGCTGAGATGCGGCGCGCGCGCGCGCGCGCGCAACC 269
QY 241 CCGTGGCGACCTCTCAACCCGCTGAAGCTCCTGCTGAGACAGCTGGGCAATCCCGTGAAC 300
DB 270 CCGTGGCGACCTCTCAACCCGCTGAAGCTCCTGCTGAGACAGCTGGGCAATCCCGTGAAC 329
QY 301 ACCTCATAGAGAGGCTCCAGAGTGTGTGCTGAGCTGGGTCGCCAGCGCTGGGGCGG 360
DB 330 ACCTCATAGAGAGGCTCCAGAGTGTGTGCTGAGCTGGGTCGCCAGCGCTGGGGCGG 389
QY 361 TGAAGGCGCTGAAAGGCGCTGCTGGGGGCGCTGAGAGTGTGGCTGAGCGGAGACTGGAG 420
DB 390 TGAAGGCGCTGAAAGGCGCTGCTGGGGGCGCTGAGAGTGTGGCTGAGCGGAGACTGGAG 449
QY 421 CATCTACACTGAGAGCAAGAGCTGCGCAACCCGCGAGGGGTGAAGAACCCCGCGCGAGG 480
DB 450 CATCTACACTGAGAGCAAGAGCTGCGCAACCCGCGAGGGGTGAAGAACCCCGCGCGAGG 509
QY 481 AGGACCGTCCATCCCTTCCCGCGCGCGCTCTCAATAAAGCTGGTTAAGAGCA 533
DB 510 AGGACCGTCCATCCCTTCCCGCGCGCGCTCTCAATAAAGCTGGTTAAGAGCA 562
```

## RESULT 12

US-09-549-342A-8

; Sequence 8, Application US/09549342A

; GENERAL INFORMATION:

; APPLICANT: Abbott Laboratories

; APPLICANT: Colpitts, Tracey L.

; APPLICANT: Russell, John C.

; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR

; FILE REFERENCE: 5972 US P6

; CURRENT APPLICATION NUMBER: US/09/549,342A

; CURRENT FILING DATE: 2000-04-13

; PRIOR APPLICATION NUMBER: US 09/467,602

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: US 09/215,818

; PRIOR FILING DATE: 1998-12-18

; PRIOR APPLICATION NUMBER: US 08/912,276

; PRIOR FILING DATE: 1997-08-17

; PRIOR APPLICATION NUMBER: US 08/697,105

; PRIOR FILING DATE: 1996-08-19

; PRIOR APPLICATION NUMBER: US 08/912,149

; PRIOR FILING DATE: 1997-08-15

; PRIOR APPLICATION NUMBER: US 08/697,106

; PRIOR FILING DATE: 1996-08-19

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO: 8

; LENGTH: 562

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (17)...(17)

; OTHER INFORMATION: n = a or g or c or t/u, unknown or other at

; OTHER INFORMATION: position 17

US-09-549-342A-8

Query Match 98.1%; Score 532.6; DB 24; Length 562;  
 Best Local Similarity 99.8%; Pred. No. 3.6e-86;  
 Matches 532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 CCGGCGCTGGAGGGGCGAGGACCGGGATTAAGAAAGCTCTGCGCTTGGCCCGGCGGACCG 60
   |||
Db 30 CCGGCGCTGGAGGGGCGAGGACCGGGATTAAGAAAGCTCTGCGCTTGGCCCGGCGGACCG 89
QY 61 CAGGTTCCCGCGCGCGCCGAGCCCGCGCATGAAGCTCGCGCCCTCTGGGCTCT 120
   |||
Db 90 CAGGTTCCCGCGCGCGCCGAGCCCGCGCATGAAGCTCGCGCCCTCTGGGCTCT 149
QY 121 GCGTGCGCTGCTGAGCTCGCGCTGCTCTTTTAACTGAGGCTCGGCGCAAGCTGTGG 180
   |||
Db 150 GCGTGCGCTGCTGAGCTCGCGCTGCTCTTTTAACTGAGGCTCGGCGCAAGCTGTGG 209
QY 181 CCCAGCTGCTGCTGCTGAGTCCGCGCGGAGGCGCGGCGCGGAGACCTGCGCAACC 240
   |||
Db 210 CCCAGCTGCTGCTGCTGAGTCCGCGCGGAGGCGCGGCGCGGAGACCTGCGCAACC 269
QY 241 CCGTGGGACCTCAACCCGCTGAAGCTCTGCTGAGCAAGCTGGGCAATCCCGTGAAC 300
   |||
Db 270 CCGTGGGACCTCAACCCGCTGAAGCTCTGCTGAGCAAGCTGGGCAATCCCGTGAAC 329
QY 301 ACCTCATAGAGGCTCCGAGAAAGTGTGGCTGAGAGTGGGATCCCAAGGCGGTGGGGCCG 360
   |||
Db 330 ACCTCATAGAGGCTCCGAGAAAGTGTGGCTGAGAGTGGGATCCCAAGGCGGTGGGGCCG 389
QY 361 TGAAGGCGCTGAAGGCGCTGCTGGGGGCGCTGACAGTGTGGCTGAGCGGAGACTGGAG 420
   |||
Db 390 TGAAGGCGCTGAAGGCGCTGCTGGGGGCGCTGACAGTGTGGCTGAGCGGAGACTGGAG 449
QY 421 CATCTACACCTGAGGACAAAGAGCTGCGCACCGCGGAGGCTGAAACCCCGCGGGG 480
   |||
Db 450 CATCTACACCTGAGGACAAAGAGCTGCGCACCGCGGAGGCTGAAACCCCGCGGGG 509

```

```

QY 481 AGACCGCTGCATCCCTTCCCGGCGCCCTCTCAATAAAGCTGTTAAGACA 533
   |||
Db 510 AGACCGCTGCATCCCTTCCCGGCGCCCTCTCAATAAAGCTGTTAAGACA 562

```

## RESULT 13

US-09-770-175-8431

; Sequence 8431, Application US/09770175

; GENERAL INFORMATION:

; APPLICANT: Gearling, David P.

; APPLICANT: Holtzman, Douglas A.

; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES

; FILE REFERENCE: 1600,2058-001

; CURRENT APPLICATION NUMBER: US/09/770,175

; CURRENT FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: US 60/178,874

; PRIOR FILING DATE: 2000-01-28

; NUMBER OF SEQ ID NOS: 8967

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO: 8431

; LENGTH: 714

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-770-175-8431

Query Match 97.7%; Score 530.4; DB 33; Length 714;  
 Best Local Similarity 99.8%; Pred. No. 9e-86;  
 Matches 531; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 CCGGCGCTGGAGGGGCGAGGACCGGGATTAAGAAAGCTCTGCGCTTGGCCCGGCGGACCG 60
   |||
Db 98 CCGGCGCTGGAGGGGCGAGGACCGGGATTAAGAAAGCTCTGCGCTTGGCCCGGCGGACCG 157
QY 61 CAGGTTCCCGCGCGCGCCGAGCCCGCGCATGAAGCTCGCGCCCTCTGGGCTCT 120
   |||
Db 158 CAGGTTCCCGCGCGCGCCGAGCCCGCGCATGAAGCTCGCGCCCTCTGGGCTCT 217
QY 121 GCGTGCGCTGCTGAGCTCGCGCTGCTCTTTTAACTGAGGCTCGGCGCAAGCTGTGG 180
   |||
Db 218 GCGTGCGCTGCTGAGCTCGCGCTGCTCTTTTAACTGAGGCTCGGCGCAAGCTGTGG 277
QY 181 CCCAGCTGCTGCTGCTGAGTCCGCGCGGAGGCGCGGCGCGGAGACCTGCGCAACC 240
   |||
Db 278 CCCAGCTGCTGCTGCTGAGTCCGCGCGGAGGCGCGGCGCGGAGACCTGCGCAACC 337
QY 241 CCGTGGGACCTCAACCCGCTGAAGCTCTGCTGAGCAAGCTGGGCAATCCCGTGAAC 300
   |||
Db 338 CCGTGGGACCTCAACCCGCTGAAGCTCTGCTGAGCAAGCTGGGCAATCCCGTGAAC 397
QY 301 ACCTCATAGAGGCTCCGAGAAAGTGTGGCTGAGAGTGGTCCAGGCGGTGGGGCCG 360
   |||
Db 398 ACCTCATAGAGGCTCCGAGAAAGTGTGGCTGAGAGTGGTCCAGGCGGTGGGGCCG 457
QY 361 TGAAGGCGCTGAAGGCGCTGCTGGGGGCGCTGACAGTGTGGCTGAGCGGAGACTGGAG 420
   |||
Db 458 TGAAGGCGCTGAAGGCGCTGCTGGGGGCGCTGACAGTGTGGCTGAGCGGAGACTGGAG 517
QY 421 CATCTACACCTGAGGACAAAGAGCTGCGCACCGCGGAGGCTGAAACCCCGCGGGG 480
   |||
Db 518 CATCTACACCTGAGGACAAAGAGCTGCGCACCGCGGAGGCTGAAACCCCGCGGGG 577
QY 481 AGGACCGTCAATCCCTTCCCGGCGCCCTCTCAATAAAGCTGTTAAGAGC 532
   |||
Db 578 AGGACCGTCAATCCCTTCCCGGCGCCCTCTCAATAAAGCTGTTAAGAGC 629

```

## RESULT 14

US-09-927-796-27

; Sequence 27, Application US/09927796

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Gunney, Austin L.  
 APPLICANT: Hillan, Kenneth J.  
 APPLICANT: Marsters, Scot A.  
 APPLICANT: Pan, James  
 APPLICANT: Pitti, Robert M.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Smith, Victoria  
 APPLICANT: Stone, Donna M.  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Wood, William T.  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR  
 FILE REFERENCE: P2931R1C1  
 CURRENT APPLICATION NUMBER: US/09/927,796  
 CURRENT FILING DATE: 2001-08-09  
 PRIOR APPLICATION NUMBER: 60/014699  
 PRIOR FILING DATE: 1996-04-01  
 PRIOR APPLICATION NUMBER: 60/026943  
 PRIOR FILING DATE: 1996-09-23  
 PRIOR APPLICATION NUMBER: 60/059121  
 PRIOR FILING DATE: 1997-07-17  
 PRIOR APPLICATION NUMBER: 60/059352  
 PRIOR FILING DATE: 1997-09-19  
 PRIOR APPLICATION NUMBER: 60/062037  
 PRIOR FILING DATE: 1997-10-10  
 PRIOR APPLICATION NUMBER: 60/063755  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/063045  
 PRIOR FILING DATE: 1997-10-24  
 PRIOR APPLICATION NUMBER: 60/063046  
 PRIOR FILING DATE: 1997-10-24  
 PRIOR APPLICATION NUMBER: 60/066511  
 PRIOR FILING DATE: 1997-11-24  
 PRIOR APPLICATION NUMBER: 60/066772  
 PRIOR FILING DATE: 1997-11-24  
 PRIOR APPLICATION NUMBER: 60/067411  
 PRIOR FILING DATE: 1997-12-03  
 PRIOR APPLICATION NUMBER: 60/069862  
 PRIOR FILING DATE: 1997-12-17  
 PRIOR APPLICATION NUMBER: 60/082700  
 PRIOR FILING DATE: 1998-04-22  
 PRIOR APPLICATION NUMBER: 60/095929  
 PRIOR FILING DATE: 1998-08-10  
 PRIOR APPLICATION NUMBER: 60/097978  
 PRIOR FILING DATE: 1998-08-26  
 PRIOR APPLICATION NUMBER: 60/103396  
 PRIOR FILING DATE: 1998-10-07  
 PRIOR APPLICATION NUMBER: 60/108867  
 PRIOR FILING DATE: 1998-11-17  
 PRIOR APPLICATION NUMBER: 60/112851  
 PRIOR FILING DATE: 1998-12-16  
 PRIOR APPLICATION NUMBER: 60/119965  
 PRIOR FILING DATE: 1999-02-12  
 PRIOR APPLICATION NUMBER: 60/123972  
 PRIOR FILING DATE: 1999-03-11  
 PRIOR APPLICATION NUMBER: 60/134459  
 PRIOR FILING DATE: 1999-05-11  
 PRIOR APPLICATION NUMBER: 60/140650  
 PRIOR FILING DATE: 1999-06-22  
 PRIOR APPLICATION NUMBER: 60/140653  
 PRIOR FILING DATE: 1999-06-22  
 PRIOR APPLICATION NUMBER: 60/144758  
 PRIOR FILING DATE: 1999-07-20  
 PRIOR APPLICATION NUMBER: 60/145698  
 PRIOR FILING DATE: 1999-07-26  
 PRIOR APPLICATION NUMBER: 60/146222  
 PRIOR FILING DATE: 1999-07-28  
 PRIOR APPLICATION NUMBER: 60/149395  
 PRIOR FILING DATE: 1999-08-17  
 PRIOR APPLICATION NUMBER: 60/151689  
 PRIOR FILING DATE: 1999-08-31  
 PRIOR APPLICATION NUMBER: 08/625328

PRIOR FILING DATE: 1996-04-01  
 PRIOR APPLICATION NUMBER: 08/710802  
 PRIOR FILING DATE: 1996-09-23  
 PRIOR APPLICATION NUMBER: 08/800699  
 PRIOR FILING DATE: 1997-02-14  
 PRIOR APPLICATION NUMBER: 08/828683  
 PRIOR FILING DATE: 1997-03-31  
 PRIOR APPLICATION NUMBER: 08/829270  
 PRIOR FILING DATE: 1997-03-31  
 PRIOR APPLICATION NUMBER: 08/928069  
 PRIOR FILING DATE: 1997-09-11  
 PRIOR APPLICATION NUMBER: 08/934494  
 PRIOR FILING DATE: 1997-09-19  
 PRIOR APPLICATION NUMBER: 09/143068  
 PRIOR FILING DATE: 1998-08-28  
 PRIOR APPLICATION NUMBER: 09/143707  
 PRIOR FILING DATE: 1998-08-28  
 PRIOR APPLICATION NUMBER: 09/151889  
 PRIOR FILING DATE: 1998-09-11  
 PRIOR APPLICATION NUMBER: 09/169104  
 PRIOR FILING DATE: 1998-10-09  
 PRIOR APPLICATION NUMBER: 09/202089  
 PRIOR FILING DATE: 1998-12-08  
 PRIOR APPLICATION NUMBER: 09/254311  
 PRIOR FILING DATE: 1999-03-03  
 PRIOR APPLICATION NUMBER: 09/304003  
 PRIOR FILING DATE: 1999-04-30  
 PRIOR APPLICATION NUMBER: 09/380137  
 PRIOR FILING DATE: 1999-08-25  
 PRIOR APPLICATION NUMBER: 09/380138  
 PRIOR FILING DATE: 1999-08-25  
 PRIOR APPLICATION NUMBER: 09/380139  
 PRIOR FILING DATE: 1999-08-25  
 PRIOR APPLICATION NUMBER: 09/403297  
 PRIOR FILING DATE: 1999-10-18  
 PRIOR APPLICATION NUMBER: 09/423844  
 PRIOR FILING DATE: 1999-11-12  
 PRIOR APPLICATION NUMBER: 09/511133  
 PRIOR FILING DATE: 2000-02-23  
 PRIOR APPLICATION NUMBER: 09/511631  
 PRIOR FILING DATE: 2000-02-23  
 PRIOR APPLICATION NUMBER: 09/664610  
 PRIOR FILING DATE: 2000-09-18  
 PRIOR APPLICATION NUMBER: 09/665350  
 PRIOR FILING DATE: 2000-09-18  
 PRIOR APPLICATION NUMBER: 09/690169  
 PRIOR FILING DATE: 2000-10-16  
 PRIOR APPLICATION NUMBER: 09/690189  
 PRIOR FILING DATE: 2000-10-16  
 PRIOR APPLICATION NUMBER: 09/709238  
 PRIOR FILING DATE: 2000-11-18  
 PRIOR APPLICATION NUMBER: 09/866034  
 PRIOR FILING DATE: 2001-05-25  
 PRIOR APPLICATION NUMBER: 09/872035  
 PRIOR FILING DATE: 2001-06-01  
 PRIOR APPLICATION NUMBER: 09/884733  
 PRIOR FILING DATE: 2001-06-19  
 PRIOR APPLICATION NUMBER: 09/886342  
 PRIOR FILING DATE: 2001-06-19  
 PRIOR APPLICATION NUMBER: 09/866028  
 PRIOR FILING DATE: 2001-08-25  
 PRIOR APPLICATION NUMBER: PCT/US97/05230  
 PRIOR FILING DATE: 1997-03-31  
 PRIOR APPLICATION NUMBER: PCT/US98/19094  
 PRIOR FILING DATE: 1998-09-14  
 PRIOR APPLICATION NUMBER: PCT/US98/19330  
 PRIOR FILING DATE: 1998-09-16  
 PRIOR APPLICATION NUMBER: PCT/US98/21407  
 PRIOR FILING DATE: 1998-10-09  
 PRIOR APPLICATION NUMBER: PCT/US98/25108  
 PRIOR FILING DATE: 1998-12-01  
 PRIOR APPLICATION NUMBER: PCT/US99/05028

```

PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: PCT/US99/20111
PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: PCT/US99/28634
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: PCT/US00/04341
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/US00/04342
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/US00/06884
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: PCT/US00/13705
PRIOR FILING DATE: 2000-05-17
PRIOR APPLICATION NUMBER: PCT/US00/14941
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 258
SEQ ID NO 27
LENGTH: 569

```

Query Match 97.4% Score 529; DB 39; Length 569;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-85;  
 Matches 529; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

15 GCGAGAGCGGGTATAGAGAGCTCGGAGCTTGCCCGGACCGGAGTTCCCGCGC 74
1 GCGAGAGCGGGTATAGAGAGCTCGGAGCTTGCCCGGACCGGAGTTCCCGCGC 60
75 GCGCGGAGCGCGCGGCATGAGAGCTGCGCCCTCTGGGGCTGCGGAGCCGTGTC 134
61 GCGCGGAGCGCGCGGCATGAGAGCTGCGCCCTCTGGGGCTGCGGAGCCGTGTC 120
135 TGCAGCTCGCTCTGCTTTCTTAGTGAGCTGCGGCAAGCTGTGGCCAGCCTGTGCT 194
121 TGCAGCTCGCTCTGCTTTCTTAGTGAGCTGCGGCAAGCTGTGGCCAGCCTGTGCT 180
195 GCGCTGAGAGTGGCGGAGCGCGGCGCGGAGCCCTGGGCAACCCCTCGGACCTTC 254
181 GCGCTGAGAGTGGCGGAGCGCGGCGCGGAGCCCTGGGCAACCCCTCGGACCTTC 240
255 AACCCCTGAGAGCTCTGCTGAGAGCAGCTGGGAGCTCCCGGTGAGCAACCTCATAGAGGC 314

```

```

DB 241 AACCCGCTGAGAGCTCTGCTGAGAGCTGGGAGCTCCCGGTGAGCAACCTCATAGAGGC 300
QY 315 TCCGAGAGTGTGTGAGCTGAGCTGCTGCCAGGCGCTGGGGGCGGTGAAGGCCCTGAG 374
DB 301 TCCGAGAGTGTGTGAGCTGAGCTGCTGCCAGGCGCTGGGGGCGGTGAAGGCCCTGAG 360
QY 375 GCGCTGAGAGTGGCGGAGCGCGGCGCGGAGCCCTGGGCAACCCCTCGGACCTTC 434
DB 361 GCGCTGAGAGTGGCGGAGCGCGGCGCGGAGCCCTGGGCAACCCCTCGGACCTTC 420
QY 435 GACAAGAGCTGCGCCAGCGCGGAGGAGTGAAGAACCCCGCGGAGGAGACCTTCATCC 494
DB 421 GACAAGAGCTGCGCCAGCGCGGAGGAGTGAAGAACCCCGCGGAGGAGACCTTCATCC 480
QY 495 CCTTCCCCCGGCGCTCTCATATAGAGTGTGAAGCAAAAAAAAA 543
DB 481 CCTTCCCCCGGCGCTCTCATATAGAGTGTGAAGCAAAAAAAAA 529

```

# RESULT 15 US-10-210-951-27

```

Sequence 27, Application US/10210951
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gunney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Pan, James
APPLICANT: Pitt, Robert M.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stone, Donna M.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
FILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
TITLE REFERENCE: P2931R1C1
CURRENT APPLICATION NUMBER: US/10/210,951
PRIOR APPLICATION NUMBER: 2002-08-02
PRIOR FILING DATE: 1996-04-01
PRIOR APPLICATION NUMBER: 60/014699
PRIOR FILING DATE: 1996-04-01
PRIOR APPLICATION NUMBER: 60/026943
PRIOR FILING DATE: 1996-09-23
PRIOR APPLICATION NUMBER: 60/059121
PRIOR FILING DATE: 1997-07-17
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/062037
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: 60/063755
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063045
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/06511
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/06772
PRIOR FILING DATE: 1997-11-24
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 258
SEQ ID NO 27
LENGTH: 569
TYPE: DNA
ORGANISM: Homo sapiens
US-10-210-951-27

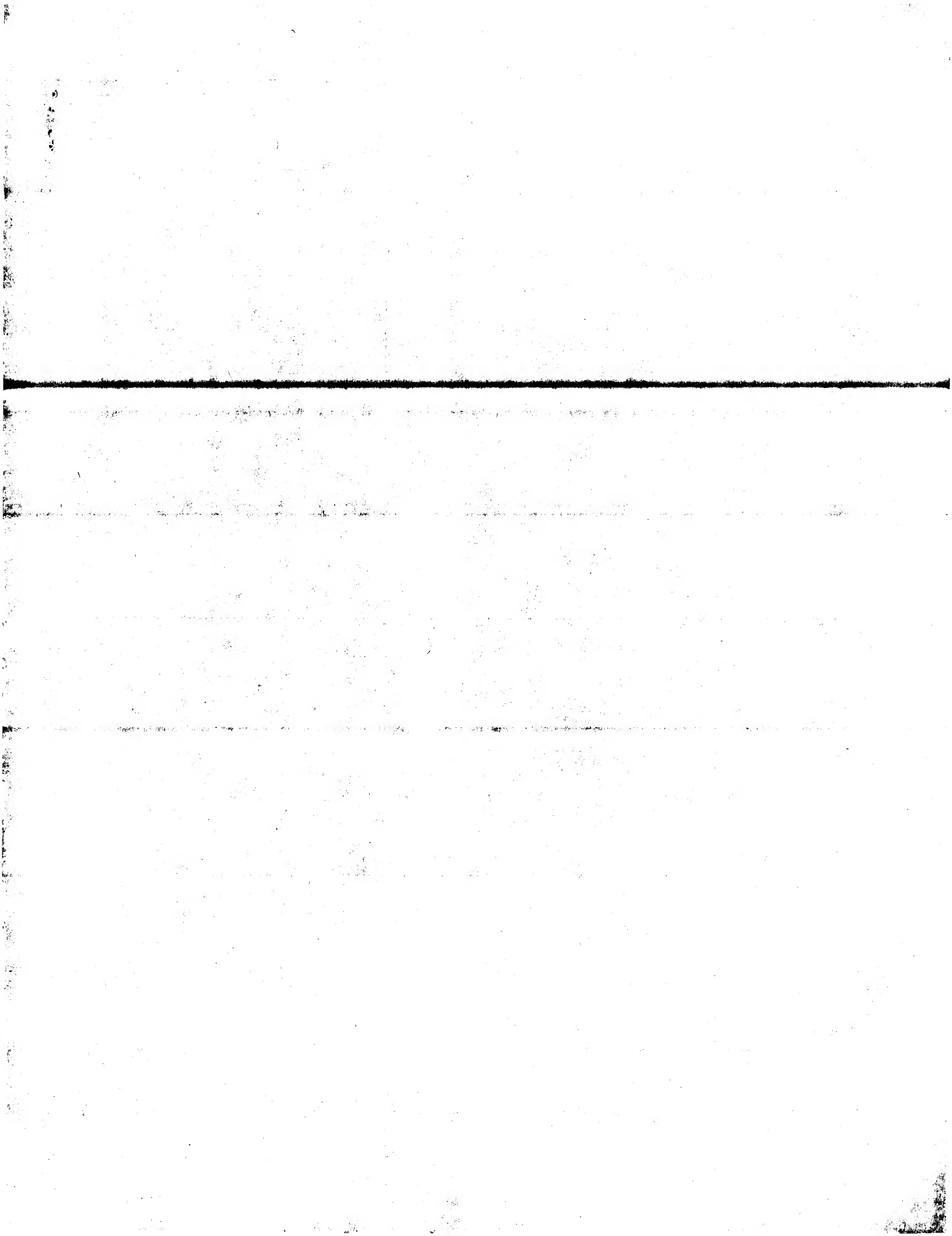
```

Query Match 97.4% Score 529; DB 48; Length 569;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-85;  
 Matches 529; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      15 GCGAGACCGGGTATTAAGAGCCTCGTGGCTTCCCGGCGACCGCAGGTTCCCGCGC 74
      1 |
      1 GCGAGGACCGGGTATTAAGAGCCTCGTGGCTTCCCGGCGACCGCAGGTTCCCGCGC 60
QY      75 GCGCGGAGCCCGCGGCATGAAGCTCGCCGCCCTCCGCGGCTCGCGGCTCGCGGCTCGCGC 134
      61 |
      61 GCGCGGAGCCCGCGGCATGAAGCTCGCCGCCCTCCGCGGCTCGCGGCTCGCGGCTCGCGC 120
QY      135 TGCAGCTCCGCTGCTGCTTCTTAAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTGCT 194
      121 |
      121 TGCAGCTCCGCTGCTGCTTCTTAAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTGCT 180
QY      195 GCGCTGAGTCTGGCGGCGGAGCGCCGGGCGCGGAGCCTGCGCAACCCCTCGGCACCTTC 254
      181 |
      181 GCGCTGAGTCTGGCGGCGGAGCGCCGGGCGCGGAGCCTGCGCAACCCCTCGGCACCTTC 240
QY      255 AACCGGTGAAGCTCCTGCTGAGCAGCGCTGGGCATCCCGGTGAACCACTCATAGAGGC 314
      241 |
      241 AACCGGTGAAGCTCCTGCTGAGCAGCGCTGGGCATCCCGGTGAACCACTCATAGAGGC 300
QY      315 TCCAGAAAGTGTGGCTGAGCTGGGTCCCAAGCGCTGGGGCCGTGAAGCCCTGAAG 374
      301 |
      301 TCCAGAAAGTGTGGGTGAGCTGGGTCCCAAGCGCTGGGGCCGTGAAGCCCTGAAG 360
QY      375 GCGCTGCTGGGGCCCTGACAGTGTGGCTGAGCCGAGACTGAGCATCTACACTGAG 434
      361 |
      361 GCGCTGCTGGGGCCCTGACAGTGTGGCTGAGCCGAGACTGAGCATCTACACTGAG 420
QY      435 GACAAGACGCTGCGCAACCGCGGAGGGCTGAACCCCGCGGGGAGGACCGTCCATCC 494
      421 |
      421 GACAAGACGCTGCGCAACCGCGGAGGGCTGAACCCCGCGGGGAGGACCGTCCATCC 480
QY      495 CTTTCCCGCGCCCTCTCAATAAAGCTGGTTAAGACAAAAA 543
      481 |
      481 CTTTCCCGCGCCCTCTCAATAAAGCTGGTTAAGACAAAAA 529
      481 CTTTCCCGCGCCCTCTCAATAAAGCTGGTTAAGACAAAAA 529
```

Search completed: October 10, 2003, 05:19:33  
Job time : 1924.32 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2003, 13:55:42 ; Search time 1114 Seconds  
(without alignments)  
9377.568 Million cell updates/sec

Title: US-09-700-770-4

Perfect score: 315  
1 taacactgactcagattt.....tggtatattacttatgc 315

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 33363688 seqs, 1658189874 residues

Total number of hits satisfying chosen parameters: 66727376

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Pending\_Patents\_NA\_Main:\*

1: /cgn2\_6/ptodata/2/pna/PCRTUS.COMB.seq.\*  
2: /cgn2\_6/ptodata/2/pna/PCRTUS.COMB.seq.\*  
3: /cgn2\_6/ptodata/2/pna/US06.COMB.seq.\*  
4: /cgn2\_6/ptodata/2/pna/US07.COMB.seq.\*  
5: /cgn2\_6/ptodata/2/pna/US08.COMB.seq.\*  
6: /cgn2\_6/ptodata/2/pna/US081.COMB.seq.\*  
7: /cgn2\_6/ptodata/2/pna/US082.COMB.seq.\*  
8: /cgn2\_6/ptodata/2/pna/US083.COMB.seq.\*  
9: /cgn2\_6/ptodata/2/pna/US084.COMB.seq.\*  
10: /cgn2\_6/ptodata/2/pna/US085.COMB.seq.\*  
11: /cgn2\_6/ptodata/2/pna/US086.COMB.seq.\*  
12: /cgn2\_6/ptodata/2/pna/US087.COMB.seq.\*  
13: /cgn2\_6/ptodata/2/pna/US088.COMB.seq.\*  
14: /cgn2\_6/ptodata/2/pna/US089.COMB.seq.\*  
15: /cgn2\_6/ptodata/2/pna/US090.COMB.seq.\*  
16: /cgn2\_6/ptodata/2/pna/US091.COMB.seq.\*  
17: /cgn2\_6/ptodata/2/pna/US092.COMB.seq.\*  
18: /cgn2\_6/ptodata/2/pna/US093.COMB.seq.\*  
19: /cgn2\_6/ptodata/2/pna/US093A.COMB.seq.\*  
20: /cgn2\_6/ptodata/2/pna/US093B.COMB.seq.\*  
21: /cgn2\_6/ptodata/2/pna/US094.COMB.seq.\*  
22: /cgn2\_6/ptodata/2/pna/US095.COMB.seq.\*  
23: /cgn2\_6/ptodata/2/pna/US095A.COMB.seq.\*  
24: /cgn2\_6/ptodata/2/pna/US095C.COMB.seq.\*  
25: /cgn2\_6/ptodata/2/pna/US095D.COMB.seq.\*  
26: /cgn2\_6/ptodata/2/pna/US096A.COMB.seq.\*  
27: /cgn2\_6/ptodata/2/pna/US096B.COMB.seq.\*  
28: /cgn2\_6/ptodata/2/pna/US096C.COMB.seq.\*  
29: /cgn2\_6/ptodata/2/pna/US096E.COMB.seq.\*  
30: /cgn2\_6/ptodata/2/pna/US096F.COMB.seq.\*  
31: /cgn2\_6/ptodata/2/pna/US097A.COMB.seq.\*  
32: /cgn2\_6/ptodata/2/pna/US097B.COMB.seq.\*  
33: /cgn2\_6/ptodata/2/pna/US097C.COMB.seq.\*  
34: /cgn2\_6/ptodata/2/pna/US098A.COMB.seq.\*  
35: /cgn2\_6/ptodata/2/pna/US098B.COMB.seq.\*  
36: /cgn2\_6/ptodata/2/pna/US098C.COMB.seq.\*  
37: /cgn2\_6/ptodata/2/pna/US098D.COMB.seq.\*  
38: /cgn2\_6/ptodata/2/pna/US099A.COMB.seq.\*  
39: /cgn2\_6/ptodata/2/pna/US099B.COMB.seq.\*  
40: /cgn2\_6/ptodata/2/pna/US099C.COMB.seq.\*  
41: /cgn2\_6/ptodata/2/pna/US099D.COMB.seq.\*  
42: /cgn2\_6/ptodata/2/pna/US099E.COMB.seq.\*  
43: /cgn2\_6/ptodata/2/pna/US099F.COMB.seq.\*

44: /cgn2\_6/ptodata/2/pna/US100A.COMB.seq.\*  
45: /cgn2\_6/ptodata/2/pna/US100B.COMB.seq.\*  
46: /cgn2\_6/ptodata/2/pna/US101A.COMB.seq.\*  
47: /cgn2\_6/ptodata/2/pna/US101B.COMB.seq.\*  
48: /cgn2\_6/ptodata/2/pna/US102A.COMB.seq.\*  
49: /cgn2\_6/ptodata/2/pna/US102B.COMB.seq.\*  
50: /cgn2\_6/ptodata/2/pna/US103A.COMB.seq.\*  
51: /cgn2\_6/ptodata/2/pna/US103B.COMB.seq.\*  
52: /cgn2\_6/ptodata/2/pna/US104A.COMB.seq.\*  
53: /cgn2\_6/ptodata/2/pna/US104B.COMB.seq.\*  
54: /cgn2\_6/ptodata/2/pna/US6000.COMB.seq.\*  
55: /cgn2\_6/ptodata/2/pna/US6001.COMB.seq.\*  
56: /cgn2\_6/ptodata/2/pna/US6002.COMB.seq.\*  
57: /cgn2\_6/ptodata/2/pna/US6003.COMB.seq.\*  
58: /cgn2\_6/ptodata/2/pna/US6004.COMB.seq.\*  
59: /cgn2\_6/ptodata/2/pna/US6005.COMB.seq.\*  
60: /cgn2\_6/ptodata/2/pna/US6006.COMB.seq.\*  
61: /cgn2\_6/ptodata/2/pna/US6007.COMB.seq.\*  
62: /cgn2\_6/ptodata/2/pna/US6008.COMB.seq.\*  
63: /cgn2\_6/ptodata/2/pna/US6009.COMB.seq.\*  
64: /cgn2\_6/ptodata/2/pna/US6010.COMB.seq.\*  
65: /cgn2\_6/ptodata/2/pna/US6011.COMB.seq.\*  
66: /cgn2\_6/ptodata/2/pna/US6012.COMB.seq.\*  
67: /cgn2\_6/ptodata/2/pna/US6013.COMB.seq.\*  
68: /cgn2\_6/ptodata/2/pna/US6014.COMB.seq.\*  
69: /cgn2\_6/ptodata/2/pna/US6015.COMB.seq.\*  
70: /cgn2\_6/ptodata/2/pna/US6016.COMB.seq.\*  
71: /cgn2\_6/ptodata/2/pna/US6017.COMB.seq.\*  
72: /cgn2\_6/ptodata/2/pna/US6018.COMB.seq.\*  
73: /cgn2\_6/ptodata/2/pna/US6019.COMB.seq.\*  
74: /cgn2\_6/ptodata/2/pna/US6020.COMB.seq.\*  
75: /cgn2\_6/ptodata/2/pna/US6021.COMB.seq.\*  
76: /cgn2\_6/ptodata/2/pna/US6022.COMB.seq.\*  
77: /cgn2\_6/ptodata/2/pna/US6023.COMB.seq.\*  
78: /cgn2\_6/ptodata/2/pna/US6024.COMB.seq.\*  
79: /cgn2\_6/ptodata/2/pna/US6025.COMB.seq.\*  
80: /cgn2\_6/ptodata/2/pna/US6026.COMB.seq.\*  
81: /cgn2\_6/ptodata/2/pna/US6027.COMB.seq.\*  
82: /cgn2\_6/ptodata/2/pna/US6028.COMB.seq.\*  
83: /cgn2\_6/ptodata/2/pna/US6029.COMB.seq.\*  
84: /cgn2\_6/ptodata/2/pna/US6030.COMB.seq.\*  
85: /cgn2\_6/ptodata/2/pna/US6031.COMB.seq.\*  
86: /cgn2\_6/ptodata/2/pna/US6032.COMB.seq.\*  
87: /cgn2\_6/ptodata/2/pna/US6033.COMB.seq.\*  
88: /cgn2\_6/ptodata/2/pna/US6034.COMB.seq.\*  
89: /cgn2\_6/ptodata/2/pna/US6035.COMB.seq.\*  
90: /cgn2\_6/ptodata/2/pna/US6036.COMB.seq.\*  
91: /cgn2\_6/ptodata/2/pna/US6037.COMB.seq.\*  
92: /cgn2\_6/ptodata/2/pna/US6038.COMB.seq.\*  
93: /cgn2\_6/ptodata/2/pna/US6039.COMB.seq.\*  
94: /cgn2\_6/ptodata/2/pna/US6040.COMB.seq.\*  
95: /cgn2\_6/ptodata/2/pna/US6041.COMB.seq.\*  
96: /cgn2\_6/ptodata/2/pna/US6042.COMB.seq.\*  
97: /cgn2\_6/ptodata/2/pna/US6043.COMB.seq.\*  
98: /cgn2\_6/ptodata/2/pna/US6044.COMB.seq.\*  
99: /cgn2\_6/ptodata/2/pna/US6045.COMB.seq.\*  
100: /cgn2\_6/ptodata/2/pna/US6046.COMB.seq.\*  
101: /cgn2\_6/ptodata/2/pna/US6047.COMB.seq.\*  
102: /cgn2\_6/ptodata/2/pna/US6047.COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	315	100.0	315	1	PCT-US99-10344-4
2	315	100.0	315	2	PCT-US99-10344-4
3	315	100.0	315	24	US-09-540-212a-28392
4	315	100.0	315	31	US-09-700-770-4

Sequence 4, Appl1  
Sequence 4, Appl1  
Sequence 28392, A  
Sequence 4, Appl1

```

C 5 315 100.0 315 31 US-09-705-256A-3132 Sequence 3132, Ap
C 6 315 100.0 315 70 US-60-164-285-3132 Sequence 3132, Ap
C 7 315 100.0 532 44 US-10-016-349A-8 Sequence 8, Appl1
C 8 315 100.0 636 1 PCT-US02-10421-2868 Sequence 2868, Ap
C 9 315 100.0 636 46 US-10-112-699-2868 Sequence 2868, Ap
C 10 315 100.0 705 44 US-10-016-349A-9 Sequence 9, Appl1
C 11 263.2 73.3 270 24 US-09-540-212A-5244 Sequence 5244, Ap
C 12 224.6 81.2 265 24 US-09-540-212A-14244 Sequence 14244, Ap
C 13 204 64.8 204 23 US-08-879-204-208 Sequence 208, App
C 14 204 64.8 204 24 US-09-540-212A-41340 Sequence 41340, A
C 15 43.6 13.4 32768 75 US-60-213-177-120 Sequence 120, App
C 16 39.2 12.4 452 25 US-09-521-640-41263 Sequence 41263, A
C 17 39.2 12.4 452 25 US-09-552-087-12715 Sequence 12715, A
C 18 39.2 12.4 452 25 US-09-552-087B-12715 Sequence 12715, A
C 19 38.2 12.1 1452321 40 US-09-947-911-267 Sequence 267, App
C 20 38 1821 68 US-60-147-189-343 Sequence 343, App
C 21 38 12.1 1664976 1 PCT-US97-14900A-1 Sequence 1, Appl1
C 22 38 12.1 1664976 30 PCT-US97-14900A-1 Sequence 1, Appl1
C 23 38 12.1 1664976 30 US-09-692-570-1 Sequence 4370, Ap
C 24 37.6 11.9 455 21 US-09-431-517-4370 Sequence 49, Appl
C 25 37.6 11.9 3436920 40 US-09-947-911-49 Sequence 49, Appl
C 26 37.4 11.9 497 22 US-09-528-409-110693 Sequence 110693,
C 27 37.4 11.9 497 39 US-09-933-524-110693 Sequence 110693,
C 28 37.4 11.9 497 39 US-09-933-524-110693 Sequence 110693,
C 29 37.4 11.9 2028 29 US-09-663-779-822 Sequence 822, App
C 30 37 11.7 512 52 US-10-424-599-56068 Sequence 56068, A
C 31 36.6 11.6 585 27 US-09-634-306B-193218 Sequence 193218,
C 32 36.6 11.6 12401 101 US-10-027-632-193218 Sequence 193218,
C 33 36.6 11.6 965 51 US-60-466-412-83338 Sequence 83338, A
C 34 36.4 11.6 965 51 US-10-369-493-30243 Sequence 30243, A
C 35 36.4 11.6 965 91 US-60-360-039-30243 Sequence 30243, A
C 36 36.4 11.6 1193 21 US-09-491-404-1596 Sequence 1596, Ap
C 37 36.4 11.6 1193 39 US-09-922-279-1596 Sequence 1596, Ap
C 38 36.4 11.6 1193 39 US-09-922-279A-1596 Sequence 501, App
C 39 36.4 11.6 53926 79 US-60-243-468-501 Sequence 524, App
C 40 36.4 11.6 68251 23 US-09-534-859-524 Sequence 524, App
C 41 36.4 11.6 68251 34 US-09-803-736-524 Sequence 60203, A
C 42 36.2 11.5 438 33 US-09-785-276A-60203 Sequence 60203, A
C 43 36.2 11.5 480 33 US-10-357-930-60203 Sequence 59667, A
C 44 36.2 11.5 480 33 US-09-785-276A-59667 Sequence 59667, A
C 45 36.2 11.5 480 51 US-10-357-930-59667

```

## ALIGNMENTS

```

RESULT 1
PCT-US99-10344-4
; Sequence 4, Application PC/TUS9910344
; GENERAL INFORMATION:
; APPLICANT: Yang, Fel
; APPLICANT: Macina, Roberto A.
; APPLICANT: Sun, Yongming
; TITLE OF INVENTION: A Novel Method of Diagnosing, Monitoring and Staging
; TITLE OF INVENTION: Lung Cancer
; FILE REFERENCE: DEX-0036
; CURRENT APPLICATION NUMBER: PCT/US99/10344
; CURRENT FILING DATE: 1999-05-12
; EARLIER APPLICATION NUMBER: 60/086,212
; EARLIER FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US99-10344-4

```

```

Query Match 100.0%; Score 315; DB 1; Length 315;
Best Local Similarity 100.0%; Pred. No. 4,1e-72;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 TAAACACTGACTGAGATTTTAAAGAAATTAACCTTTTGAGAAATAGAACAAATGCAATCAGTT 60

```

```

|||||
Db 1 TAAACACTGACTGAGATTTTAAAGAAATTAACCTTTTGAGAAATAGAACAAATGCAATCAGTT 60
61 TCCACCACTTAAAGATATCTTTAGAGATCTACAGCCTCCCTTAGGGGACATACAAA 120
61 TCCACCACTTAAAGATATCTTTAGAGATCTACAGCCTCCCTTAGGGGACATACAAA 120
61 TCCACCACTTAAAGATATCTTTAGAGATCTACAGCCTCCCTTAGGGGACATACAAA 120
61 TCCACCACTTAAAGATATCTTTAGAGATCTACAGCCTCCCTTAGGGGACATACAAA 120
121 GTGAGTTGTGTCCTTTGTGAGTCCACCTTATATTCAGTAGGTATGATACAAAT 180
121 GTGAGTTGTGTCCTTTGTGAGTCCACCTTATATTCAGTAGGTATGATACAAAT 180
121 GTGAGTTGTGTCCTTTGTGAGTCCACCTTATATTCAGTAGGTATGATACAAAT 180
121 GTGAGTTGTGTCCTTTGTGAGTCCACCTTATATTCAGTAGGTATGATACAAAT 180
181 TTGAAATATGATTTGTACACAAATTAACCTGAGTTATGGAACATCAGTAGAAGAAATA 240
181 TTGAAATATGATTTGTACACAAATTAACCTGAGTTATGGAACATCAGTAGAAGAAATA 240
181 TTGAAATATGATTTGTACACAAATTAACCTGAGTTATGGAACATCAGTAGAAGAAATA 240
241 CAACATTCATCCCTTTACAGAGATCATTTAGTGCACCTGAGTATTTGTCAATGT 300
241 CAACATTCATCCCTTTACAGAGATCATTTAGTGCACCTGAGTATTTGTCAATGT 300
301 ATTATCTACTTATGC 315
301 ATTATCTACTTATGC 315

```

```

RESULT 2
PCT-US99-10344-4
; Sequence 4, Application PC/TUS9910344
; GENERAL INFORMATION:
; APPLICANT: Yang, Fel
; APPLICANT: Macina, Roberto A.
; APPLICANT: Sun, Yongming
; TITLE OF INVENTION: A Novel Method of Diagnosing, Monitoring and Staging
; TITLE OF INVENTION: Lung Cancer
; FILE REFERENCE: DEX-0036
; CURRENT APPLICATION NUMBER: PCT/US99/10344
; CURRENT FILING DATE: 1999-05-12
; EARLIER APPLICATION NUMBER: 60/086,212
; EARLIER FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US99-10344-4

```

```

Query Match 100.0%; Score 315; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 4,1e-72;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 TAAACACTGACTGAGATTTTAAAGAAATTAACCTTTTGAGAAATAGAACAAATGCAATCAGTT 60
1 TAAACACTGACTGAGATTTTAAAGAAATTAACCTTTTGAGAAATAGAACAAATGCAATCAGTT 60
61 TCCACCACTTAAAGATATCTTTAGAGATCTACAGCCTCCCTTAGGGGACATACAAA 120
61 TCCACCACTTAAAGATATCTTTAGAGATCTACAGCCTCCCTTAGGGGACATACAAA 120
61 TCCACCACTTAAAGATATCTTTAGAGATCTACAGCCTCCCTTAGGGGACATACAAA 120
61 TCCACCACTTAAAGATATCTTTAGAGATCTACAGCCTCCCTTAGGGGACATACAAA 120
121 GTGAGTTGTGTCCTTTGTGAGTCCACCTTATATTCAGTAGGTATGATACAAAT 180
121 GTGAGTTGTGTCCTTTGTGAGTCCACCTTATATTCAGTAGGTATGATACAAAT 180
121 GTGAGTTGTGTCCTTTGTGAGTCCACCTTATATTCAGTAGGTATGATACAAAT 180
121 GTGAGTTGTGTCCTTTGTGAGTCCACCTTATATTCAGTAGGTATGATACAAAT 180
181 TTGAAATATGATTTGTACACAAATTAACCTGAGTTATGGAACATCAGTAGAAGAAATA 240
181 TTGAAATATGATTTGTACACAAATTAACCTGAGTTATGGAACATCAGTAGAAGAAATA 240
181 TTGAAATATGATTTGTACACAAATTAACCTGAGTTATGGAACATCAGTAGAAGAAATA 240
241 CAACATTCATCCCTTTACAGAGATCATTTAGTGCACCTGAGTATTTGTCAATGT 300
241 CAACATTCATCCCTTTACAGAGATCATTTAGTGCACCTGAGTATTTGTCAATGT 300
301 ATTATCTACTTATGC 315
301 ATTATCTACTTATGC 315

```

## RESULT 3

US-09-540-212A-28392/c

; Sequence 28392, Application US/09540212A

; GENERAL INFORMATION:

; APPLICANT: Seilheimer, Jeffrey J.

; APPLICANT: Deleage, Angelo M.

; APPLICANT: Stuart, Susan G.

; APPLICANT: Stuve, Laura L.

; APPLICANT: Mullaby, Sara J.

; APPLICANT: Naughton, Rebecca E.

; TITLE OF INVENTION: POLYNUCLEOTIDES OF AIRWAY AND LUNG SYSTEM TISSUE

; FILE REFERENCE: PD-1034 CIP

; CURRENT APPLICATION NUMBER: US/09/540,212A

; CURRENT FILING DATE: 2000-03-31

; NUMBER OF SEQ ID NOS: 67551

; SOFTWARE: PERL Program

; SEQ ID NO 28392

; LENGTH: 315

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc-feature

; OTHER INFORMATION: Incyte ID No: hu00551794

US-09-540-212A-28392

Query Match

Best Local Similarity 100.0%; Score 315; DB 24; Length 315;

Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAACACTGACTGAGATTTTAAAGAAATTAACCTTTGAGAAATAGAACAAATGAATCACTT 60  
 DB 315 TAAACACTGACTGAGATTTTAAAGAAATTAACCTTTGAGAAATAGAACAAATGAATCACTT 256

QY 61 TCTCCACCACTTAAGTATATCTCTTAGAGATCTACAGCTCCCTTTAGGGGACATACAA 120  
 DB 255 TCTCCACCACTTAAGTATATCTCTTAGAGATCTACAGCTCCCTTTAGGGGACATACAA 196

QY 121 GTCAGTTGTGTCCTTTGTGAGTCCCACTTAATTCAGATGCTATGCTATCAATTT 180  
 DB 195 GTCAGTTGTGTCCTTTGTGAGTCCCACTTAATTCAGATGCTATGCTATCAATTT 136

QY 181 TTGAATAATAGATGTGCACACATTAATCTGAGATCTACAGCTCCCTTTAGGGGACATACAA 240  
 DB 135 TTGAATAATAGATGTGCACACATTAATCTGAGATCTACAGCTCCCTTTAGGGGACATACAA 76

QY 241 CAACATTCATCCCTTTACAGAGATCATTTACTTGCAACTGAGATTAATTTGTCATGTGT 300  
 DB 75 CAACATTCATCCCTTTACAGAGATCATTTACTTGCAACTGAGATTAATTTGTCATGTGT 16

QY 301 ATTATCTACTTATGC 315  
 DB 15 ATTATCTACTTATGC 1

## RESULT 4

US-09-700-770-4

; Sequence 4, Application US/09700770

; GENERAL INFORMATION:

; APPLICANT: Yang Fel

; APPLICANT: Macina, Roberto A.

; APPLICANT: Sun, Yongming

; APPLICANT: Stuve, Laura L.

; APPLICANT: Mullaby, Sara J.

; APPLICANT: Naughton, Rebecca E.

; TITLE OF INVENTION: A Novel Method of Diagnosing, Monitoring and Staging Lung Cancer

; FILE REFERENCE: DEX-0036

; CURRENT APPLICATION NUMBER: US/09/700,770

; CURRENT FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: 60/086,212

; PRIOR FILING DATE: 1998-05-21

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 315

; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-700-770-4

Query Match

Best Local Similarity 100.0%; Score 315; DB 31; Length 315;

Best Local Similarity 100.0%; Pred. No. 4.1e-72;

Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAACACTGACTGAGATTTTAAAGAAATTAACCTTTGAGAAATAGAACAAATGAATCACTT 60  
 DB 315 TAAACACTGACTGAGATTTTAAAGAAATTAACCTTTGAGAAATAGAACAAATGAATCACTT 60

QY 61 TCTCCACCACTTAAGTATATCTCTTAGAGATCTACAGCTCCCTTTAGGGGACATACAA 120  
 DB 61 TCTCCACCACTTAAGTATATCTCTTAGAGATCTACAGCTCCCTTTAGGGGACATACAA 120

QY 121 GTCAGTTGTGTCCTTTGTGAGTCCCACTTAATTCAGATGCTATGCTATCAATTT 180  
 DB 121 GTCAGTTGTGTCCTTTGTGAGTCCCACTTAATTCAGATGCTATGCTATCAATTT 180

QY 181 TTGAATAATAGATGTGCACACATTAATCTGAGATCTACAGCTCCCTTTAGGGGACATACAA 240  
 DB 181 TTGAATAATAGATGTGCACACATTAATCTGAGATCTACAGCTCCCTTTAGGGGACATACAA 240

QY 241 CAACATTCATCCCTTTACAGAGATCATTTACTTGCAACTGAGATTAATTTGTCATGTGT 300  
 DB 241 CAACATTCATCCCTTTACAGAGATCATTTACTTGCAACTGAGATTAATTTGTCATGTGT 300

QY 301 ATTATCTACTTATGC 315  
 DB 301 ATTATCTACTTATGC 315

## RESULT 5

US-09-705-256A-3132/c

; Sequence 3132, Application US/09705256A

; GENERAL INFORMATION:

; APPLICANT: Ma, Xiao-Jun; Dotson, Stanton B.; Monsanto Company

; TITLE OF INVENTION: Tumor Associated Molecules (TAMs): Targets for diagnosis, trea

; FILE REFERENCE: 3214

; CURRENT APPLICATION NUMBER: US/09/705,256A

; CURRENT FILING DATE: 1999-05-11

; PRIOR APPLICATION NUMBER: US 60/164,285

; PRIOR FILING DATE: 1999-11-05

; NUMBER OF SEQ ID NOS: 8259

; SEQ ID NO 3132

; LENGTH: 315

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-705-256A-3132

Query Match 100.0%; Score 315; DB 31; Length 315;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-72;

Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAACACTGACTGAGATTTTAAAGAAATTAACCTTTGAGAAATAGAACAAATGAATCACTT 60  
 DB 315 TAAACACTGACTGAGATTTTAAAGAAATTAACCTTTGAGAAATAGAACAAATGAATCACTT 256

QY 61 TCTCCACCACTTAAGTATATCTCTTAGAGATCTACAGCTCCCTTTAGGGGACATACAA 120  
 DB 255 TCTCCACCACTTAAGTATATCTCTTAGAGATCTACAGCTCCCTTTAGGGGACATACAA 196

QY 121 GTCAGTTGTGTCCTTTGTGAGTCCCACTTAATTCAGATGCTATGCTATCAATTT 180  
 DB 121 GTCAGTTGTGTCCTTTGTGAGTCCCACTTAATTCAGATGCTATGCTATCAATTT 136

QY 181 TTGAATAATAGATGTGCACACATTAATCTGAGATCTACAGCTCCCTTTAGGGGACATACAA 240  
 DB 181 TTGAATAATAGATGTGCACACATTAATCTGAGATCTACAGCTCCCTTTAGGGGACATACAA 76

QY 241 CAACATTCATCCCTTTACAGAGATCATTTACTTGCAACTGAGATTAATTTGTCATGTGT 300

```

Db      75 CAACATTCATCCCTTTACAGAGATCATTTACTGCACTCAGATTAATTGTCATGTCT 16
      301 ATTATCTACTTATGC 315
      15 ATTATCTACTTATGC 1

```

# RESULT 6

```

US-60-164-285-3132/c
; Sequence 3132, Application US/60164285
; GENERAL INFORMATION:
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Tumor Associated Molecules (TAMs): Targets for diagnosis, treatme
; FILE REFERENCE: 3214
; CURRENT APPLICATION NUMBER: US/60/164,285
; CURRENT FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 8259
; SEQ ID NO 3132
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-164-285-3132

```

```

Query Match      100.0%; Score 315; DB 70; Length 315;
Best Local Similarity 100.0%; Pred. No. 4,1e-72;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 TAAACACTGACTCAGATTTTAAAGAAATTAACCTTTGAGAAATAGAAATGAATGAGTT 60
      315 TAAACACTGACTCAGATTTTAAAGAAATTAACCTTTGAGAAATAGAAATGAATGAGTT 256
      61 TCTCCACCACTTAAGTATATCTCTTAGAGATCTACACCTCCCTTTAGGGGACATACAA 120
      121 GTGAGTTGTGTCCTTTGTTGAGTCCACCTTATATTCAAGTAGAGTAGATCAATTAAT 180
      195 GTGAGTTGTGTCCTTTGTTGAGTCCACCTTATATTCAAGTAGAGTAGATCAATTAAT 136
      181 TTGAAATAGATTTGTACACAAATTAACCTGAGTTTATGAAACATCAGTAGAAGAAATA 240
      135 TTGAAATAGATTTGTACACAAATTAACCTGAGTTTATGAAACATCAGTAGAAGAAATA 76
      241 CAACATTCATCCCTTTACAGAGATCATTTACTTGAACACAGATTAATTGTCATGTCT 300
      75 CAACATTCATCCCTTTACAGAGATCATTTACTTGAACACAGATTAATTGTCATGTCT 16
      301 ATTATCTACTTATGC 315
      15 ATTATCTACTTATGC 1

```

## RESULT 7

```

US-10-016-349A-8/c
; Sequence 8, Application US/10016349A
; GENERAL INFORMATION:
; APPLICANT: Recipon, Herve
; APPLICANT: Sun, Yongming
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Liu, Chenghua
; APPLICANT: Turner, Leah
; TITLE OF INVENTION: Compositions and Methods relating to Lung Specific Genes and Prot
; FILE REFERENCE: DEX-0243
; CURRENT APPLICATION NUMBER: US/10/016,349A
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/243,459
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 244
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 532
; TYPE: DNA

```

```

; ORGANISM: Homo sapiens
US-10-016-349A-8

```

```

Query Match      100.0%; Score 315; DB 44; Length 532;
Best Local Similarity 100.0%; Pred. No. 4,7e-72;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 TAAACACTGACTCAGATTTTAAAGAAATTAACCTTTGAGAAATAGAAATGAATGAGTT 60
      315 TAAACACTGACTCAGATTTTAAAGAAATTAACCTTTGAGAAATAGAAATGAATGAGTT 256
      61 TCTCCACCACTTAAGTATATCTCTTAGAGATCTACACCTCCCTTTAGGGGACATACAA 120
      121 GTGAGTTGTGTCCTTTGTTGAGTCCACCTTATATTCAAGTAGAGTAGATCAATTAAT 180
      195 GTGAGTTGTGTCCTTTGTTGAGTCCACCTTATATTCAAGTAGAGTAGATCAATTAAT 136
      181 TTGAAATAGATTTGTACACAAATTAACCTGAGTTTATGAAACATCAGTAGAAGAAATA 240
      135 TTGAAATAGATTTGTACACAAATTAACCTGAGTTTATGAAACATCAGTAGAAGAAATA 76
      241 CAACATTCATCCCTTTACAGAGATCATTTACTTGAACACAGATTAATTGTCATGTCT 300
      75 CAACATTCATCCCTTTACAGAGATCATTTACTTGAACACAGATTAATTGTCATGTCT 16
      301 ATTATCTACTTATGC 315
      15 ATTATCTACTTATGC 1

```

## RESULT 8

```

PCT-US02-10421-2868/c
; Sequence 2868, Application PC/TUS0210421
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Wang, Tonglong
; APPLICANT: Wang, Siding
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Gaiger, Alexander
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.565PC
; CURRENT APPLICATION NUMBER: PCT/US02/10421
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 2959
; SEQ ID NO 2868
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 587..588
; OTHER INFORMATION: n = A,T,C or G
PCT-US02-10421-2868

```

```

Query Match      100.0%; Score 315; DB 1; Length 636;
Best Local Similarity 100.0%; Pred. No. 4,9e-72;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 TAAACACTGACTCAGATTTTAAAGAAATTAACCTTTGAGAAATAGAAATGAATGAGTT 60
      315 TAAACACTGACTCAGATTTTAAAGAAATTAACCTTTGAGAAATAGAAATGAATGAGTT 256
      61 TCTCCACCACTTAAGTATATCTCTTAGAGATCTACACCTCCCTTTAGGGGACATACAA 120
      121 GTGAGTTGTGTCCTTTGTTGAGTCCACCTTATATTCAAGTAGAGTAGATCAATTAAT 180
      195 GTGAGTTGTGTCCTTTGTTGAGTCCACCTTATATTCAAGTAGAGTAGATCAATTAAT 136

```

QY 181 TTGAAATAGATGTCACACAAATACTGGAGTTTATGAAACATCAGTAGAGAAATA 240  
Db 135 TTGAAATAGATGTCACACAAATACTGGAGTTTATGAAACATCAGTAGAGAAATA 76  
QY 241 CAACATTCACATCCCTTACAGAGATCTTACTGCAACCTCAGATTAATTTGTCATGCT 300  
Db 75 CAACATTCACATCCCTTACAGAGATCTTACTGCAACCTCAGATTAATTTGTCATGCT 16  
QY 301 ATTATCTACTTATGC 315  
Db 15 ATTATCTACTTATGC 1

RESULT 9  
US-10-112-699-2868/C  
; Sequence 2868, Application US/10112699  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tonglong  
; APPLICANT: Bangur, Siqing  
; APPLICANT: Gaiger, Alexander  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF CANCER  
; FILE REFERENCE: 210121.565  
; CURRENT APPLICATION NUMBER: US/10/112.699  
; CURRENT FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 2959  
; SEQ ID NO 2868  
; LENGTH: 636  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc-feature  
; LOCATION: 587, 588  
; OTHER INFORMATION: n = A,T,C or G  
US-10-112-699-2868

Query Match 100.0%; Score 315; DB 46; Length 636;  
Best Local Similarity 100.0%; Pred. No. 4.9e-72;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAACACTGACTGATTTTAAAGAAATTAACCTTTGAGAAATAGAAACAATGAATCAGT 60  
Db 315 TAAACACTGACTGATTTTAAAGAAATTAACCTTTGAGAAATAGAAACAATGAATCAGT 256  
QY 61 TCTCCACACTTAAGTATATCTCTTAGAGATCTACAGCCTCCCTTAAAGGACATACAA 120  
Db 255 TCTCCACACTTAAGTATATCTCTTAGAGATCTACAGCCTCCCTTAAAGGACATACAA 196  
QY 121 GTCAGTTGTGCTTGTGTTGAGTCCACCTTAATTCAGTAGATGACTACAAAT 180  
Db 195 GTCAGTTGTGCTTGTGTTGAGTCCACCTTAATTCAGTAGATGACTACAAAT 136  
QY 181 TTGAAATAGATGTCACACAAATACTGGAGTTTATGAAACATCAGTAGAGAAATA 240  
Db 135 TTGAAATAGATGTCACACAAATACTGGAGTTTATGAAACATCAGTAGAGAAATA 76  
QY 241 CAACATTCACATCCCTTACAGAGATCTTACTGCAACCTCAGATTAATTTGTCATGCT 300  
Db 75 CAACATTCACATCCCTTACAGAGATCTTACTGCAACCTCAGATTAATTTGTCATGCT 16  
QY 301 ATTATCTACTTATGC 315  
Db 15 ATTATCTACTTATGC 1

RESULT 10  
US-10-016-349A-9/C  
; Sequence 9, Application US/10016349A  
; GENERAL INFORMATION:  
; APPLICANT: Recipon, Herve  
; APPLICANT: Sun, Yungming  
; APPLICANT: Chen, Sel-yu

; APPLICANT: Liu, Chenghua  
; APPLICANT: Turner, Leah  
; TITLE OF INVENTION: Compositions and Methods relating to Lung Specific Genes and P  
; FILE REFERENCE: DEX-0243  
; CURRENT APPLICATION NUMBER: US/10/016.349A  
; CURRENT FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: US 60/243,459  
; PRIOR FILING DATE: 2000-10-26  
; NUMBER OF SEQ ID NOS: 244  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 705  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc-feature  
; LOCATION: (656)..(657)  
; OTHER INFORMATION: n = a, c, g or t  
US-10-016-349A-9

Query Match 100.0%; Score 315; DB 44; Length 705;  
Best Local Similarity 100.0%; Pred. No. 5.1e-72;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAACACTGACTGATTTTAAAGAAATTAACCTTTGAGAAATAGAAACAATGAATCAGT 60  
Db 384 TAAACACTGACTGATTTTAAAGAAATTAACCTTTGAGAAATAGAAACAATGAATCAGT 325  
QY 61 TCTCCACACTTAAGTATATCTCTTAGAGATCTACAGCCTCCCTTAAAGGACATACAA 120  
Db 324 TCTCCACACTTAAGTATATCTCTTAGAGATCTACAGCCTCCCTTAAAGGACATACAA 265  
QY 121 GTCAGTTGTGCTTGTGTTGAGTCCACCTTAATTCAGTAGATGACTACAAAT 180  
Db 264 GTCAGTTGTGCTTGTGTTGAGTCCACCTTAATTCAGTAGATGACTACAAAT 205  
QY 181 TTGAAATAGATGTCACACAAATACTGGAGTTTATGAAACATCAGTAGAGAAATA 240  
Db 204 TTGAAATAGATGTCACACAAATACTGGAGTTTATGAAACATCAGTAGAGAAATA 145  
QY 241 CAACATTCACATCCCTTACAGAGATCTTACTGCAACCTCAGATTAATTTGTCATGCT 300  
Db 144 CAACATTCACATCCCTTACAGAGATCTTACTGCAACCTCAGATTAATTTGTCATGCT 85  
QY 301 ATTATCTACTTATGC 315  
Db 84 ATTATCTACTTATGC 70

RESULT 11  
US-09-540-212A-5244/C  
; Sequence 5244, Application US/09540212A  
; GENERAL INFORMATION:  
; APPLICANT: Seilhamer, Jeffrey J.  
; APPLICANT: Deleage, Angelo M.  
; APPLICANT: Stuart, Susan G.  
; APPLICANT: Stuve, Laura L.  
; APPLICANT: Mullaby, Sara J.  
; APPLICANT: Naughton, Rebecca E.  
; TITLE OF INVENTION: POLYNUCLEOTIDES OF AIRWAY AND LUNG SYSTEM TISSUE  
; FILE REFERENCE: PD-1034 CIP  
; CURRENT APPLICATION NUMBER: US/09/540.212A  
; CURRENT FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 67551  
; SOFTWARE: PERL Program  
; SEQ ID NO 5244  
; LENGTH: 270  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc-feature  
; OTHER INFORMATION: Incyte ID No: hu00812997  
; NAME/KEY: unsure

LOCATION: 130  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-540-212A-5244

## Query Match

Best Local Similarity 83.2%; Score 262.2; DB 24; Length 270;  
Matches 264; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

OY 48 AATGAATCAGTTTCCACCACTTAAGATATCTCTAGAGATCTACAGCCTCCCTTTA 107
DB 268 AATGAATCAGTTTCCACCACTTAAGATATCTCTAGAGATCTACAGCCTCCCTTTA 209
OY 108 GGGGACATCAAGAGTCAGTTGTGTCCTTTGTAGTCCCACTTATATCAAGTAGT 167
DB 208 GGGGACATCAAGAGTCAGTTGTGTCCTTTGTAGTCCCACTTATATCAAGTAGT 149
OY 168 ATGACTACAAATTTGAAATAGATGTGCACACATAAAGCGAGTTATGGAACATCA 227
DB 148 ATGACTACAAATTTGAAATAGATGTGCACACATAAAGCGAGTTATGGAACATCA 89
OY 228 GTAGAAGAAATACACATTCACCCCTTACAGAGATCTTATCTGCACTGAGATA 287
DB 88 GTAGAAGAAATACACATTCACCCCTTACAGAGATCTTATCTGCACTGAGATA 29
OY 288 ATTGTCAATGTGATATCTACTATGTC 315
DB 28 ATTGTCAATGTGATATCTACTATGTC 1

```

## RESULT 12

US-09-540-212A-14244/c  
; Sequence 14244, Application US/09540212A  
; GENERAL INFORMATION:

```

; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Deleage, Angelo M.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Mullaly, Sara J.
; APPLICANT: Naughton, Rebecca E.
; TITLE OF INVENTION: POLYNUCLEOTIDES OF AIRWAY AND LUNG SYSTEM TISSUE
; FILE REFERENCE: PD-1034 CIP
; CURRENT APPLICATION NUMBER: US/09/540,212A
; NUMBER OF SEQ ID NOS: 2000-03-31
; SOFTWARE: PERL Program
; SEQ ID NO 14244
; LENGTH: 265
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc. feature
; OTHER INFORMATION: Incyte ID No: hu00144511
; NAME/KEY: unsure
; LOCATION: 233
; OTHER INFORMATION: a, t, c, g, or other
US-09-540-212A-14244

```

## Query Match

Best Local Similarity 71.3%; Score 224.6; DB 24; Length 265;  
Matches 260; Conservative 0; Mismatches 5; Indels 3; Gaps 3;

```

OY 48 AATGAATCAGTTTCCACCACTTAAGATATCTCTAGAGATCTACAGCCTCCCTTTA 107
DB 265 AATGAATCAGTTTCCACCACTTAAGATATCTCTAGAGATCTACAGCCTCCCTTTA 206
OY 108 GGGGACATCAAGAGTCAGTTGTGTCCTTTGTAGTCCCACTTATATCAAGTAGT 167
DB 205 GGGGACATCAAGAGTCAGTTGTGTCCTTTGTAGTCCCACTTATATCAAGTAGT 146
OY 168 ATGACTACAAATTTGAAATAGATGTGCACACATAAAGCGAGTTATGGAACATCA 227
DB 145 A-GACTACAAA-TTTGAAATAATGATGTGCACACATAAAGCGAGTTATGGAACATCA 88

```

```

OY 228 GTAGAAGAAATACACATTCACCCCTTACAGAGATCTTATCTGCACTGAGATA 287
DB 87 GTAG-AGGAAATACACATTCACCCCTTACAGAGATCTTATCTGCACTGAGATA 29
OY 288 ATTGTCAATGTGATATCTACTATGTC 315
DB 28 ATTGTCAATGTGATATCTACTATGTC 1

```

## RESULT 13

US-08-879-204-208

; Sequence 208, Application US/08879204  
; GENERAL INFORMATION:

```

; APPLICANT: Gooding, Douglas H.
; APPLICANT: Stuve, Laura L.
; APPLICANT: Stuart, Susan G.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Akerblom, Ingrid E.
; APPLICANT: Deleage, Angelo M.
; APPLICANT: Naughton, Rebecca E.
; APPLICANT: Klingler, Tod M.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
; NUMBER OF SEQUENCES: 2532
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304

```

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:

```

; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/020,195
; FILING DATE: JUNE 20, 1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/027,234
; FILING DATE: SEPTEMBER 27, 1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PD-0189 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 208:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; IMMEDIATE SOURCE:
; CLONE: 1472038
US-08-879-204-208

```

## Query Match

Best Local Similarity 64.8%; Score 204; DB 13; Length 204;  
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 83 CTGAGATCTACAGCCTCCCTTTAGGGGACATACAAAGTCAGTTGTGCTTGTGTTG 142
DB 1 CTGAGATCTACAGCCTCCCTTTAGGGGACATACAAAGTCAGTTGTGCTTGTGTTG 60

```







GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2003, 13:55:42 ; Search time 7285.19 Seconds

(without alignments)  
9377.568 Million cell updates/sec

Title: US-09-700-770-3

Perfect score: 2060  
Sequence: 1 ctgagagctcctaact.....ttccattgaaaaaaaaa 2060

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 33363688 seqs, 16581889874 residues

Total number of hits satisfying chosen parameters: 66727376

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Pending\_Patents\_NA\_Main:\*

1: /cgn2\_6/ptodata/2/pna/pctus\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/pna/pctus\_COMB.seq.\*  
3: /cgn2\_6/ptodata/2/pna/US06\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/pna/US07\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/pna/US08\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/pna/US081\_COMB.seq:\*  
7: /cgn2\_6/ptodata/2/pna/US082\_COMB.seq:\*  
8: /cgn2\_6/ptodata/2/pna/US083\_COMB.seq:\*  
9: /cgn2\_6/ptodata/2/pna/US084\_COMB.seq:\*  
10: /cgn2\_6/ptodata/2/pna/US085\_COMB.seq:\*  
11: /cgn2\_6/ptodata/2/pna/US086\_COMB.seq:\*  
12: /cgn2\_6/ptodata/2/pna/US087\_COMB.seq:\*  
13: /cgn2\_6/ptodata/2/pna/US088\_COMB.seq:\*  
14: /cgn2\_6/ptodata/2/pna/US089\_COMB.seq:\*  
15: /cgn2\_6/ptodata/2/pna/US090\_COMB.seq:\*  
16: /cgn2\_6/ptodata/2/pna/US091\_COMB.seq:\*  
17: /cgn2\_6/ptodata/2/pna/US092\_COMB.seq:\*  
18: /cgn2\_6/ptodata/2/pna/US092B\_COMB.seq:\*  
19: /cgn2\_6/ptodata/2/pna/US093A\_COMB.seq:\*  
20: /cgn2\_6/ptodata/2/pna/US093B\_COMB.seq:\*  
21: /cgn2\_6/ptodata/2/pna/US094\_COMB.seq:\*  
22: /cgn2\_6/ptodata/2/pna/US095A\_COMB.seq:\*  
23: /cgn2\_6/ptodata/2/pna/US095B\_COMB.seq:\*  
24: /cgn2\_6/ptodata/2/pna/US095C\_COMB.seq:\*  
25: /cgn2\_6/ptodata/2/pna/US095D\_COMB.seq:\*  
26: /cgn2\_6/ptodata/2/pna/US096A\_COMB.seq:\*  
27: /cgn2\_6/ptodata/2/pna/US096B\_COMB.seq:\*  
28: /cgn2\_6/ptodata/2/pna/US096C\_COMB.seq:\*  
29: /cgn2\_6/ptodata/2/pna/US096D\_COMB.seq:\*  
30: /cgn2\_6/ptodata/2/pna/US096E\_COMB.seq:\*  
31: /cgn2\_6/ptodata/2/pna/US097A\_COMB.seq:\*  
32: /cgn2\_6/ptodata/2/pna/US097B\_COMB.seq:\*  
33: /cgn2\_6/ptodata/2/pna/US097C\_COMB.seq:\*  
34: /cgn2\_6/ptodata/2/pna/US098A\_COMB.seq:\*  
35: /cgn2\_6/ptodata/2/pna/US098B\_COMB.seq:\*  
36: /cgn2\_6/ptodata/2/pna/US098C\_COMB.seq:\*  
37: /cgn2\_6/ptodata/2/pna/US098D\_COMB.seq:\*  
38: /cgn2\_6/ptodata/2/pna/US099A\_COMB.seq:\*  
39: /cgn2\_6/ptodata/2/pna/US099B\_COMB.seq:\*  
40: /cgn2\_6/ptodata/2/pna/US099C\_COMB.seq:\*  
41: /cgn2\_6/ptodata/2/pna/US099D\_COMB.seq:\*  
42: /cgn2\_6/ptodata/2/pna/US099E\_COMB.seq:\*  
43: /cgn2\_6/ptodata/2/pna/US099F\_COMB.seq:\*

44: /cgn2\_6/ptodata/2/pna/US100A\_COMB.seq:\*  
45: /cgn2\_6/ptodata/2/pna/US100B\_COMB.seq:\*  
46: /cgn2\_6/ptodata/2/pna/US101A\_COMB.seq:\*  
47: /cgn2\_6/ptodata/2/pna/US101B\_COMB.seq:\*  
48: /cgn2\_6/ptodata/2/pna/US102A\_COMB.seq:\*  
49: /cgn2\_6/ptodata/2/pna/US102B\_COMB.seq:\*  
50: /cgn2\_6/ptodata/2/pna/US103A\_COMB.seq:\*  
51: /cgn2\_6/ptodata/2/pna/US103B\_COMB.seq:\*  
52: /cgn2\_6/ptodata/2/pna/US104B\_COMB.seq:\*  
53: /cgn2\_6/ptodata/2/pna/US104C\_COMB.seq:\*  
54: /cgn2\_6/ptodata/2/pna/US600\_COMB.seq:\*  
55: /cgn2\_6/ptodata/2/pna/US6001\_COMB.seq:\*  
56: /cgn2\_6/ptodata/2/pna/US6002\_COMB.seq:\*  
57: /cgn2\_6/ptodata/2/pna/US6003\_COMB.seq:\*  
58: /cgn2\_6/ptodata/2/pna/US6004\_COMB.seq:\*  
59: /cgn2\_6/ptodata/2/pna/US6005\_COMB.seq:\*  
60: /cgn2\_6/ptodata/2/pna/US6006\_COMB.seq:\*  
61: /cgn2\_6/ptodata/2/pna/US6007\_COMB.seq:\*  
62: /cgn2\_6/ptodata/2/pna/US6008\_COMB.seq:\*  
63: /cgn2\_6/ptodata/2/pna/US6009\_COMB.seq:\*  
64: /cgn2\_6/ptodata/2/pna/US6010\_COMB.seq:\*  
65: /cgn2\_6/ptodata/2/pna/US6011\_COMB.seq:\*  
66: /cgn2\_6/ptodata/2/pna/US6012\_COMB.seq:\*  
67: /cgn2\_6/ptodata/2/pna/US6013\_COMB.seq:\*  
68: /cgn2\_6/ptodata/2/pna/US6014\_COMB.seq:\*  
69: /cgn2\_6/ptodata/2/pna/US6015\_COMB.seq:\*  
70: /cgn2\_6/ptodata/2/pna/US6016\_COMB.seq:\*  
71: /cgn2\_6/ptodata/2/pna/US6017\_COMB.seq:\*  
72: /cgn2\_6/ptodata/2/pna/US6018\_COMB.seq:\*  
73: /cgn2\_6/ptodata/2/pna/US6019\_COMB.seq:\*  
74: /cgn2\_6/ptodata/2/pna/US6020\_COMB.seq:\*  
75: /cgn2\_6/ptodata/2/pna/US6021\_COMB.seq:\*  
76: /cgn2\_6/ptodata/2/pna/US6022\_COMB.seq:\*  
77: /cgn2\_6/ptodata/2/pna/US6023A\_COMB.seq:\*  
78: /cgn2\_6/ptodata/2/pna/US6023B\_COMB.seq:\*  
79: /cgn2\_6/ptodata/2/pna/US6024\_COMB.seq:\*  
80: /cgn2\_6/ptodata/2/pna/US6025\_COMB.seq:\*  
81: /cgn2\_6/ptodata/2/pna/US6026\_COMB.seq:\*  
82: /cgn2\_6/ptodata/2/pna/US6027\_COMB.seq:\*  
83: /cgn2\_6/ptodata/2/pna/US6028\_COMB.seq:\*  
84: /cgn2\_6/ptodata/2/pna/US6029\_COMB.seq:\*  
85: /cgn2\_6/ptodata/2/pna/US6030\_COMB.seq:\*  
86: /cgn2\_6/ptodata/2/pna/US6031\_COMB.seq:\*  
87: /cgn2\_6/ptodata/2/pna/US6032\_COMB.seq:\*  
88: /cgn2\_6/ptodata/2/pna/US6033\_COMB.seq:\*  
89: /cgn2\_6/ptodata/2/pna/US6034\_COMB.seq:\*  
90: /cgn2\_6/ptodata/2/pna/US6035\_COMB.seq:\*  
91: /cgn2\_6/ptodata/2/pna/US6036\_COMB.seq:\*  
92: /cgn2\_6/ptodata/2/pna/US6037\_COMB.seq:\*  
93: /cgn2\_6/ptodata/2/pna/US6038\_COMB.seq:\*  
94: /cgn2\_6/ptodata/2/pna/US6039\_COMB.seq:\*  
95: /cgn2\_6/ptodata/2/pna/US6040\_COMB.seq:\*  
96: /cgn2\_6/ptodata/2/pna/US6041\_COMB.seq:\*  
97: /cgn2\_6/ptodata/2/pna/US6042\_COMB.seq:\*  
98: /cgn2\_6/ptodata/2/pna/US6043\_COMB.seq:\*  
99: /cgn2\_6/ptodata/2/pna/US6044\_COMB.seq:\*  
100: /cgn2\_6/ptodata/2/pna/US6045\_COMB.seq:\*  
101: /cgn2\_6/ptodata/2/pna/US6046\_COMB.seq:\*  
102: /cgn2\_6/ptodata/2/pna/US6047\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2060	100.0	2060	1	PCT-US99-10344-3
2	2060	100.0	2060	2	PCT-US99-10344-3
3	2060	100.0	2060	31	US-09-700-770-3
4	2060	100.0	2061	28	US-09-659-151-16





Db	781	CCACACTGATATCCCATCCCTCTTCATCGATGATCCAACTGGACAGGACCACTTAACCTTAC	840
QY	841	TGAGGGGATGAGAGAAACCAAGAGACTCTCCCAAGTTGGGAGCCCAATCCCTGGGAGCA	900
Db	841	TGAGGGGATGAGAGAAACCAAGAGACTCTCCCAAGTTGGGAGCCCAATCCCTGGGAGCA	900
QY	901	AGCCATCTTCTTACCTCTCTCCAGATGACAGGATGTGAGTATTTTGGGAAATTTGGG	960
Db	901	AGCCATCTTCTTACCTCTCTCCAGATGACAGGATGTGAGTATTTTGGGAAATTTGGG	960
QY	961	TGGGAACGGCTCCACAAAACCTTACCTGTTGCCCTTTGACACTGGCTCTCAATCTCTGGG	1020
Db	961	TGGGAACGGCTCCACAAAACCTTACCTGTTGCCCTTTGACACTGGCTCTCAATCTCTGGG	1020
QY	1021	TCCCGTCAGAGATGCGCACTTCTTCAGTGAGTGCCCGAGTTCACCAACCAATTTGATC	1080
Db	1021	TCCCGTCAGAGATGCGCACTTCTTCAGTGAGTGCCCGAGTTCACCAACCAATTTGATC	1080
QY	1081	CCAAAGCCCTAGCTCTTCCAGGCCAATGGAGCAAGTTTGCAATATGAACTG	1140
Db	1081	CCAAAGCCCTAGCTCTTCCAGGCCAATGGAGCAAGTTTGCAATATGAACTG	1140
QY	1141	GGCGGGTATATGAATTCCTGACGAGGAAACACTGACTATTTGGTGAATCAAGGTCAT	1200
Db	1141	GGCGGGTATATGAATTCCTGACGAGGAAACACTGACTATTTGGTGAATCAAGGTCAT	1200
QY	1201	CAGTATTTTCGGGAGGCTCTCTGGAGCCAGCTGCTCTCGTTTGGCCATTTTG	1260
Db	1201	CAGTATTTTCGGGAGGCTCTCTGGAGCCAGCTGCTCTCGTTTGGCCATTTTG	1260
QY	1261	ATGGGATATTTGGGCGCTTGTCCCATCTCTGTGTGAGAGAGTTGGGCCCCGATGG	1320
Db	1261	ATGGGATATTTGGGCGCTTGTCCCATCTCTGTGTGAGAGAGTTGGGCCCCGATGG	1320
QY	1321	ATGTACTGTGAGAGAGGGGCTATTTGATTAAGCCGTCTTCCCTTTTAACTCAACAGGG	1380
Db	1321	ATGTACTGTGAGAGAGGGGCTATTTGATTAAGCCGTCTTCCCTTTTAACTCAACAGGG	1380
QY	1381	ACCTGAAAGAGCTTATGAGAGAGAGCTGTCTTGGGGGCTGGAGACCGGCACTACA	1440
Db	1381	ACCTGAAAGAGCTTATGAGAGAGAGCTGTCTTGGGGGCTGGAGACCGGCACTACA	1440
QY	1441	TCCACCCCTCACTCTGTGCAGTACAGGATCCCGCTACGTGAGAGATCCCAATGGAGC	1500
Db	1441	TCCACCCCTCACTCTGTGCAGTACAGGATCCCGCTACGTGAGAGATCCCAATGGAGC	1500
QY	1501	GTGTGAAGTGGGCCAGGGCTGACTCTGTGCGCAAGGGCTGTCTGCATTCGTGATA	1560
Db	1501	GTGTGAAGTGGGCCAGGGCTGACTCTGTGCGCAAGGGCTGTCTGCATTCGTGATA	1560
QY	1561	CGGGAGCTTCCCTATATCAGAGACCAATGAGAGATTCGGGGCTTCGATGACGCAATTG	1620
Db	1561	CGGGAGCTTCCCTATATCAGAGACCAATGAGAGATTCGGGGCTTCGATGACGCAATTG	1620
QY	1621	GGGGAATCCCTTGTGGCTGGGAGTACATATCTGTCTGGGAAATCCCAAAGCTCC	1680
Db	1621	GGGGAATCCCTTGTGGCTGGGAGTACATATCTGTCTGGGAAATCCCAAAGCTCC	1680
QY	1681	CCGAGATCTCTTCTTGTGGGGGCTGTGTTTAACTCAGGAGCCCATATTAACGTCA	1740
Db	1681	CCGAGATCTCTTCTTGTGGGGGCTGTGTTTAACTCAGGAGCCCATATTAACGTCA	1740
QY	1741	TCCAGACTACTGAAATGAGCGTCCGCTCTCTGTCCGGTTTCCAGGCGCTGATGTCC	1800
Db	1741	TCCAGACTACTGAAATGAGCGTCCGCTCTCTGTCCGGTTTCCAGGCGCTGATGTCC	1800
QY	1801	CTCGCGCTGACAGGCGCTTCTGATTCCTCGGTGACGTCTTCTTGGGAGCATGTGGCG	1860
Db	1801	CTCGCGCTGACAGGCGCTTCTGATTCCTCGGTGACGTCTTCTTGGGAGCATGTGGCG	1860
QY	1861	TCTTCACCGGGGACATGAAGCAGGCGCGGGTGGGCTGAGCGCGCTGGCACTC	1920
Db	1861	TCTTCACCGGGGACATGAAGCAGGCGCGGGTGGGCTGAGCGCGCTGGCACTC	1920

Db	1861	TTCTTCGACCCGGGGGACATGAGAGCAGACGCCCGGGGTGGGCGTGGCGGCTTCGCACTC	1920
Qy	1921	GCGGAGCGGACCTTCGATGTGGGAGAGACTCGCAGCGGCATTTCCCGGGGTGAGCGCCAA	1980
Db	1921	GCGGAGCGGACCTTCGATGTGGGAGAGACTCGCAGCGGCATTTCCCGGGGTGAGCGCCAA	1980
Qy	1981	GTGAAGCGCATCGCCAGCGGGTGTCCGCGAGGTCTGCTAACCAGTAAAAATTCACATAT	2040
Db	1981	GTGAAGCGCATCGCCAGCGGGTGTCCGCGAGGTCTGCTAACCAGTAAAAATTCACATAT	2040
Qy	2041	TTCCATGTAAAAAATTTTTTTTTT	2060
Db	2041	TTCCATGTAAAAAATTTTTTTTTT	2060

```

RESULT 3
US-09-700-770-3
: Sequence 3, Application US/09700770
: GENERAL INFORMATION:
: APPLICANT: Yang Fei
: APPLICANT: Macina, Roberto A.
: TITLE OF INVENTION: A Novel Method of Diagnosing, Monitoring and Staging Lung Canc
: FILE REFERENCE: DEX-0036
: CURRENT APPLICATION NUMBER: US/09/700,770
: CURRENT FILING DATE: 2000-11-20
: PRIOR APPLICATION NUMBER: 60/086,212
: PRIOR FILING DATE: 1998-05-21
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 3
: LENGTH: 2060
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-700-770-3

```

Query Match	100.0%;	Score 2060;	DB 31,	Length 2060;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2060;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CTTGAGAGCTCTCAAAATACTTGGTCATGATGAGAACCCGACCGAATACTGATATGATGATTT	60	
DB	1	CTTGAGAGCTCTCAAAATACTTGGTCATGATGAGAACCCGACCGAATACTGATATGATGATTT	60	
QY	61	TGAGACAGAGGTGGACAAGGCTCGAAGATCGGAAAACATTCCTCTTCTCTGCCACCATGAC	120	
DB	61	TGAGACAGAGGTGGACAAGGCTCGAAGATCGGAAAACATTCCTCTTCTCTGCCACCATGAC	120	
QY	121	CAAGAAAGGTCAAAAACCTTCAGCGAGAGCGCTCGAACAATCTGTGAATATGTCGCGTTTC	180	
DB	121	CAAGAAAGGTCAAAAACCTTCAGCGAGAGCGCTCGAACAATCTGTGAATATGTCGCGTTTC	180	
QY	181	CTCTAAATNCCACACAGGTTGAAAAATATACGCAATATATATTTTATTCCTCTAAATT	240	
DB	181	CTCTAAATNCCACACAGGTTGAAAAATATACGCAATATATATTTTATTCCTCTAAATT	240	
QY	241	CAAGATACCTACCTGGTTTATATTTCTTAATGAAATGGCTGGAACCCCTTATGATATT	300	
DB	241	CAAGATACCTACCTGGTTTATATTTCTTAATGAAATGGCTGGAACCCCTTATGATATT	300	
QY	301	CTGCACACCTCTGAATTAATTAACCCACAGAACACGCTTGGTCTACTGCGAAATCTTGGCTTAC	360	
DB	301	CTGCACACCTCTGAATTAATTAACCCACAGAACACGCTTGGTCTACTGCGAAATCTTGGCTTAC	360	
QY	361	TGCGATCCCCCTCCATGAGCAATAGATGAGATGAAGCGCTTAGAGTCCCTTATATAAGTT	420	
DB	361	TGCGATCCCCCTCCATGAGCAATAGATGAGATGAAGCGCTTAGAGTCCCTTATATAAGTT	420	
QY	421	TAAAGCGAAGGCGCGTTCATCTTCTAGCACTGACGTTGCCAGCCGAGGTTTGACAT	480	
DB	421	TAAAGCGAAGGCGCGTTCATCTTCTAGCACTGACGTTGCCAGCCGAGGTTTGACAT	480	
QY	481	ACCTCATGTAGATGTGGTTGTCAACTTGTACATCTCTACCCAAATCCAAAGATATACATCCA	540	





; INFORMATION FOR SEQ ID NO: 16:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2061 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: LUNGA5T01  
 ; CLONE: 877617  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 16 :  
 ; US-09-659-151-16

Query Match 100.0%; Score 2060; DB 28; Length 2061;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 2060; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGAGCTCTCAAAATCTGTCATGTGATGAAGCCGACCCGAATCTGAATGTGATTT 60  
 Db 1 CTGAGAGCTCTCAAAATCTGTCATGTGATGAAGCCGACCCGAATCTGAATGTGATTT 60  
 QY 61 TGAAGACAGAGTTGACAGCCCTGAGATGGAAGAACATTCCTTCTGCGACCATGAC 120  
 Db 61 TGAAGACAGAGTTGACAGCCCTGAGATGGAAGAACATTCCTTCTGCGACCATGAC 120  
 QY 121 CAAGAAGTTCAAAAATCTCAGAGACGCTGGAAGATCCGTGAAATGTGCGGTTTC 180  
 Db 121 CAAGAAGTTCAAAAATCTCAGAGACGCTGGAAGATCCGTGAAATGTGCGGTTTC 180  
 QY 181 CTCCTAATAACAGACAGTGAATAATACAGCAATATATATTTTATTCCTCTAAT 240  
 Db 181 CTCCTAATAACAGACAGTGAATAATACAGCAATATATATTTTATTCCTCTAAT 240  
 QY 241 CAAGATACCTACCGTGTATATCTAATGATTTGGCTGGAACCTCTTATGATAT 300  
 Db 241 CAAGATACCTACCGTGTATATCTAATGATTTGGCTGGAACCTCTTATGATAT 300  
 QY 301 CTGACAGACCTTAATTAATACCAGAGACAGCTTTGCTACTGCGAAATCTTGCGTTAC 360  
 Db 301 CTGACAGACCTTAATTAATACCAGAGACAGCTTTGCTACTGCGAAATCTTGCGTTAC 360  
 QY 361 TGCCATCCCCCTCCATGAGCAATATGTCAGATGAAGCGCTAGATCCCTTAATAGTT 420  
 Db 361 TGCCATCCCCCTCCATGAGCAATATGTCAGATGAAGCGCTAGATCCCTTAATAGTT 420  
 QY 421 TAAGGCCAAGGCCGCTTCATCTCTAAGCAATGACGCTGCGACCCGAGGTTTGAAT 480  
 Db 421 TAAGGCCAAGGCCGCTTCATCTCTAAGCAATGACGCTGCGACCCGAGGTTTGAAT 480  
 QY 481 ACCTATGTAGATGTGTTGTCAACTTTCACATTCCTACCCATTCAGAGATTAATCCA 540  
 Db 481 ACCTATGTAGATGTGTTGTCAACTTTCACATTCCTACCCATTCAGAGATTAATCCA 540  
 QY 541 TCGAGTAGTAGAAGCTAGAGCTGAGGCGCTCCGGAAGAGCTATTTTGTACACA 600  
 Db 541 TCGAGTAGTAGAAGCTAGAGCTGAGGCGCTCCGGAAGAGCTATTTTGTACACA 600  
 QY 601 GTATGATGTGAACCTCTTCAGCGCATAGAACACTTAATTTGGAAGAACTACCGAGTT 660  
 Db 601 GTATGATGTGAACCTCTTCAGCGCATAGAACACTTAATTTGGAAGAACTACCGAGTT 660  
 QY 661 TTCGAACACAGATATGAGTTATGATGCTACAGAACAGCGTCCCGACGATGTCTCAC 720  
 Db 661 TTCGAACACAGATATGAGTTATGATGCTACAGAACAGCGTCCCGACGATGTCTCAC 720  
 QY 721 CACGCGTGTCAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
 Db 721 CACGCGTGTCAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
 QY 781 CCACACTGATCCGATCCCTTCTCATGAGTCAAACTGACGAGAGACCTGTAACCTAC 840  
 Db 781 CCACACTGATCCGATCCCTTCTCATGAGTCAAACTGACGAGAGACCTGTAACCTAC 840  
 QY 841 TGAAGGATGAGAAACAGACAGCTCCCAAGATTGGGGGCCCATCCCTCGGGGACA 900

Db 841 TGAAGGATGAGAAACAGACAGAGCTCCCAAGTTGGGGGCCCATCCCTCGGGGACA 900  
 QY 901 AGCCATCTTCTGACCTCTCTGAACTACAGGATGTGAGATTTTGGGAAATTTGGGC 960  
 Db 901 AGCCATCTTCTGACCTCTCTGAACTACAGGATGTGAGATTTTGGGAAATTTGGGC 960  
 QY 961 TGGGAACGCTCCACAAAATCTCAGTGTGCTTTGACACTGGCTCTCCAAATCTCTGG 1020  
 Db 961 TGGGAACGCTCCACAAAATCTCAGTGTGCTTTGACACTGGCTCTCCAAATCTCTGG 1020  
 QY 1021 TCCCGTCCAGAGATGCGCACTTCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
 Db 1021 TCCCGTCCAGAGATGCGCACTTCTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
 QY 1081 CCAAAAGCTCTAGCTCTCTCCAGGCCAATGGGACCAAGTTTGCCTCAATATGAACTG 1140  
 Db 1081 CCAAAAGCTCTAGCTCTCTCCAGGCCAATGGGACCAAGTTTGCCTCAATATGAACTG 1140  
 QY 1141 GCGGATGATGGAATCCGAGAGCAAGGCAAGCTACTATTTGATGATCAAGGTGCAT 1200  
 Db 1141 GCGGATGATGGAATCCGAGAGCAAGGCAAGCTACTATTTGATGATCAAGGTGCAT 1200  
 QY 1201 CAGTATTTTGGGAGAGCTCTCTGAGAGCCAGCCTGCTGCTTTGCGCTTTGCGCTTTG 1260  
 Db 1201 CAGTATTTTGGGAGAGCTCTCTGAGAGCCAGCCTGCTGCTTTGCGCTTTGCGCTTTG 1260  
 QY 1261 ATGGATATTTGGGCTCGGTTTCCCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320  
 Db 1261 ATGGATATTTGGGCTCGGTTTCCCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320  
 QY 1321 ATGACTGATGAGAGAGGCTATTTGATTAAGCCTGCTTCTCTTACTTACCTCAACAGG 1380  
 Db 1321 ATGACTGATGAGAGAGGCTATTTGATTAAGCCTGCTTCTCTTACTTACCTCAACAGG 1380  
 QY 1381 ACCCGAAGAGCTGATGAGAGAGAGCTGTCTGAGGAGGCTGAGACCCGACACTACA 1440  
 Db 1381 ACCCGAAGAGCTGATGAGAGAGAGCTGTCTGAGGAGGCTGAGACCCGACACTACA 1440  
 QY 1441 TCCCAACCCCTACCTGCTGCGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500  
 Db 1441 TCCCAACCCCTACCTGCTGCGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500  
 QY 1501 GTGTGAAGTGGGCCAGGCTGACTCTCTGTGCAAGAGGCTGTGCTGCTGCTGCTGCTG 1560  
 Db 1501 GTGTGAAGTGGGCCAGGCTGACTCTCTGTGCAAGAGGCTGTGCTGCTGCTGCTGCTG 1560  
 QY 1561 CGGCAAGTCCCTCATCAAGAGACCACTGAGAGATCCGAGGCTGCTGCTGCTGCTGCTG 1620  
 Db 1561 CGGCAAGTCCCTCATCAAGAGACCACTGAGAGATCCGAGGCTGCTGCTGCTGCTGCTG 1620  
 QY 1621 GGGGAATCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
 Db 1621 GGGGAATCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
 QY 1681 CCGAGTCTCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740  
 Db 1681 CCGAGTCTCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740  
 QY 1741 TCCAGACTACTCGAATAGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800  
 Db 1741 TCCAGACTACTCGAATAGGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800  
 QY 1801 CTCGCTGACAGGAGGCTCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860  
 Db 1801 CTCGCTGACAGGAGGCTCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860  
 QY 1861 TCTTCAAGCCGCGGAGATCAAGAGAGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920  
 Db 1861 TCTTCAAGCCGCGGAGATCAAGAGAGCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920  
 QY 1921 GCGAGCGGAGCTCGGATGAGGAGAGCTGCGAGGCGAGTTCCCGGGTGAAGGCCAA 1980



Db 1921 GCGGAGCGGACCTCGGATGGGAGAGACTGCCGACAGTCCCGGGGTGAGGCCCA 1980  
 QY 1981 GTGAAGCGCATGCGAGCGGGTGTGCGGAGAGTCTGTACCCAGTAAATTCACAT 2040  
 Db 1981 GTGAAGCGCATGCGAGCGGGTGTGCGGAGAGTCTGTACCCAGTAAATTCACAT 2040  
 QY 2041 TTCATTTGAAAAAATAA 2060  
 Db 2041 TTCATTTGAAAAAATAA 2060

## RESULT 5

US-09-968-415-16

Sequence 16, Application US/09968415

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

Yue, Henry

Guebler, Karl J.

Corley, Neil C.

Tang, Tom Y.

Shah, Puryl

TITLE OF INVENTION: HUMAN PROTEASE MOLECULES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Dr.

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/968,415

FILING DATE: 26-Sep-2001

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 09/659,151

FILING DATE: &lt;unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Mohan-Peterson, Sheela

REGISTRATION NUMBER: 41,201

REFERENCE/DOCKET NUMBER: PF-0458 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 2061 base pairs.

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: LUNCAST01

CLONE: 877617

SEQUENCE DESCRIPTION: SEQ ID NO: 16 :

US-09-968-415-16

Query Match 100.0%; Score 2060; DB 42; Length 2061;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2060; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGAGAGCTCTCAAACTCTGTCATGATGAGGAGCGGACCGCATATGATGAT 60  
 Db 1 CTGAGAGCTCTCAAACTCTGTCATGATGAGGAGCGGACCGCATATGATGAT 60  
 QY 61 TGAGAGAGGTTGACAGAGCTCGAGATCGGAAAAATCTCTCTCTGACCATGAC 120  
 Db 61 TGAGAGAGGTTGACAGAGCTCGAGATCGGAAAAATCTCTCTCTGACCATGAC 120

QY 121 CAAGAAGTTTCAAAAATCTCAGCGAGAGCTGTGAAGATCCTGTGAATGTGCCGTTTC 180  
 Db 121 CAAGAAGTTTCAAAAATCTCAGCGAGAGCTGTGAAGATCCTGTGAATGTGCCGTTTC 180  
 QY 181 GTCTAAATACGACAGAGTTGAAAAATACAGCAATTTATTTTATTCCTCTTAAT 240  
 Db 181 GTCTAAATACGACAGAGTTGAAAAATACAGCAATTTATTTTATTCCTCTTAAT 240  
 QY 241 CAAGATTAACCTACCTGGTTATATCTAATGAATGGGTGGAATCCTTATGATAT 300  
 Db 241 CAAGATTAACCTACCTGGTTATATCTAATGAATGGGTGGAATCCTTATGATAT 300  
 QY 301 CTGACAGACCTGTAAATATACCGAGAAACAGCTTGTACTGCAAAATCTTGCTTAC 360  
 Db 301 CTGACAGACCTGTAAATATACCGAGAAACAGCTTGTACTGCAAAATCTTGCTTAC 360  
 QY 361 TGCCATCCCCCTCCATGAGCAAAATGATGAGTAAGCCGCTAAGATTCCTTAATAG 420  
 Db 361 TGCCATCCCCCTCCATGAGCAAAATGATGAGTAAGCCGCTAAGATTCCTTAATAG 420  
 QY 421 TAAGCCAAAGGCCGTTCCATTTCTTACCACTGACAGTTCGCAAGGAGTTGACAT 480  
 Db 421 TAAGCCAAAGGCCGTTCCATTTCTTACCACTGACAGTTCGCAAGGAGTTGACAT 480  
 QY 481 ACCTCATGTAGATGTGGTGTCAACTTTCATTTCCATCCATTCAGAGATTAATCCA 540  
 Db 481 ACCTCATGTAGATGTGGTGTCAACTTTCATTTCCATCCATTCAGAGATTAATCCA 540  
 QY 541 TCAGTAGTGTGAAGAGCTAGAGCTGGGCGCTCCGAAAGGCTATTTCTTACACA 600  
 Db 541 TCAGTAGTGTGAAGAGCTAGAGCTGGGCGCTCCGAAAGGCTATTTCTTACACA 600  
 QY 601 GTATGATGTGAAGCTCTCCAGGCAATGAACTTAATTTGGGAAGAACTACAGGTT 660  
 Db 601 GTATGATGTGAAGCTCTCCAGGCAATGAACTTAATTTGGGAAGAACTACAGGTT 660  
 QY 661 TCCAAACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
 Db 661 TCCAAACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720  
 QY 721 CACCGCTGTGCAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
 Db 721 CACCGCTGTGCAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
 QY 781 CCACACTGATCCGATCCCTCTTATGATGATGATGATGATGATGATGATGATGATGAT 840  
 Db 781 CCACACTGATCCGATCCCTCTTATGATGATGATGATGATGATGATGATGATGATGAT 840  
 QY 841 TGAAGGATGAG 900  
 Db 841 TGAAGGATGAG 900  
 QY 901 AGCCATCTTCTGATCTCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 960  
 Db 901 AGCCATCTTCTGATCTCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 960  
 QY 961 TGGAAGGCTTCACAAAATCTTCACTGCTTGGACACTGCTCTCTCAATCTCTGAG 1020  
 Db 961 TGGAAGGCTTCACAAAATCTTCACTGCTTGGACACTGCTCTCTCAATCTCTGAG 1020  
 QY 1021 TCCGTCAG 1080  
 Db 1021 TCCGTCAG 1080  
 QY 1081 CCAAGGCTTCTGATCTCTTCCAGGCAATGAGCAATTTGTCATTAATATGAACTG 1140  
 Db 1081 CCAAGGCTTCTGATCTCTTCCAGGCAATGAGCAATTTGTCATTAATATGAACTG 1140  
 QY 1141 GCGGGTAG 1200  
 Db 1141 GCGGGTAG 1200  
 QY 1201 CAGTATTTTGGGGAGGCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260

Db 1201 CAGTATTTGGGGAGGCTCTCTGAGACCAGCTGCTCTTCCCTTTGGCCATTTTG 1260  
 Qy 1261 ATGGATATTTGGGCTCGGTTTTCCTATCTCTCTGTGAAGAGTTGGCCCGGATGG 1320  
 Db 1261 ATGGATATTTGGGCTCGGTTTTCCTATCTCTCTGTGAAGAGTTGGCCCGGATGG 1320  
 Qy 1321 ATGACTGTGAGAGAGGAGGCTATTTGATTAAGCTGTCTCTCTTTTACCTCAACAGG 1380  
 Db 1321 ATGACTGTGAGAGAGGAGGCTATTTGATTAAGCTGTCTCTCTTTTACCTCAACAGG 1380  
 Qy 1381 ACCCTGAAGAGCTGTGAAGAGAGAGTGTCTGTGGGGGCTGGACCCGGGACACTACA 1440  
 Db 1381 ACCCTGAAGAGCTGTGAAGAGAGAGTGTCTGTGGGGGCTGGACCCGGGACACTACA 1440  
 Qy 1441 TCCACCCCTCACCTCTGTGAGAGAGTGTCTGTGGGGGCTGGACCCGGGACACTACA 1440  
 Db 1441 TCCACCCCTCACCTCTGTGAGAGAGTGTCTGTGGGGGCTGGACCCGGGACACTACA 1440  
 Qy 1501 GTGTGAAGTGGGGCCAGAGGCTGTCTGTGCAAGAGGCTGTCTGTGCAAGAGGCTGTG 1500  
 Db 1501 GTGTGAAGTGGGGCCAGAGGCTGTCTGTGCAAGAGGCTGTCTGTGCAAGAGGCTGTG 1500  
 Qy 1561 CGGGACAGTCCCTCTATCAAGAGAGAGTGTCTGTGCAAGAGGCTGTCTGTGCAAGAGG 1560  
 Db 1561 CGGGACAGTCCCTCTATCAAGAGAGAGTGTCTGTGCAAGAGGCTGTCTGTGCAAGAGG 1560  
 Qy 1621 GGGGAATCCCTTCTGTGAGAGAGTGTCTGTGCAAGAGGCTGTCTGTGCAAGAGGCTGTG 1620  
 Db 1621 GGGGAATCCCTTCTGTGAGAGAGTGTCTGTGCAAGAGGCTGTCTGTGCAAGAGGCTGTG 1620  
 Qy 1681 CCGCAGTCTCTCTCTCTGTGAGAGAGTGTCTGTGCAAGAGGCTGTCTGTGCAAGAGGCTGTG 1680  
 Db 1681 CCGCAGTCTCTCTCTCTGTGAGAGAGTGTCTGTGCAAGAGGCTGTCTGTGCAAGAGGCTGTG 1680  
 Qy 1741 TCCAGACTACTGAAATGAGGCTGTCTGTGCAAGAGGCTGTCTGTGCAAGAGGCTGTGCA 1740  
 Db 1741 TCCAGACTACTGAAATGAGGCTGTCTGTGCAAGAGGCTGTCTGTGCAAGAGGCTGTGCA 1740  
 Qy 1801 CTCCGCTCTGAGAGGCTGTCTGTGCAAGAGGCTGTCTGTGCAAGAGGCTGTCTGTGCAAG 1800  
 Db 1801 CTCCGCTCTGAGAGGCTGTCTGTGCAAGAGGCTGTCTGTGCAAGAGGCTGTCTGTGCAAG 1800  
 Qy 1861 TCTTCGAGCGGGGGGACATGAAGAGAGGCTGTCTGTGCAAGAGGCTGTCTGTGCAAGAGG 1860  
 Db 1861 TCTTCGAGCGGGGGGACATGAAGAGAGGCTGTCTGTGCAAGAGGCTGTCTGTGCAAGAGG 1860  
 Qy 1921 GCGGAGCGGAGCTGTGAGAGAGGCTGTCTGTGCAAGAGGCTGTCTGTGCAAGAGGCTGTG 1920  
 Db 1921 GCGGAGCGGAGCTGTGAGAGAGGCTGTCTGTGCAAGAGGCTGTCTGTGCAAGAGGCTGTG 1920  
 Qy 1981 GTGAAGCGGAGCTGTGAGAGAGGCTGTCTGTGCAAGAGGCTGTCTGTGCAAGAGGCTGTG 1980  
 Db 1981 GTGAAGCGGAGCTGTGAGAGAGGCTGTCTGTGCAAGAGGCTGTCTGTGCAAGAGGCTGTG 1980  
 Qy 2041 TTCCATTGAAAAA 2060  
 Db 2041 TTCCATTGAAAAA 2060  
 Qy 2041 TTCCATTGAAAAA 2060  
 Db 2041 TTCCATTGAAAAA 2060

RESULT 6  
 US-10-180-719-16  
 Sequence 16, Application US/10180719  
 GENERAL INFORMATION:  
 APPLICANT: Bandman, Olga  
 Hillman, Jennifer L.  
 Yue, Henry  
 Guegler, Karl J.  
 Corley, Neil C.  
 Tang, Tom Y.  
 Shah, Puri  
 TITLE OF INVENTION: HUMAN PROTEASE MOLECULES  
 NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Dr.  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/180,719  
 FILING DATE: 25-Jun-2002  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/008,271  
 FILING DATE: 16-Jan-1998  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mohan-Peterson, Sheela  
 REGISTRATION NUMBER: 41,201  
 REFERENCE/DOCKET NUMBER: PF-0458 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-855-0555  
 TELEFAX: 650-845-4166  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2061 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: LUNGAST01  
 CLONE: 877617  
 SEQUENCE DESCRIPTION: SEQ ID NO: 16 :  
 US-10-180-719-16  
 Query Match 100.0%; Score 2060; DB 47; Length 2061;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2060; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 CTTGAGAGCTCTCAAAATCTGTGATGATGAGAGCCGACCGAATAGTGAATATGATTT 60  
 Qy 1 CTTGAGAGCTCTCAAAATCTGTGATGATGAGAGCCGACCGAATAGTGAATATGATTT 60  
 Db 61 TGAGACAGAGGTTGACAAAGCTCGAGATCGGAAACATTCCTCTCTCTGCGACCATGAC 120  
 Qy 61 TGAGACAGAGGTTGACAAAGCTCGAGATCGGAAACATTCCTCTCTCTGCGACCATGAC 120  
 Db 121 CAAGAAGGTTCAAAACCTTAGCGAGAGCTGTGAAGATCTGTGAATATGATTTATTTATTT 180  
 Qy 121 CAAGAAGGTTCAAAACCTTAGCGAGAGCTGTGAAGATCTGTGAATATGATTTATTTATTT 180  
 Db 181 CTCTAAATACAGACAGTGAAGAAATTAAGCAATATTAATTTATTTATTTATTTATTT 240  
 Qy 181 CTCTAAATACAGACAGTGAAGAAATTAAGCAATATTAATTTATTTATTTATTTATTT 240  
 Db 241 CAGGATACCTACCTGTTTATATCTTAATGAATGCTGGAATCTCTTATATGATTT 300  
 Qy 241 CAGGATACCTACCTGTTTATATCTTAATGAATGCTGGAATCTCTTATATGATTT 300  
 Db 301 CTGAGACCTCTGTAATATATACAGAGAAAGCTTTGCTACTGGAATCTTGGCTTAC 360  
 Qy 301 CTGAGACCTCTGTAATATATACAGAGAAAGCTTTGCTACTGGAATCTTGGCTTAC 360  
 Db 361 TGGCATCCCTCCATAGAGAAATGATCAGAGTGAAGAGGCTGAGATCCCTTATATAGT 420  
 Qy 361 TGGCATCCCTCCATAGAGAAATGATCAGAGTGAAGAGGCTGAGATCCCTTATATAGT 420  
 Db 421 TAGGCGAAGGCCCGTTCCATCTCTAGCAATGACGTTGCCAGCGAGGTTTGACAT 480  
 Qy 421 TAGGCGAAGGCCCGTTCCATCTCTAGCAATGACGTTGCCAGCGAGGTTTGACAT 480

[illegible]

Dh	1561	CGGGCAGCTCCCTCATCACAGAACCCACTGAGGAGATCCGGGCCCTCAGTCAGACATTG	1620
Qy	1621	GGGGAATCCCTTGCTGCTGGGAGTACATCATCTGTGCTGGGAAATCCCAAGCTCC	1680
Dh	1621	GGGGAATCCCTTGCTGCTGGGAGTACATCATCTGTGCTGGGAAATCCCAAGCTCC	1680
Qy	1681	CCGAGCTCCTCTCTCTTGGGGGGGGCTGGTTAACTCCACGGCCCATGATTACGTCA	1740
Dh	1681	CCGAGCTCCTCTCTCTTGGGGGGGGCTGGTTAACTCCACGGCCCATGATTACGTCA	1740
Qy	1741	TCCAGACTACTCGAAATGGCGTCCGCCCTCTGCTTGCGGTTTCCAGGCCCTGAGTATCC	1800
Dh	1741	TCCAGACTACTCGAAATGGCGTCCGCCCTCTGCTTGCGGTTTCCAGGCCCTGAGTATCC	1800
Qy	1801	CTCCGCTGCAGGAGCCCTTCTGATTCCTCGGTACGTTCTTTTGGGAGCATATGTGGCG	1860
Dh	1801	CTCCGCTGCAGGAGCCCTTCTGATTCCTCGGTACGTTCTTTTGGGAGCATATGTGGCG	1860
Qy	1861	TCTTCGACCCGGGGGAGACATGAAAGACAGCGCCGGGGTGGGCTCGGCGGACCTCGCACTC	1920
Dh	1861	TCTTCGACCCGGGGGAGACATGAAAGACAGCGCCGGGGTGGGCTCGGCGGACCTCGCACTC	1920
Qy	1921	GCAGAGCGAGCTCGGATGGGAGAGACTGCGCAGCGCAGTTCCGCCGGGTAGAGCCCAA	1980
Dh	1921	GCAGAGCGAGCTCGGATGGGAGAGACTGCGCAGCGCAGTTCCGCCGGGTAGAGCCCAA	1980
Qy	1981	GTGAAGCCGATGCCGAGCGGGTGTCTGGGGAGTCTGTACCCAGTAAAAATCCACTAT	2040
Dh	1981	GTGAAGCCGATGCCGAGCGGGTGTCTGGGGAGTCTGTACCCAGTAAAAATCCACTAT	2040
Qy	2041	TTCCATTGAAAAAATAAAAAA 2060	
Dh	2041	TTCCATTGAAAAAATAAAAAA 2060	

## RESULT 7

US-09-116-641-2  
Sequence 2 A

; Sequence 2, Application US/09116641D

; GENERAL INFORMATION:

APPLICANT: Xu, Hong

APPLICANT: Elsenboss, Laura A.

APPLICANT: Fogliano, Michael

APPLICANT: Cohan, Victoria L.

APPLICANT: Bandman, Olga

TITLE OF INVENTION: HUMAN ASPARTIC PROTEASES

FILE REFERENCE: PF-0458-1 CIP

CURRENT APPLICATION NUMBER: US/09/116,

CURRENT FILING DATE: 1998-07-16  
EABITFB APPLICATION NUMBER: 09/008 271

EARLIER FILING DATE: 1998-01-16

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: Fast

; SEQ ID NO 2  
: LENGTH: 2061

TYPE: DNA

ORGANISM: HOMO SAPIENS

FEATURE: 827617 INNCASE01  
COVER INFORMATION.

OTHER INFO  
US-09-116-641-2

Query Match 99.98; Score 2058.4; DB 16; Length 2061;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2059;	Conservative 0;	Mismatches 1;	Inserts 0;	Gaps 0;
---------------	-----------------	---------------	------------	---------

1 CTTGAGAGCTCTCAATACTTGGTCATGGATGAAGCCGACCGAATACTGAATATGGA'TT 60

[illegible]

Dd 1 CTGAGAGCTCTCAATACCTTGGTCATGGATGAGCCGACCGAATACCGAATATGGATT 60

61 TGAGACAGAGGTTGACAAGCCTCGAGATCGGAACATTCCTCTTCTCTGCGCACCATGAC 120

100





OY		701	GTCGCCAGCGATGCTCTCAACACCGGTGTGCACAACCCCTGCTGTAACCCCTGCTGCTGCTGCTGCTCTCT	Indels	0;	Gaps	0;
Db		44	GTCCCCAGGAGTGTCTCCACCAACCGTGCTGCACACCCCTGCTGCACCCCTGCTGCTGCTGCTGCTCTCT				760
OY		761	GAATGSGAGCCTTCCGGGGCACACTGATCCGCAATCCCCTTTATATGAGTCCAACCTCG				103
Db		104	GAATGTGGAGCCCTCCGGGGCCACACTATCCGATCCCTTTATGAGTCCAACCTCG				820
OY		821	ACGAGAGACCCCTGAACCTACTGAGGGGATGAGAGAACCAGCAGAGCTCCCAAATTGGG				153
Db		154	AOCGAGATCCTGAACTCTGAGAGGGGATGAGAGAACCAGCAGAGCTCCCAAATTGGG				880
OY		881	GGCCCATCCCTCTGGGGACAAGCCATCTTCGTAACCTCTCTGTAACCTACAGGATGTGA				223
Db		224	GGCCCATCCCTCTGGGGACAAGCCATCTTCGTAACCTCTCTGTAACCTACAGGATGTGA				940
OY		941	GTAATTTGGGAAATTGGGCTGGGAACGCTCCACAAAATCTCACTGTGCTTTGACAC				283
Db		284	GTAATTTGGGAAATTGGGCTGGGAACGCTCCACAAAATCTCACTGTGCTTTGACAC				1000
OY		1001	TGGCTCTCCAAATCTGTGGGTCCCGTCCAGAGAGATGCCAATCTTCAATGAGCTGCTG				343
Db		344	TGGCTCTCCAAATCTGTGGGTCCCGTCCAGAGAGATGCCAATCTTCAATGAGCTGCTG				1060
OY		1061	GTTAACACACGAGTTGATCCCAAAAGCCTCTAGCTCCCTCCAGGCCAATGGGAACAATT				403
Db		404	GTTAACACACGAGTTGATCCCAAAAGCCTCTAGCTCCCTCCAGGCCAATGGGAACAATT				1120
OY		1121	TGCCATTCAATATGGAATCGGGGGGTAGATGAAATCTGAGGAGAACAACTGACTAT				463
Db		464	TGCCATTCAATATGGAATCGGGGGGTAGATGAAATCTGAGGAGAACAACTGACTAT				1180
OY		1181	TGATGGAATCAAGGCTGCATCAATGATTTTCGGGGAGGCTCTGTGGAGCCAGCCTGAT				523
Db		524	TGATGGAATCAAGGCTGCATCAATGATTTTCGGGGAGGCTCTGTGGAGCCAGCCTGAT				1240
OY		1241	CTTGGCTTTTGGCCATTTTGATGGAATTTGGGCTCGGTTTTCCCATTTCTGTGTGGA				583
Db		584	CTTGGCTTTTGGCCATTTTGATGGAATTTGGGCTCGGTTTTCCCATTTCTGTGTGGA				1300
OY		1301	AGGAGTTGGCCCCCGATGATGTATCGGTGTGACAGAGGGCTATTGGATAAGCCTGCTT				643
Db		644	AGGAGTTGGCCCCCGATGATGTATCGGTGTGACAGAGGGCTATTGGATAAGCCTGCTT				1360
OY		1361	CTCCTTTTACCTCAACAGGGACCTGTGAAGACCTGATGAGAGAGAGCTGTGCTTGGGGG				703
Db		704	CTCCTTTTACCTCAACAGGGACCTGTGAAGACCTGATGAGAGAGAGCTGTGCTTGGGGG				1420
OY		1421	CTGGAACCCGGACAACATACCAACCCCTCACCTTGTGCAAGTACAGGTCCTGCGCTTA				763
Db		764	CTGGAACCCGGACAACATACCAACCCCTCACCTTGTGCAAGTACAGGTCCTGCGCTTA				1480
OY		1481	CTGGCAGATCCACATGAGCGTGTGAAGTGGGCCAAGGCTGACTCTGTGCCAAGG				823
Db		824	CTGGCAGATCCACATGAGCGTGTGAAGTGGGCCAAGGCTGACTCTGTGCCAAGG				1540
							883

TELECOMMUNICATION INFORMATION

TELEPHONE: 610-407-0700  
TELEFAX: 610-407-0701



TELEX:  
 : INFORMATION FOR SEQ ID NO: 3:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 1519 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: cDNA  
 : US-09-111-727-3

Query Match 65.6%; Score 1350.4; DB 16; Length 1519;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 1354; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

OY 701 GTCCCAAGCATGTCCTCACCACCGCTGCTCAACCCCTGCTGCTGCTGCTGCTGCT 760
DB 109 GTCCCAAGCATGTCCTCACCACCGCTGCTCAACCCCTGCTGCTGCTGCTGCTGCT 168
OY 761 GAATGTGAGGCTTCCGGGGCCACATGATCCGATCCCTCTTCATGAGTCCAACTGG 820
DB 169 GAATGTGAGGCTTCCGGGGCCACATGATCCGATCCCTCTTCATGAGTCCAACTGG 228
OY 821 ACCGAGACCCCTGACCTACTGAGGGAGTGAAGAAACACAGAGCTCCCAAGTTGG 880
DB 229 ACCGAGATCTCTGAACCTACTGAGGGAGTGAAGAAACACAGAGCTCCCAAGTTGG 288
OY 881 GGGCCCATCCCTGCGGGGACAAAGCCATCTGTACCTCTCTGAACTACAGAGATGTGA 940
DB 289 GGGCCCATCCCTGCGGGGACAAAGCCATCTGTACCTCTCTGAACTACAGAGATGTGA 348
OY 941 GTATTGTGGGAATTTGGGCTGGGAGAGCCCTCCCAAAAACCTTCATCTGTGCTTTGAC 1000
DB 349 GTATTGTGGGAATTTGGGCTGGGAGAGCCCTCCCAAAAACCTTCATCTGTGCTTTGAC 408
OY 1001 TGAGTCTCCATCTCTGAGTCCGCTCCAGAGAGATGCATCTTCACAGTGTGCTGCTG 1060
DB 409 TGAGTCTCCATCTCTGAGTCCGCTCCAGAGAGATGCATCTTCACAGTGTGCTGCTG 468
OY 1061 GTTACACACCGATTTGATCCCAAGCCCTTACCTCTTCAGGACCAATGGACCAAGTT 1120
DB 469 GTTACACACCGATTTGATCCCAAGCCCTTACCTCTTCAGGACCAATGGACCAAGTT 528
OY 1121 TGGCATCAATATGGAATCTGGGCGGGGTGATGGAATCTCTGAGGACCAAGCTGACTAT 1180
DB 529 TGGCATCAATATGGAATCTGGGCGGGGTGATGGAATCTCTGAGGACCAAGCTGACTAT 588
OY 1181 TGTGTGAATCAAGGGTGCATGATGATTTTGGGAGAGCTCTGAGGAGCCAGAGCTGT 1240
DB 589 TGTGTGAATCAAGGGTGCATGATGATTTTGGGAGAGCTCTGAGGAGCCAGAGCTGT 648
OY 1241 CTTCGCTTTTGGCCATTTTGATGGGAGATTTGGGCTCGGTTTCCCATTTGCTGTGGA 1300
DB 649 CTTCGCTTTTGGCCATTTTGATGGGAGATTTGGGCTCGGTTTCCCATTTGCTGTGGA 708
OY 1301 AGGAGTCCGGCCCGGAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1360
DB 709 AGGAGTCCGGCCCGGAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 768
OY 1361 CTTCCTTTTACCTCAACAGGAGACCTCTGAAGAGCTGATGAGAGAGAGAGAGAGAG 1420
DB 769 CTTCCTTTTACCTCAACAGGAGACCTCTGAAGAGCTGATGAGAGAGAGAGAGAGAG 828
OY 1421 CTTCGAGCCCGGACATGATCCACCCCTGACCTTGTGTCAGTCAAGGATGCTGCTTA 1480
DB 829 CTTCGAGCCCGGACATGATCCACCCCTGACCTTGTGTCAGTCAAGGATGCTGCTTA 888
OY 1481 CTGCAATATCAATGAGAGTGTGAAGGTGGGCGGAGGCTGACTCTCTGTGCAAGGG 1540
DB 889 CTGCAATATCAATGAGAGTGTGAAGGTGGGCGGAGGCTGACTCTCTGTGCAAGGG 948
OY 1541 CTGTGCTGCAATCTCTGATGAGGAGGCTGCTCATATCAAGAGACCACTGAGAGATCCG 1600
DB 949 CTGTGCTGCAATCTCTGATGAGGAGGCTGCTCATATCAAGAGACCACTGAGAGATCCG 1008

```

```

OY 1601 GGGCTGATCAGACCATTTGGGGGAATCCCTTGTGCTGGGAGTACATATCTGTG 1660
DB 1009 GGGCTGATCAGACCATTTGGGGGAATCCCTTGTGCTGGGAGTACATATCTGTG 1068
OY 1661 CTGGAATATCCCAAGCTCCCGCAGTCTCTCTTTTGGGGGGTCTGTTAACTT 1720
DB 1069 CTGGAATATCCCAAGCTCCCGCAGTCTCTCTTTTGGGGGGTCTGTTAACTT 1128
OY 1721 CACGGCCATGATTAAGTATCAAGTACAGTACAGTAAATGGGCTCCGCTCTGCTGTCCG 1780
DB 1129 CACGGCCATGATTAAGTATCAAGTACAGTAAATGGGCTCCGCTCTGCTGTCCG 1188
OY 1781 TTTCAGGCTCCGATGTCCTCCGCTGACAGGAGCCCTTCGATCTCTGATGAGTCTT 1840
DB 1189 TTTCAGGCTCCGATGTCCTCCGCTGACAGGAGCCCTTCGATCTCTGATGAGTCTT 1248
OY 1841 CTGGGGACATATGTCGGCTCTTTCGACCGGGGGACATGAAGACAGCCCGGGTGG 1900
DB 1249 CTGGGGACATATGTCGGCTCTTTCGACCGGGGGACATGAAGACAGCCCGGGTGG 1308
OY 1901 CTTGGCGGCGCTGCACTCGCGGAGGAGACCTGGATGGGAGAGACTGGGAGGCGCA 1960
DB 1309 CTTGGCGGCGCTGCACTCGCGGAGGAGACCTGGATGGGAGAGACTGGGAGGCGCA 1368
OY 1961 GTTCCCGGATGACGCCCAAGTGAAGCATGCGAGCGGGTGTGCGGAGTCTGCT 2020
DB 1369 GTTCCCGGATGACGCCCAAGTGAAGCATGCGAGGAGGAGGAGGAGTGTGCTGCT 1428
OY 2021 ACCGATTAATCACTATTTCATTTGAAAAA 2060
DB 1429 ACCGATTAATCACTATTTCATTTGAAAAA 1468

```

## RESULT 11

US-09-791-231-3

Sequence 3, Application US/09791231

GENERAL INFORMATION:

APPLICANT: POWELL, DAVID J.

APPLICANT: KAY, JOHN

APPLICANT: HILL, JEFFREY

APPLICANT: SMITH, TREDD

TITLE OF INVENTION: ASP5

FILE REFERENCE: GH-70067-C1

CURRENT APPLICATION NUMBER: US/09/791,231

CURRENT FILING DATE: 2001-02-22

PRIOR APPLICATION NUMBER: 60/056,480

PRIOR FILING DATE: 1997-08-21

PRIOR APPLICATION NUMBER: 09/111,727

PRIOR FILING DATE: 1998-07-08

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 3

LENGTH: 1519

TYPE: DNA

ORGANISM: HOMO SAPIENS

FEATURE:

NAME/KEY: UNSURE

LOCATION: (8)(9)

US-09-791-231-3

Query Match 65.6%; Score 1350.4; DB 33; Length 1519;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1354; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

OY 701 GTCCCAAGCATGTCCTCACCACCGCTGCTCAACCCCTGCTGCTGCTGCTGCT 760
DB 109 GTCCCAAGCATGTCCTCACCACCGCTGCTCAACCCCTGCTGCTGCTGCTGCT 168
OY 761 GAATGTGAGGCTTCCGGGGCCACATGATCCGATCCCTCTTCATGAGTCCAACTGG 820
DB 169 GAATGTGAGGCTTCCGGGGCCACATGATCCGATCCCTCTTCATGAGTCCAACTGG 228

```





OY	881	GGCCCAATCCCTGGGGACAAGCCCAATCTTCACCTCTCTCGAACAATACAGAGATGAGCA	940
Db	418	GGCCCAATCCCTGGGGACAAGCCCAATCTTCGACCTCTCTCGAACAATACAGAGATGAGCA	477
OY	941	GTATTTTGGGAAATTTGGGCTGGGAGAGCCCTCCACAATACTTCACTGTGTGCTTTGACAC	1000
Db	478	GTATTTTGGGAAATTTGGGCTGGGAGAGCCCTCCACAATACTTCACTGTGTGCTTTGACAC	537
OY	1001	TGCGTCTCTCCAAATCTCTGGGTCCCGCTCAGAGAAATGCCACTTCTTCAAGTGTGCCCTCTG	1060
Db	538	TGCGTCTCTCCAAATCTCTGGGTCCCGCTCAGAGAAATGCCACTTCTTCAAGTGTGCCCTCTG	597
OY	1061	GTACACACACGATTTTGATCCCAAAAGCCTGACCTCTCCAGGCCCAATGGGACCAAGTT	1120
Db	598	GTACACACACGATTTTGATCCCAAAAGCCTGACCTCTCCAGGCCCAATGGGACCAAGTT	657
OY	1121	TGCCATTCAAATATGAAACTGGGCGGGATGATGAAATCCTGAGCGAGGACAACGTACTAT	1180
Db	658	TGCCATTCAAATATGAAACTGGGCGGGATGATGAAATCCTGAGCGAGGACAACGTACTAT	717
OY	1181	TGGTGGAAATCAAGGCTGCATCAGATGATTTTCGGGGAGGCTCTCTGGGAGGCCCAACCTGCT	1240
Db	718	TGGTGGAAATCAAGGCTGCATCAGATGATTTTCGGGGAGGCTCTCTGGGAGGCCCAACCTGCT	777
OY	1241	CTTGCTTTTGCCCAATTTTGATGGGAATTTGGGCGCTCGTTTCCCATCTGTCTGTGGA	1300
Db	778	CTTGCTTTTGCCCAATTTTGATGGGAATTTGGGCGCTCGTTTCCCATCTGTCTGTGGA	837
OY	1301	AGGAGTTCCGGCCCCCGGATGATGTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1360
Db	838	AGGAGTTCCGGCCCCCGGATGATGTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	897
OY	1361	CTCCTTTTACCTCAACAAGGAGCCCTGTAAGAAGCCTGATGTAGAGAGAGAGCCTGCGGGGG	1420
Db	898	CTCCTTTTACCTCAACAAGGAGCCCTGTAAGAAGCCTGATGTAGAGAGAGAGCCTGCGGGGG	957
OY	1421	CTCGGACCCGGACACTACATCCCAACCCCTTACCTGTGTGTGTGTGTGTGTGTGTGTGTGT	1480
Db	958	CTCGGACCCGGACACTACATCCCAACCCCTTACCTGTGTGTGTGTGTGTGTGTGTGTGTGT	1017
OY	1481	CTGCGAGATCCAGATGAGGCGGTGTGAAGGTGGGGCCAGGGGTGACTCTGTGTGTGTGTGT	1540
Db	1018	CTGCGAGATCCAGATGAGGCGGTGTGAAGGTGGGGCCAGGGGTGACTCTGTGTGTGTGTGT	1077
OY	1541	CTGT	1600
Db	1078	CTGT	1137
OY	1601	GGCCCTGTGATCAGACCAATTTGGGGGAATTCCTTGTGTGTGTGTGTGTGTGTGTGTGTGT	1660
Db	1138	GGCCCTGTGATCAGACCAATTTGGGGGAATTCCTTGTGTGTGTGTGTGTGTGTGTGTGTGT	1197
OY	1661	CTGCGAAATCCCAAGCTCCCGGAGAGCTCTTCTCTTGTGTGTGTGTGTGTGTGTGTGTGT	1720
Db	1198	CTGCGAAATCCCAAGCTCCCGGAGAGCTCTTCTCTTGTGTGTGTGTGTGTGTGTGTGTGT	1257
OY	1721	CAGGCGCCATGATTAAGCTATCAGACTACTCGAATATGCGCTCGCCTCTGTGTGTGTGT	1780
Db	1258	CAGGCGCCATGATTAAGCTATCAGACTACTCGAATATGCGCTCGCCTCTGTGTGTGTGT	1317
OY	1781	TTTCCAGGCGCTGTGATGTCCCTCGCGCTGCAAGGGCCCTTGTGAAATCCTCGGTGTGACGT	1840
Db	1318	TTTCCAGGCGCTGTGATGTCCCTCGCGCTGCAAGGGCCCTTGTGAAATCCTCGGTGTGACGT	1377
OY	1841	CTTGGGGAGCATGTGTGGCCGTCTTTCGACCGCGGGGAGCATGAAAGACAGCGCCCGGTGGG	1900
Db	1378	CTTGGGGAGCATGTGTGGCCGTCTTTCGACCGCGGGGAGCATGAAAGACAGCGCCCGGTGGG	1437
OY	1901	CTTGGGGAGCATGTGTGGCCGTCTTTCGACCGCGGGGAGCATGAAAGACAGCGCCCGGTGGG	1960
Db	1438	CTTGGGGAGCATGTGTGGCCGTCTTTCGACCGCGGGGAGCATGAAAGACAGCGCCCGGTGGG	1497

QY	1961	GTCCCGGGGAGCGCCCAAGTGAAGGCAATGCGCAGCGGTGTGCTCCGGAAGTCCCTGCT	2020
Db	1498	GTCCCGGGGAGCGCCCAAGTGAAGGCAATGCGCAGCGGTGTGCTCCGGAAGTCCCTGCT	1557
QY	2021	ACCCAGTAAATCCACATATTCCATTGTAATAAAAAAAAAA	2060
Db	1558	ACCCAGTAAATCCACATATTCCATTGTAATAAAAAAAAAA	1597
RESULT 13			
US-09-791-231-1			
; Sequence 1, Application US/09791231			
; GENERAL INFORMATION:			
; APPLICANT: POWELL, DAVID J.			
; APPLICANT: KAT, JOHN			
; APPLICANT: HILL, JEFFREY			
; APPLICANT: SMITH, TRUDI			
; TITLE OF INVENTION: ASP5			
; FILE REFERENCE: GH-70067-C1			
; CURRENT APPLICATION NUMBER: US/09/791,231			
; CURRENT FILING DATE: 2001-02-22			
; PRIOR APPLICATION NUMBER: 60/056,480			
; PRIOR FILING DATE: 1997-08-21			
; PRIOR APPLICATION NUMBER: 09/111,727			
; PRIOR FILING DATE: 1998-07-08			
; NUMBER OF SEQ ID NOS: 5			
; SOFTWARE: FastSeq for Windows Version 3.0			
; SEQ ID NO 1			
; LENGTH: 1648			
; TYPE: DNA			
; ORGANISM: HOMO SAPIENS			
US-09-791-231-1			
Query Match			
Best Local Similarity 99.6%; Score 1350.4; DB 33; Length 1648;			
Matches 1354; Conservative 0; Mismatches 6; Indels 0; Gaps 0;			
QY	701	GTCCCAAGCAAGTCTCCACCAAGCGTGCAGCAACCCCTGCTGCTGCTGCTGCTGCTGCT	760
Db	238	GTCCCAAGCAAGTCTCCACCAAGCGTGCAGCAACCCCTGCTGCTGCTGCTGCTGCTGCT	297
QY	761	GAATGTGAGAGCTTCGAGGGGCGACACTGATCCGATCCCTTCATGAGTCAAACTGG	820
Db	298	GAATGTGAGAGCTTCGAGGGGCGACACTGATCCGATCCCTTCATGAGTCAAACTGG	357
QY	821	ACGCAAGCACTGAACCTACTGAGGGGATGAGAGAACACAGACAGACTCCCAAGTTGGG	880
Db	358	ACGCAAGCACTGAACCTACTGAGGGGATGAGAGAACACAGACAGACTCCCAAGTTGGG	417
QY	881	GGCCCAATCCCTGGGGGCAAGCCATCTGTACCTCTCTCGAAGCTAACAGGATGTGCA	940
Db	418	GGCCCAATCCCTGGGGGCAAGCCATCTGTACCTCTCTCGAAGCTAACAGGATGTGCA	477
QY	941	GTAATTTGGGAAAAATTGGGCTGGGGAACGCTCCACAAAACCTCACTGTTGGCTTGAAC	1000
Db	478	GTAATTTGGGAAAAATTGGGCTGGGGAACGCTCCACAAAACCTCACTGTTGGCTTGAAC	537
QY	1001	TGCTCTCTCAATCTCTGGGTCCGCTCCAGAGATGCCACTTCTTCAGTGTGCCCTGCTG	1060
Db	538	TGCTCTCTCAATCTCTGGGTCCGCTCCAGAGATGCCACTTCTTCAGTGTGCCCTGCTG	597
QY	1061	GTTACACACCGAATTTGATTCACCAAAAGCCTAGCTCTCTCCAGGCCAATGGGACCAAGTT	1120
Db	598	GTTACACACCGAATTTGATTCACCAAAAGCCTAGCTCTCTCCAGGCCAATGGGACCAAGTT	657
QY	1121	TGCCATTCAAAATGGAATCTGGGCGGGTATGATGAATCCTGAGCAGAGACAAGTGAATAT	1180
Db	658	TGCCATTCAAAATGGAATCTGGGCGGGTATGATGAATCCTGAGCAGAGACAAGTGAATAT	717
QY	1181	TGCTGGAATCAAGGCTGATCATGATGATTTTCGGGGAAGCTCTCTGGGAGCCCAAGCTGCT	1240
Db	718	TGCTGGAATCAAGGCTGATCATGATGATTTTCGGGGAAGCTCTCTGGGAGCCCAAGCTGCT	777

```

QY      1241 CTTCGCTTTTGGCCATTTTGTATGGATATTGGGCGTCGGTTTCCATTCCTGTCTGTGA 1300
      778 CTTCGCTTTTGGCCATTTTGTATGGATATTGGGCGTCGGTTTCCATTCCTGTCTGTGA 837
QY      1301 AGGAGTTCGCCCCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1360
      838 AGGAGTTCGCCCCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1360
QY      1361 CTTCCTTTTACCTCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 897
      898 CTTCCTTTTACCTCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1420
QY      1421 CTGCGACCCGCGACACTACATCCACCCCTGACCTTCGTCGACAGTACAGTCCCTGCTA 1480
      958 CTGCGACCCGCGACACTACATCCACCCCTGACCTTCGTCGACAGTACAGTCCCTGCTA 1480
QY      1481 CTGGAGATCCACATGAGAGCTGTGAAGGTGGGCCAGAGGCTGACTCTCTGTGCCAAGG 1540
      1018 CTGGAGATCCACATGAGAGCTGTGAAGGTGGGCCAGAGGCTGACTCTCTGTGCCAAGG 1540
QY      1541 CTGTGCTGCATCTCTGATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1077
      1078 CTGTGCTGCATCTCTGATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1600
QY      1601 GGCCCTGCATGACAGCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1137
      1138 GGCCCTGCATGACAGCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1660
QY      1661 CTGGAAATCCCAAGAGTCCCGCAGTCTCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGG 1197
      1198 CTGGAAATCCCAAGAGTCCCGCAGTCTCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGG 1257
QY      1721 CAGGCGCATGATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1780
      1258 CAGGCGCATGATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1840
QY      1781 TTTCAGAGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1840
      1318 TTTCAGAGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1317
QY      1841 CTTCGAGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1377
      1378 CTTCGAGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1900
QY      1901 CCTGCGCGCGCTGCTGACCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1437
      1438 CCTGCGCGCGCTGCTGACCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1960
QY      1961 GTTCCCGGCGGCTGCTGACCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1497
      1498 GTTCCCGGCGGCTGCTGACCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2020
QY      2021 ACCGAGTAAATCCATATTTTCAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 1557
      1558 ACCGAGTAAATCCATATTTTCAATGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 1557

```

## RESULT 14

```

US-10-036-657-15
/ Sequence 15, Application US/10036657
/ GENERAL INFORMATION:
/ APPLICANT: Earl Francis Albone, et al.
/ TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES
/ FILE REFERENCE: GP-707/8B-C1
/ CURRENT APPLICATION NUMBER: US/10/036,657
/ NUMBER OF SEQ ID NOS: 107
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 15
/ LENGTH: 1648
/ TYPE: DNA
/ ORGANISM: HOMO SAPIENS
US-10-036-657-15

```

Query Match 65.6%; Score 1350.4; DB 44; Length 1648;  
 Best Local Similarity 99.6%; Pred No. 0;  
 Matches 1354; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

QY      701 GTCCCCAGGATGTCTCCACACCGCTCTGCAACCCCTGCGTGGTCTGCTCTCTCTCT 760
      238 GTCCCCAGGATGTCTCCACACCGCTCTGCAACCCCTGCGTGGTCTGCTCTCTCTCTCT 297
QY      761 GAATGTGAGGCTTCGCGGCGGACACATGATCCGATCCCTCTTATGATGATCAACCTG 820
      298 GAATGTGAGGCTTCGCGGCGGACACATGATCCGATCCCTCTTATGATGATCAACCTG 357
QY      821 ACGGAGACCTGTAACCTACTGAGGAGGATGAGAGAACCGACAGAGCTCCCAAGTGGG 880
      358 ACGGAGATCCTGAACCTACTGAGGAGGATGAGAGAACCGACAGAGCTCCCAAGTGGG 417
QY      881 GGCCCGATCCCTGCGGAGCAAGCCCATCTTGTACTCTCTGCAACTCTGCAAGGAGTGTGCA 940
      418 GGCCCGATCCCTGCGGAGCAAGCCCATCTTGTACTCTCTGCAACTCTGCAAGGAGTGTGCA 477
QY      941 GTATTTGGGGAATTTGGGCTGGGAAAGCCCTCCACAAACTTACTGCTTTGACAC 1000
      478 GTATTTGGGGAATTTGGGCTGGGAAAGCCCTCCACAAACTTACTGCTTTGACAC 537
QY      1001 TGCGCTCCCAATCTCTGGGTCCGTCAGAGAGATGCCAATTCTGATGATGCTGCTG 1060
      538 TGCGCTCCCAATCTCTGGGTCCGTCAGAGAGATGCCAATTCTGATGATGCTGCTG 597
QY      1061 GTTACACACCGATTTGATGCCAAGCCCTGATGCTCTTCCAGGCCAATGGAGCAAGTT 1120
      598 GTTACACACCGATTTGATGCCAAGCCCTGATGCTCTTCCAGGCCAATGGAGCAAGTT 657
QY      1121 TGCATTCATATGGAATCGGCGGGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1180
      658 TGCATTCATATGGAATCGGCGGGTATGATGATGATGATGATGATGATGATGATGATGATGAT 717
QY      1181 TGGTGAATCAAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1240
      718 TGGTGAATCAAAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 777
QY      1241 CTTCGCTTTGCGCCATTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1300
      778 CTTCGCTTTGCGCCATTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 837
QY      1301 AGGAGTTCGCCCCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1360
      838 AGGAGTTCGCCCCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 897
QY      1361 CTCTTTTACCTCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1420
      898 CTCTTTTACCTCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 957
QY      1421 CTGCGACCCGCGACACTACATCCACCCCTGACCTTCGTCGACAGTACAGTCCCTGCTA 1480
      958 CTGCGACCCGCGACACTACATCCACCCCTGACCTTCGTCGACAGTACAGTCCCTGCTA 1017
QY      1481 CTGGAGATCCACATGAGAGCTGTGAAGGTGGGCCAGAGGCTGACTCTCTGTGCCAAGG 1540
      1018 CTGGAGATCCACATGAGAGCTGTGAAGGTGGGCCAGAGGCTGACTCTCTGTGCCAAGG 1077
QY      1541 CTGTGCTGCATCTCTGATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1600
      1078 CTGTGCTGCATCTCTGATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1137
QY      1601 GGCCCTGCATGACAGCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1660
      1138 GGCCCTGCATGACAGCCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1197
QY      1661 CTGGAAATCCCAAGAGTCCCGCAGTCTCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGG 1720
      1198 CTGGAAATCCCAAGAGTCCCGCAGTCTCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGG 1257

```

QY	1121	CACGGCCCATATTACGCATCCAGACACTACGAATAGCGCTCCGCCCTCTGCTGTCCGG	1780
Db	1258	CACGGCCCATATTACGCATCCAGACACTACACTCGAATAGCGCTCCGCCCTCTGCTGTCCGG	1317
QY	1781	TTTTCACAGCCCTGGATGTCCCTCCGCCCTGCAGGGCCCTTCTCGATCTCGGTGACGTCCT	1840
Db	1318	TTTTACAGGCCCTGGATGTCCCTCCGCCCTGCAGGGCCCTTCTCGATCTCCGGTGAAGTCCT	1377
QY	1841	CTTGGGGACGATGTGGCCGCTTCGACCCGCGGGGACATGGAAGACACAGCCCGCGGTGGG	1900
Db	1378	CTTGGGGACGATGTGGCCGCTTCGACCCGCGGGGACATGGAAGACACAGCCCGCGGTGGG	1437
QY	1901	CTGTGGCGCGGCTCTGCACCTGCGGAGCGGACCTTGATGGGAGAGACTGCGCAGGCGCA	1960
Db	1438	CTGTGGCGCGGCTCTGCACCTGCGGAGCGGACCTTGATGGGAGAGACTGCGCAGGCGCA	1497
QY	1961	GTTTCCCGGGGAGCGCCCAAGTAGAGCGCATGTCACAGCGGGTGGTCGCGGAGTCTGCTCT	2020
Db	1498	GTTTCCCGGGGAGCGCCCAAGTAGAGCGCATGTCACAGCGGGTGGTCTGCGGTAGTCTGCTCT	1557
QY	2021	ACCCAGTAAAAATCCACTATTTCCTATTGAAAAA	2060
Db	1558	ACCCAGTAAAAATCCACTATTTCCTATTGAAAAA	1597

```

RESULT 15
US-60-452-680-7764
: Sequence 7764, Application US/60452680
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: APPLICANT: GROPE, Andrew
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: FILE REFERENCE: CLO01450
: CURRENT APPLICATION NUMBER: US/60/452,680
: CURRENT FILING DATE: 2003-03-07
: NUMBER OF SEQ ID NOS: 116213
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 7764
: LENGTH: 1398
: TYPE: DNA
: ORGANISM: Homo sapiens
US-60-452-680-7764

```

Query Match	65.4%;	Score 1347.6;	DB 100;	Length 1398;
Best Local Similarity	99.5%;	Pred. No. 0;		
Matches 1347;	Conservative	4;	Mismatches	3; Indels 0; Gaps 0;

QY	701	GTCCCCAGCATGTCCTCACACACGGCTGCAACCCCTGGTGTGGTGGCCCTGACT	760
Db	44	GTCCCCAGCATGTCCTCACACACGGCTGCAACCCCTGGTGTGGTGGCCCTGACT	103
QY	761	GAATGTGGAGCTTCCGGGGCCACACATGATCCGATCCCTCTTATGAGTCAACCTGG	820
Db	104	GAATGTGGAGCTTCCGGGGCCACACATGATCCGATCCCTCTTATGAGTCAACCTGG	163
QY	821	ACGAGAGACCCCTGAACTACTGAGGGGATGGAGAAACAAGACAGCTCCCAAGTTGGG	880
Db	164	ACGAGAGATCCTGAACCTACTGAGGGGATGGAGAAACAAGACAGAGTCCCAAGTTGGG	223
QY	881	GGCCCCATCCCCCTGGGGACAAGCCCATCTTGTAAGTCTCTCGAATCAAGGATGTGCA	940
Db	224	GGCCCCATCCCCCTGGGGACAAGCCCATCTTGTAAGTCTCTCGAATCAAGGATGTGCA	283
QY	941	GTAATTTTGGGGAATTTGGCTGGGGAAGCGCTCCACAACATGCATGCTTGGACAC	1000
Db	284	GTAATTTTGGGGAATTTGGCTGGGGAAGCGCTCCACAACATGCATGCTTGGACAC	343
QY	1001	TGGCTCCTCCAAATCTCTGGGTGCCGATCCAGAGATGCACTTCTTCAAGTGGCCCTCTG	1060
Db	344	TGGCTCCTCCAAATCTCTGGGTGCCGATCCAGAGATGCACTTCTTCAAGTGGCCCTCTG	403
QY	1061	GTTTACACACCATGTTTATCCCAAGACGCTCTAGCTCTTCGAGGCAATGGGACCAATT	1120

D	404	GTTCACACACGAGTTTATGCCAAAGCCTAGTCTCTCCAGGCCAATGGACCAAGTT	463
Q	1121	TGCCATTCAATATGGAACCTGGCGGGGTAGATGCATCTTAGCGAGGACAAGCTACTAT	1180
D	464	TGCATTCAATATGGAAGCTGGCGGGTAGATGATCTAGCGAGGACAAGCTACTAT	523
Q	1181	TGCTGGAATCAAGGGTGCATCAGATTTTCGGGGAGGCTCTCTGGAGGCCAAGCTGCT	1240
D	524	TGGTGAATCAAGGGTGCATCAGATTTTCGGGGAGGCTCTCTGGAGGCCAAGCTGCT	583
Q	1241	CTTCGCTTTTGCCATTTTATGAGGATATTGGCCCTGGTTTCCATTCCTGTCTGTGA	1300
D	584	CTTCGCTTTTGCCATTTTATGAGGATATTGGCCCTGGTTTCCATTCCTGTCTGTGA	643
Q	1301	AGGAGTTCGGCCCCCGGATGATGTAACGTGTGGACAGGGGCTATTGATTAAGCTGTCT	1360
D	644	AGGAGTTCGGCCCCCGGATGATGTAACGTGTGGACAGGGGCTATTGATTAAGCTGTCT	703
Q	1361	CTCCTTTTACCTCAACAGGAGACCTGTGAAGACCTGATGAGAGAGAGTGTGCTCGGGGG	1420
D	704	CTCCTTTTACCTCAACAGGAGACCTGTGAAGACCTGATGAGAGAGAGTGTGCTCGGGGG	763
Q	1421	CTGGAGCCGGACACTACATCCACCCTACCTTGTCGCACTGACGGTCCCTGCTTA	1480
D	764	CTGGAGCCGGACACTACATCCACCCTACCTTGTCGCACTGACGGTCCCTGCTTA	823
Q	1481	CTGGCAATCAATCGAGGGGTGAGAGTGGGGCCGAGGGCTGACTCTGTCTGCCAAGG	1540
D	824	CTGGCAATCAATCGAGGGGTGAGAGTGGGGCCGAGGGCTGACTCTGTCTGCCAAGG	883
Q	1541	CTGTGCTGCATCTGTGATACGGGACAGCTCCCTATACAGAGACCCTAGAGAGATCCG	1600
D	884	CTGTGCTGCATCTGTGATACGGGACAGCTCCCTATACAGAGACCCTAGAGAGATCCG	943
Q	1601	GGCCCTCAGTGAAGCCATTGGGGGAAACCCCTTGCTGGGTGGGAGTACATCTCTGTG	1660
D	944	GGCCCTCAGTGAAGCCATTGGGGGAAACCCCTTGCTGGGTGGGAGTACATCTCTGTG	1003
Q	1661	CTGGGAATCCCAAGCTCCCGCAGTCTCTTCCTCTTTGGGGGGGTGTGTGTTAACT	1720
D	1004	CTGGGAATCCCAAGCTCCCGCAGTCTCTTCCTCTTTGGGGGGGTGTGTGTTAACT	1063
Q	1721	CAGGGCCCATGATTACTCATCCAGACTACTCGAAATGGGGTCCGCTCTGTGCTTGTCCG	1780
D	1064	CAGGGCCCATGATTACTCATCCAGACTACTCGAAATGGGGTCCGCTCTGTGCTTGTCCG	1123
Q	1781	TTTTCAGAGCCCTGGATGTCCCTCCGCTCGAGAGGCCCTTGTGATCTCTCGGTACGTCT	1840
D	1124	TTTTCAGAGCCCTGGATGTCCCTCCGCTCGAGAGGCCCTTGTGATCTCTCGGTACGTCT	1183
Q	1841	CTTGGGGAGCTATGTGGCGCTCTTTCGACCGCGGGGACATGAAGAGCAGCCCGGGGTGG	1900
D	1184	CTTGGGGAGCTATGTGGCGCTCTTTCGACCGCGGGGACATGAAGAGCAGCCCGGGGTGG	1243
Q	1901	CTGGAGCGGGCTGCGACTCGCGGAGGGACCTCGATGGGGGAGACTCTCCGAGGGGCA	1960
D	1244	CTGGAGCGGGCTGCGACTCGCGGAGGGACCTCGGATGGGGGAGACTCTCCGAGGGGCA	1303
Q	1961	GTTTCCCGGGTGAACGCCCAAGTGAAGAGCATGTGCGACAGGGTGTGTCGAGAGTCTGCT	2020
D	1304	GTTTCCCGGGTGAACGCCCAAGTGAAGAGCATGTGCGACAGGGTGTGTCGAGAGTCTGCT	1363
Q	2021	ACCACGTAATAATTCATATTTTCATTGAAAAA	2054
D	1364	ACCACGTAATAATTCATATTTTCATTGACGAA	1397

Search completed: October 10, 2003, 05:19:17  
Job time : 7290.19 secs





Query Match	2.4%	Score 41	DB 6	length 4353
Best Local Similarity	46.9%	Fred. No. 0.26		
Matches 128	Conservative 0	Mismatches 145	Indels 0	Gaps 0
QY	315	AAAGCCAGCCGAGAGATCCCTGTGCTGGCGGCGCTGGTAAACGCTCTGTAAGCATATC	374	
Db	1708	AAGGCCATCGGAGCCGTCTGTCTGGGCCACCCCGTAGCATATCGGACGGAACCTG	1767	
QY	375	ATCTGGCTGAAGGTGATCATACAGCTAACATCTCCAGCTGAGGTGAGGCTCTGGCCAAAT	434	
Db	1768	CTGACCCGAGATCGGCTGACACCTGAACTTCCCATCAGGCCCATCGAGACGCTGGCCCTG	1827	
QY	435	GACGACGAGCTGTAGTCAAGATCCCCCTGGACATGGTGGCTGATTTCAACACGCCCCCTG	494	

```

RESULT 5
PCT-US02-29560A-393
:
: Sequence 393, Application PC/TUS0229560A
:
GENERAL INFORMATION:
:
APPLICANT: Afar, Daniel
:
APPLICANT: Aziz, Natasha
:
APPLICANT: Gish, Kurt C
:
APPLICANT: Hevezl, Peter A.
:
APPLICANT: Mack, David H.
:
APPLICANT: Wilson, Keith E.
:
APPLICANT: Zlotnik, Albert
:
APPLICANT: Eos Biotechnology, Inc.
:
TITLE OF INVENTION: Methods of diagnosis of Cancer, Compositions and
:
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
:
FILE REFERENCE: 018501-002710PC
:
CURRENT APPLICATION NUMBER: PCT/US02/29560A
:
CURRENT FILING DATE: 2002-09-17

```

;; PRIOR APPLICATION NUMBER: US 60/323,469  
;; PRIOR FILING DATE: 2001-09-17  
;; NUMBER OF SEQ ID NOS: 412  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 393  
;; LENGTH: 1609  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
PCT-US02-29560A-393

Query Match 2.4%; Score 39.8; DB 1; Length 1609;  
Best local Similarity 46.5%; Pred. No. 0.39;  
Matches 128; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY 351 GTGAACACCGCTCTGAAGCATCATCTGTGAAGGTATCATACAGTCAACATCTCCACG 410  
DB 1238 GTGATCAATCTTCTGAGTTCTTCACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1297  
QY 411 GTGACAGTGAAGCCCTGGCCCAATGACAGAGCTGTAGTCAAGATCCCTGGACATG 470  
DB 1298 ATCTGGCTGCGCCACAGAAAGCTGAGTGAAGCGGCCCATCAAGGTGAACCTGGCCCTG 1357  
QY 471 GTGGCGGATGCAACAGCGCCCTGTGCAAGACCATGTGTGAGTCCACATGACGACTGAG 530  
DB 1358 CCTGTCTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1417  
QY 531 GCCCAAGCCACCATCGCATGTGAGACCAAGTGAAGGCGCCCGCTGGTCTGACTG 590  
DB 1418 GTGAGATGTGGCATCGGCTTCAACATCATCTCCACAGGGGCTGCGCTTACTTCTTG 1477  
QY 591 GACTGTGCCACCAAGCCATGGAGCCCTGCCATCCA 625  
DB 1478 GTCTGTGGAAAAACAAAGCCCAAGTGGCTCTCCA 1512

RESULT 6  
US-60-485-450-262  
;; Sequence 262, Application US/60485450  
;; GENERAL INFORMATION:  
;; APPLICANT: CARGILL, Michele  
;; APPLICANT: CHANG, Sheng-Yung  
;; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
;; TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C  
;; TITLE OF INVENTION: VIRUS-INJECTED SUBJECTS, METHODS OF DETECTION AND USES  
;; FILE REFERENCE: CL001470  
;; CURRENT APPLICATION NUMBER: US/60/485,450  
;; CURRENT FILING DATE: 2003-07-09  
;; NUMBER OF SEQ ID NOS: 47859  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 262  
;; LENGTH: 4541  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-60-485-450-262

Query Match 2.4%; Score 39.8; DB 7; Length 4541;  
Best local Similarity 46.5%; Pred. No. 0.65;  
Matches 128; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY 351 GTGAACACCGCTCTGAAGCATCATCTGTGAAGGTATCATACAGTCAACATCTCCACG 410  
DB 1256 GTGATCAATCTTCTGAGTTCTTCACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1315  
QY 411 GTGACAGTGAAGCCCTGGCCCAATGACAGAGCTGTAGTCAAGATCCCTGGACATG 470  
DB 1316 ATCTGGCTGCGCCACAGAAAGCTGAGTGAAGCGGCCCATCAAGGTGAACCTGGCCCTG 1375  
QY 471 GTGGCGGATGCAACAGCGCCCTGTGCAAGACCATGTGTGAGTCCACATGACGACTGAG 530  
DB 1376 CCTGTCTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1435  
QY 531 GCCCAAGCCACCATCGCATGTGAGACCAAGTGAAGGCGCCCGCTGGTCTGACTG 590

DB 1436 GTGAGATGTGGCATCGGCTTCAACCATCATCTCAGGCGGCTGCGCTACTTCTTG 1495  
QY 591 GACTGTGCCACCAAGCCATGGAGGCTGGCATCCA 625  
DB 1496 GTCTGTGGAAAAACAAAGCCCAAGTGGCTCTCCA 1530

RESULT 7  
PCT-US03-28227-326/C  
;; Sequence 326, Application PC/TUS0328227  
;; GENERAL INFORMATION:  
;; APPLICANT: INCYTE CORPORATION; SCHMIDT, Jeanette P.;  
;; APPLICANT: WRIGHT, Rachel J.; BRUNS, Christopher M.;  
;; APPLICANT: MARINOVIC, Mirjana M.; SHEN, Fan;  
;; APPLICANT: HARTSHORNE, Toinette A.; SUCHOKOLSKI, Martin;  
;; APPLICANT: ALIUS, Christina M.; PITTS, Steven J.;  
;; APPLICANT: ELDER, Linda V.; MOONEY, Elizabeth M.;  
;; APPLICANT: DELBEANE, Angelo M.; PANESAR, Iqbal S.;  
;; APPLICANT: BANVILLE, Steven C.; REDDY, Thirupathi P.;  
;; APPLICANT: STEVENS, Kristian A.; BLANCHARD, John L.;  
;; APPLICANT: PANZER, Scott R.; WANG, Xinhao;  
;; APPLICANT: AU, Alan P.; GERSTIN, Edward H., Jr.;  
;; APPLICANT: PERALTA, Careyna H.; ANDERSON, Scott E.;  
;; APPLICANT: RIOUX, Pierre; SHEN, Edward J.;  
;; APPLICANT: WU, Mingham C.; STUYE, Laura L.;  
;; APPLICANT: LAGACE, Robert E.; SPIRO, Peter A.;  
;; APPLICANT: STEWART, Elizabeth A.; WINGROVE, James A.;  
;; APPLICANT: VITT, Ursula A.; KIRTON, Edward;  
;; APPLICANT: XU, Yuming; KWONG, Mary;  
;; APPLICANT: POLICKY, Jennifer L.; HURWITZ, Bonnie L.;  
;; APPLICANT: MA, Yan; JACKSON, Jennifer L.;  
;; APPLICANT: GIETZEN, Darrell; PATURY, Srikanth;  
;; APPLICANT: SHI, Xiaobing; SUAREZ, Charlyn J.  
;; TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS  
;; FILE REFERENCE: PN-0100 PCT  
;; CURRENT APPLICATION NUMBER: PCT/US03/28227  
;; CURRENT FILING DATE: 2003-09-12  
;; PRIOR APPLICATION NUMBER: US 60/410,260  
;; PRIOR FILING DATE: 2002-09-12  
;; PRIOR APPLICATION NUMBER: US 60/410,259  
;; PRIOR FILING DATE: 2002-09-12  
;; NUMBER OF SEQ ID NOS: 5444  
;; SOFTWARE: PERL Program  
;; SEQ ID NO 326  
;; LENGTH: 1247  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; OTHER INFORMATION: Incyte ID No: 1905822.PT2  
PCT-US03-28227-326

Query Match 2.4%; Score 39.6; DB 1; Length 1247;  
Best local Similarity 43.8%; Pred. No. 0.4;  
Matches 171; Conservative 0; Mismatches 219; Indels 0; Gaps 0;

QY 357 ACCGTCTTGAAGCATCATCTGTGAAGGTATCATACAGTCAACATCTCCACGCTGAG 416  
DB 1043 AGCTTCCAGTCGGAACATCGCCCGGTACAGAGGGCGCTTTCACCAAGCCACCTCCAG 984  
QY 417 GTGAACCCCTCGGCCAATGACAGAGCTGTGTAAGATCCCTGGACATGGTGGCT 476  
DB 983 TGGCTGACATCTCCCGCGAGCTGTGGCTGTGACCAAGTGGCTTACAGAAAGATGTG 924  
QY 477 GGAATCAACAGCCCTGTGTAAGACCATGTGAGTTCACATGACGACTGAGGCCCA 536  
DB 923 CTGCCCAACCTGTGAGAGCAGAGACATGGGAGAGTGAAGCAGAGCCACACACTGG 864  
QY 537 GCCACCATCGCATGTGAGACCAAGTGAAGGCGCCCGCTGGTCTGACTGACTG 596  
DB 863 GTGCCCTCTCTCAAGAAAGTGCACAGCGCGGACCCAGAGTTCCTTGTCTGCTCTTC 804



```
QY 597 GCCACGACGATGGAGCCTGGCAGTCACACTGCTGCAATAGCTCTCTCTGCTGAAC 656
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 803 GCGCCGCTCTGCTGCTGACCGGCCCATCAACCGCTGCTGCTGCGAGGCCGCTGCGC 744
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 657 GCGTAGAGTACGAGGATGATGAACTCCAGTGCATCCCTCCCAATCTAGTAAAC 716
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 743 GAGCTGTGCGAGCCGCTGATGCAATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 684
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 717 CAGCTGTGCTCCGCTGATGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 746
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 683 GACAGTTCCTCCCGAGGAGGAGCTGTCATC 654

RESULT 8
US-10-375-932-316
; Sequence 316, Application US/10375932
; GENERAL INFORMATION:
; APPLICANT: Apt, Doris
; APPLICANT: Punnonen, Juha
; APPLICANT: Brinkman, Alice M.
; TITLE OF INVENTION: NOVEL FLAVIVIRUS ANTIGENS
; FILE REFERENCE: 0322.210US
; CURRENT APPLICATION NUMBER: US/10/375,932
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 60/360,030
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 345
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 316
; LENGTH: 1341
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polynucleotide: 16G11-NPRM Round II shuffled clone no H
US-10-375-932-316

Query Match 2.3%; Score 38.6; DB 6; Length 1341;
Best Local Similarity 46.0%; Pred. No. 0.82;
Matches 168; Conservative 0; Mismatches 194; Indels 3; Gaps 1;

QY 336 GTGCTGGGCGAGCTGTGAACACGCTGCTGAAGCAGCATCATCTGCTGAAGTCAAC 395
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 748 GTGCTGGGCGAGCAGAGAGGCGCCATGACACCGCCCTGACCGGCGCCACGAGATCCAG 807
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 366 GCTAACATCTCTCAGCTGAGGTGAAGCCCTGCGCCATGACAGAGCTGCTAGTCAAG 455
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 808 ATGACAGCGGAGCACTGCTGTTCAACCGGCCACTGAAGTGCAGGCTGAGATGACAAG 867
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 456 ATCCCCCT---GGAATGTGTGCTGATTCACACAGCCCTGCTCAAGCATCTGTGAG 512
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 868 CTGACGCTGAAGGCGATGAGTACATGATGTGACCGGCAAGTTCAGATCGTGAAGGAG 927
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 513 TTCCACATGACGACTGAGGCCCAACCAATCCCATGAGACACCAAGTGAAGTGGCCCC 572
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 928 ATGCGCGAGAGCCACAGGACGACCATCTGATCAGAGGTCAATAGAGGCGCAGCGCGC 987
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 573 ACCGCGCTGTCTCAGTGAAGTGCACACCAAGTGGAGGCTGCGCATCACTGTGCTG 632
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 988 CCGTCAAGATCCCTTACAGCACCGAGGAGCGGCGCAAGGCCACCAAGCGCAGGCTG 1047
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 633 CATAGCTCTCTCTGCTGTAAGGCTTAGTGAAGAGTATGAACTCTAGTACCA 692
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1048 ATCACCAGCAACCCCATGATGATGCAAGAGAAAGCCCGTGAACATGAGCTGAGGCC 1107
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 693 TCCCT 697
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1108 CCTT 1112
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
US-10-375-932-293
; Sequence 293, Application US/10375932
; GENERAL INFORMATION:
; APPLICANT: Apt, Doris
; APPLICANT: Punnonen, Juha
; APPLICANT: Brinkman, Alice M.
; TITLE OF INVENTION: NOVEL FLAVIVIRUS ANTIGENS
; FILE REFERENCE: 0322.210US
; CURRENT APPLICATION NUMBER: US/10/375,932
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 60/360,030
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 345
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 293
; LENGTH: 1347
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polynucleotide: 12E3-NPRM Round II shuffled clone no
US-10-375-932-293

Query Match 2.3%; Score 38.6; DB 6; Length 1347;
Best Local Similarity 46.0%; Pred. No. 0.82;
Matches 168; Conservative 0; Mismatches 194; Indels 3; Gaps 1;

QY 336 GTGCTGGGCGAGCTGTGAACACGCTGCTGAAGCAGCATCATCTGCTGAAGTCAAC 395
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 754 GTGCTGGGCGAGCAGAGAGGCGCCATGACACCGCCCTGACCGGCGCCACGAGATCCAG 813
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 396 GCTAACATCTCTCAGCTGAGGTGAAGCCCTGCGCCATGACAGAGCTGCTAGTCAAG 455
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 814 ATGACAGCGGAGCACTGCTGTTCAACCGGCCACTGAAGTGCAGGCTGAGATGACAG 873
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 456 ATCCCCCT---GGAATGTGTGCTGATTCACACAGCCCTGCTCAAGCATCTGTGAG 512
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 874 CTGACGCTGAAGGCGATGAGTACAGCATGTGACCGCGCAAGTTCAGATGTAAGAG 933
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 513 TTCCACATGACGACTGAGGCCCAACCAATCCCATGAGACACCAAGTGAAGTGGCCCC 572
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 934 ATGCGCGAGAGCCACAGGCGCCATCTGATGAGGAGGCTGATGAGAGGCGAGCGGCC 993
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 573 ACCGCGCTGTCTCAGTGAAGTGCACACAGCCATGAGGAGGCTGCGCATCACTGTG 632
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 994 CCGTCAAGATCCCTTACAGCACGAGAGGCGCCAGGCGCAAGGCCACAGCGCAGGCTG 1053
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 633 CATAGCTCTCTCTGCTGTAAGGCTTAGTGAAGAGTATGAACTCTAGTACCA 692
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1054 ATCACCAGCAACCCCATGATGATGCAAGAGAAAGCCCGTGAACATGAGCTGAGGCC 1113
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 693 TCCCT 697
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1114 CCTT 1118
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 10
US-10-375-932-187
; Sequence 187, Application US/10375932
; GENERAL INFORMATION:
; APPLICANT: Apt, Doris
; APPLICANT: Punnonen, Juha
; APPLICANT: Brinkman, Alice M.
; TITLE OF INVENTION: NOVEL FLAVIVIRUS ANTIGENS
; FILE REFERENCE: 0322.210US
; CURRENT APPLICATION NUMBER: US/10/375,932
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US 60/360,030
; PRIOR FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 345
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic polynucleotide: 16G11 Round II shuffled clone
```



US-10-375-932-187

Query Match 2.3%; Score 38.6; DB 6; Length 1389;  
Best Local Similarity 46.0%; Pred. No. 0.83;  
Matches 168; Conservative 0; Mismatches 194; Indels 3; Gaps 1;

QY 336 GTGCTGGGACGCTGGTGAACACCGCTTCAAGCACAATCTGTGGCTGAAGTCAATACA 395  
DB 796 GTGCTGGGACGCGAGGAGGCGCCATGACACCGCCCTGACCGCGCCGACGAGATCCAG 855  
QY 396 GCTAACATCTCCAGCTGAGTGAACCGCTCGGCCAATGACACGAGAGCTGTAGTCAAG 455  
DB 856 ATGAGCAGCGGCAACCTGCTGTTCAACGGCCACTGTAAGTGCAGGCTGAGAGATGACAG 915  
QY 456 ATCCCCCT---GGACATGTGTGGCTGATTCACACAGCCCGCTGGTCAAGACCATGTGAG 512  
DB 916 CTGACAGCTGAAGGACATGACCTAGTATGTGACACCGGCAAGTTCCAGATCTGAAGAG 975  
QY 513 TTGCACATGACGATGAGGCCCAAGCCATCCGATGACACACAGTGCAGATGGCCCC 572  
DB 976 ATGCGCAGACCCAGCAGCGGACCATCTGATGATGATGATGATGATGATGATGATGATG 1035  
QY 573 ACCCGCTGTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 632  
DB 1036 CCTGCAAGATCCCTTCAAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1095  
QY 633 CATAGCT 692  
DB 1096 ATGACCGCCCAACCCCATCTGATGATGATGATGATGATGATGATGATGATGATGATG 1155  
QY 693 TCCTCT 697  
DB 1156 CCCTT 1160

RESULT 11

US-10-375-932-164  
; Sequence 164, Application US/10375932  
; GENERAL INFORMATION:  
; APPLICANT: Apt, Doris  
; APPLICANT: Punnonen, Juha  
; APPLICANT: Brinkman, Alice M.  
; TITLE OF INVENTION: NOVEL FLAVIVIRUS ANTIGENS  
; FILE REFERENCE: 0322.2100S  
; CURRENT APPLICATION NUMBER: US/10/375,932  
; CURRENT FILING DATE: 2003-02-26  
; PRIOR APPLICATION NUMBER: US 60/360,030  
; PRIOR FILING DATE: 2002-02-26  
; NUMBER OF SEQ ID NOS: 345  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 164  
; LENGTH: 1395  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE INFORMATION: Synthetic polynucleotide: 12E3 Round II shuffled clone  
US-10-375-932-164

Query Match 2.3%; Score 38.6; DB 6; Length 1395;

Best Local Similarity 46.0%; Pred. No. 0.84;  
Matches 168; Conservative 0; Mismatches 194; Indels 3; Gaps 1;

QY 336 GTGCTGGGACGCTGGTGAACACCGCTTCAAGCACAATCTGTGGCTGAAGTCAATACA 395  
DB 802 GTGCTGGGACGCGAGGAGGCGCCATGACACCGCCCTGACCGCGCCGACGAGATCCAG 861  
QY 396 GCTAACATCTCCAGCTGAGTGAACCGCTCGGCCAATGACACGAGAGCTGTAGTCAAG 455  
DB 862 ATGAGCAGCGGCAACCTGCTGTTCAACGGCCACTGTAAGTGCAGGCTGAGAGTGAAG 921  
QY 456 ATCCCCCT---GGACATGTGTGGCTGATTCACACAGCCCGCTGGTCAAGACCATGTGAG 512  
DB 922 CTGACAGCTGAAGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 981

QY 513 TTCCACATGACGACTGAGGCCCAAGCCACCATCCGATGACACACAGTGCAGTGGCCCC 572  
DB 982 ATGCGCCAGACCCAGCAGCAGGAGACCATGTGATGATGATGATGATGATGATGATGATG 1041  
QY 573 ACCCGCTGTCTCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 632  
DB 1042 CCTGCAAGATCCCTTCAAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1101  
QY 633 CATAGCT 692  
DB 1102 ATGACCGCCCAACCCCATCTGATGATGATGATGATGATGATGATGATGATGATGATG 1161  
QY 693 TCCTCT 697  
DB 1162 CCCTT 1166

RESULT 12

US/10/375  
; Sequence 254, Application US/10375932  
; GENERAL INFORMATION:  
; APPLICANT: Apt, Doris  
; APPLICANT: Punnonen, Juha  
; APPLICANT: Brinkman, Alice M.  
; TITLE OF INVENTION: NOVEL FLAVIVIRUS ANTIGENS  
; FILE REFERENCE: 0322.2100S  
; CURRENT APPLICATION NUMBER: US/10/375,932  
; CURRENT FILING DATE: 2003-02-26  
; PRIOR APPLICATION NUMBER: US 60/360,030  
; PRIOR FILING DATE: 2002-02-26  
; NUMBER OF SEQ ID NOS: 345  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 254  
; LENGTH: 2025  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE INFORMATION: Synthetic polynucleotide: 16G11-D4 (16G11 extended to C15/full  
US/10/375,932-254

Query Match 2.3%; Score 38.6; DB 6; Length 2025;  
Best Local Similarity 46.0%; Pred. No. 1;  
Matches 168; Conservative 0; Mismatches 194; Indels 3; Gaps 1;

QY 336 GTGCTGGGACGCTGGTGAACACCGCTTCAAGCACAATCTGTGGCTGAAGTCAATACA 395  
DB 1294 GTGCTGGGACGCGAGGAGGCGCCATGACACCGCCCTGACCGCGCCGACGAGATCCAG 1353  
QY 396 GCTAACATCTCCAGCTGAGTGAACCGCTCGGCCAATGACACGAGAGCTGTAGTCAAG 455  
DB 1354 ATGAGCAGCGGCAACCTGCTGTTCAACGGCCACTGTAAGTGCAGGCTGAGAGTGAAG 1413  
QY 456 ATCCCCCT---GGACATGTGTGGCTGATTCACACAGCCCGCTGGTCAAGACCATGTGAG 512  
DB 1414 CTGACAGCTGAAGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1473  
QY 513 TTCCACATGACGACTGAGGCCCAAGCCACCATCCGATGACACACAGTGCAGATGGGCCCC 572  
DB 1474 ATGCGCCAGACCCAGCAGCAGGAGACCATGTGATGATGATGATGATGATGATGATGATG 1533  
QY 573 ACCCGCTGTCTCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 632  
DB 1534 CCTGCAAGATCCCTTCAAGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1593  
QY 633 CATAGCT 692  
DB 1594 ATGACCGCCCAACCCCATCTGATGATGATGATGATGATGATGATGATGATGATGATG 1653  
QY 693 TCCTCT 697  
DB 1654 CCCTT 1658

Query Match	2.3%	Score 38.6;	DB 6;	Length 2025;
Best Local Similarity	46.0%	Pred. No. 1;		
Matches 168; Conservative	0;	Mismatches 194;	Indels 3;	Gaps 1;

RESULT 14  
US-10-425-114A-21298  
Sequence 21298, Application US/10425114A  
General Information

```

/ SEQ ID NO 21298
/ LENGTH: 1953
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: LIB3279-221_H9_FLI
US-10-425-114A-21298

Query Match
Best Local Similarity 2.3%; Score 38.4; DB 6; Length 1953;
Matches 126; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

OY 288 GCTCCCTCTCTCAGTGCATCGCGGAAAAGACAGCCGAGAGATCCCTGTGCGGACG 347
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 272 GCCGCCACGGCGGTGGAGCTGGCGGCCCTCGGCCGCCGCGGAGCTCTCTCGCTGGCGC 331
OY 348 CTGTTGAACACCGTCTCTGAAGCATCATCTGGCTGAGAGTCAACAGCTAAGATCCTC 407
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 332 TCGTTGAGCTGGACCTGGTCCACATCTCTGCTCGCGGTTCCGTCTGTGTCGGC 391
OY 408 CAGTGAAGTTGAAGCCCTCGGCATATGACAGAGCTGTACATAGATCCCTTGAC 467
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 392 ACGGTGACTGATGTTCGCGGCCAGGCGGTGTACTGTGTGACTTACGCTGTACAG 451
OY 468 ATGGTGGCTTGATTCAACAGCCCTGTGTCAAGACCATGTGAGTTCCACATGACACT 527
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 452 CCCCCCGCAGCTGCGCGGTGCCCTTGGCCACTTCATGAGACACGCCGCTCATACG 511
OY 528 GAGGCCCAAGCCACCATCCGCATGACACAG 559
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 512 GACGACACAGAGCGTGCCTTCCAGACCAG 543

RESULT 15
US-10-425-114A-26294
/ Sequence 26294; Application US/10425114A
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jingdong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E
/ APPLICANT: Tabaska, Jack E
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114A
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 26294
/ LENGTH: 1278
/ TYPE: DNA
/ FEATURE:
/ ORGANISM: Homo sapiens
/ OTHER INFORMATION: Clone ID: LIB4119-276-BL_FLI
US-10-425-114A-26294

Query Match
Best Local Similarity 2.3%; Score 38; DB 6; Length 1278;
Matches 107; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

OY 463 TGGACATGTTGGCTGGATTCAACAGCCCTGTGTCAAGACCATTGGAGTTCCACATGA 522
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 250 TGGACATCTGTGCACTGTCAACAGCGCTTCATCATCAAGACTTACAGATCTTTGAGA 309
OY 523 CGACGTGAGGCCCAACGCCCATTCGGANTGAGACACCAATGCAATGTGGCCGCCGCGCTGG 582
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 310 CCTCTGACGGACGGATCTTACATCATCAATGAGACTTGGCGTCCAGGCGGACCTTCGAGT 369
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 583 TCCCTAGTACTGTGCCACAGCCATGGAGGCTGCGCATCCAACTGTGCATTAAGCTT 642
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 370 TCATCAAGTGCAGGAGACCTCGATATAGAGCGTGGGACGCAAGATGTTCCAGACGCTT 429

```

```

RESULT 15
US-10-425-114A-26294
: Sequence 26294, Application US/10425114A
: GENERAL INFORMATION:
: APPLICANT: Liu, Jindong
: APPLICANT: Zhou, Yihua
: APPLICANT: Kovalic, David K.
: APPLICANT: Screen, Steven E
: APPLICANT: Tabaska, Jack E
: APPLICANT: Cao, Yongwei
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
: FILE REFERENCE: 38-21(53313)B
: CURRENT APPLICATION NUMBER: US/10/425,114A
: CURRENT FILING DATE: 2003-04-28
: NUMBER OF SEQ ID NOS: 73128
: SEQ ID NO 26294
: LENGTH: 1278
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: Clone ID: LIB4119-276-B1_FLI
: US-10-425-114A-26294

```

	Query Match	2.3%	Score38:	DB 6:	Length 1278:
	Best Local Similarity	48.2%	Pred. No. 1-2:		
	Matches 107:	Conservative	0:	Mismatches 115:	Indels 0:
				Gaps	0:
QY	463	TGGACATGGTGGCTGGATTCAACAGCCCGCTGTGCAAGACCATCTGGAGTTCCACATGA	522		
Db	250	TGGACATCTGGCACTGTCAACACGGCTCATCATCAAGACTTCAGAGATTGTGGACA	309		
QY	523	CGAGTGAAGGCCCAACCCACATCCGGCATGGACACACACTGCAAGTGGCCCGCAGCCGCTGG	582		
Db	310	CCTCTGACGGACGGATCTACATCTCATGAGACTTGGCTGTCAGGGCGAGCCCTCTCGAAT	369		
QY	583	TCCCTAGTACTGTGCCACAGCATGGAGAGCTGCCATCTCAACATGCTGTCANTAACTCT	642		
Db	370	TCATCAAGTGGCAGGAGACCCCTGATATAGAGACGTGGGACGCCAAGATTTTCCAGCACTTT	429		

QY 643 CCTTCTGTGAGCGCTTACTAGTACGAGTCAATGAACCTCC 684  
||| | ||| | | | | | | | |  
Db 430 CCTCCGCCGTCAAGTACTGCCACGACCTGGACATGTCACAC 471

Search completed: October 9, 2003, 23:55:11  
Job time : 346.992 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2003, 13:55:42 ; Search time 5941.32 Seconds  
(without alignments)  
9377.568 Million cell updates/sec

Title: US-09-700-770-2

Perfect score: 1680  
Sequence: 1 ggtgtgcagagataaagtt.....tcaataaaccttgcctgtg 1680

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 33363688 seqs, 1658189874 residues

Total number of hits satisfying chosen parameters: 66727376

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents\_NA\_Main.\*

1: /cgn2\_6/ptodata/2/pna/PCTUS\_COMB.seq.\*  
2: /cgn2\_6/ptodata/2/pna/PCTUS\_COMB.seq.\*  
3: /cgn2\_6/ptodata/2/pna/US06\_COMB.seq.\*  
4: /cgn2\_6/ptodata/2/pna/US07\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/pna/US08\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/pna/US08\_COMB.seq.\*  
7: /cgn2\_6/ptodata/2/pna/US08\_COMB.seq.\*  
8: /cgn2\_6/ptodata/2/pna/US08\_COMB.seq.\*  
9: /cgn2\_6/ptodata/2/pna/US08\_COMB.seq.\*  
10: /cgn2\_6/ptodata/2/pna/US08\_COMB.seq.\*  
11: /cgn2\_6/ptodata/2/pna/US08\_COMB.seq.\*  
12: /cgn2\_6/ptodata/2/pna/US08\_COMB.seq.\*  
13: /cgn2\_6/ptodata/2/pna/US08\_COMB.seq.\*  
14: /cgn2\_6/ptodata/2/pna/US08\_COMB.seq.\*  
15: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
16: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
17: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
18: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
19: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
20: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
21: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
22: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
23: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
24: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
25: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
26: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
27: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
28: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
29: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
30: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
31: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
32: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
33: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
34: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
35: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
36: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
37: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
38: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
39: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
40: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
41: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
42: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*  
43: /cgn2\_6/ptodata/2/pna/US09\_COMB.seq.\*

44: /cgn2\_6/ptodata/2/pna/US100A\_COMB.seq.\*  
45: /cgn2\_6/ptodata/2/pna/US100B\_COMB.seq.\*  
46: /cgn2\_6/ptodata/2/pna/US101A\_COMB.seq.\*  
47: /cgn2\_6/ptodata/2/pna/US101B\_COMB.seq.\*  
48: /cgn2\_6/ptodata/2/pna/US102A\_COMB.seq.\*  
49: /cgn2\_6/ptodata/2/pna/US102B\_COMB.seq.\*  
50: /cgn2\_6/ptodata/2/pna/US103A\_COMB.seq.\*  
51: /cgn2\_6/ptodata/2/pna/US103B\_COMB.seq.\*  
52: /cgn2\_6/ptodata/2/pna/US104A\_COMB.seq.\*  
53: /cgn2\_6/ptodata/2/pna/US104B\_COMB.seq.\*  
54: /cgn2\_6/ptodata/2/pna/US6000\_COMB.seq.\*  
55: /cgn2\_6/ptodata/2/pna/US6001\_COMB.seq.\*  
56: /cgn2\_6/ptodata/2/pna/US6002\_COMB.seq.\*  
57: /cgn2\_6/ptodata/2/pna/US6003\_COMB.seq.\*  
58: /cgn2\_6/ptodata/2/pna/US6004\_COMB.seq.\*  
59: /cgn2\_6/ptodata/2/pna/US6005\_COMB.seq.\*  
60: /cgn2\_6/ptodata/2/pna/US6006\_COMB.seq.\*  
61: /cgn2\_6/ptodata/2/pna/US6007\_COMB.seq.\*  
62: /cgn2\_6/ptodata/2/pna/US6008\_COMB.seq.\*  
63: /cgn2\_6/ptodata/2/pna/US6009\_COMB.seq.\*  
64: /cgn2\_6/ptodata/2/pna/US6010\_COMB.seq.\*  
65: /cgn2\_6/ptodata/2/pna/US6011\_COMB.seq.\*  
66: /cgn2\_6/ptodata/2/pna/US6012\_COMB.seq.\*  
67: /cgn2\_6/ptodata/2/pna/US6013\_COMB.seq.\*  
68: /cgn2\_6/ptodata/2/pna/US6014\_COMB.seq.\*  
69: /cgn2\_6/ptodata/2/pna/US6015\_COMB.seq.\*  
70: /cgn2\_6/ptodata/2/pna/US6016\_COMB.seq.\*  
71: /cgn2\_6/ptodata/2/pna/US6017\_COMB.seq.\*  
72: /cgn2\_6/ptodata/2/pna/US6018\_COMB.seq.\*  
73: /cgn2\_6/ptodata/2/pna/US6019\_COMB.seq.\*  
74: /cgn2\_6/ptodata/2/pna/US6020\_COMB.seq.\*  
75: /cgn2\_6/ptodata/2/pna/US6021\_COMB.seq.\*  
76: /cgn2\_6/ptodata/2/pna/US6022\_COMB.seq.\*  
77: /cgn2\_6/ptodata/2/pna/US6023\_COMB.seq.\*  
78: /cgn2\_6/ptodata/2/pna/US6023B\_COMB.seq.\*  
79: /cgn2\_6/ptodata/2/pna/US6024\_COMB.seq.\*  
80: /cgn2\_6/ptodata/2/pna/US6025\_COMB.seq.\*  
81: /cgn2\_6/ptodata/2/pna/US6026\_COMB.seq.\*  
82: /cgn2\_6/ptodata/2/pna/US6027\_COMB.seq.\*  
83: /cgn2\_6/ptodata/2/pna/US6028\_COMB.seq.\*  
84: /cgn2\_6/ptodata/2/pna/US6029\_COMB.seq.\*  
85: /cgn2\_6/ptodata/2/pna/US6030\_COMB.seq.\*  
86: /cgn2\_6/ptodata/2/pna/US6031\_COMB.seq.\*  
87: /cgn2\_6/ptodata/2/pna/US6032\_COMB.seq.\*  
88: /cgn2\_6/ptodata/2/pna/US6033\_COMB.seq.\*  
89: /cgn2\_6/ptodata/2/pna/US6034\_COMB.seq.\*  
90: /cgn2\_6/ptodata/2/pna/US6035\_COMB.seq.\*  
91: /cgn2\_6/ptodata/2/pna/US6036\_COMB.seq.\*  
92: /cgn2\_6/ptodata/2/pna/US6037\_COMB.seq.\*  
93: /cgn2\_6/ptodata/2/pna/US6038\_COMB.seq.\*  
94: /cgn2\_6/ptodata/2/pna/US6039\_COMB.seq.\*  
95: /cgn2\_6/ptodata/2/pna/US6040\_COMB.seq.\*  
96: /cgn2\_6/ptodata/2/pna/US6041\_COMB.seq.\*  
97: /cgn2\_6/ptodata/2/pna/US6042\_COMB.seq.\*  
98: /cgn2\_6/ptodata/2/pna/US6043\_COMB.seq.\*  
99: /cgn2\_6/ptodata/2/pna/US6044\_COMB.seq.\*  
100: /cgn2\_6/ptodata/2/pna/US6045\_COMB.seq.\*  
101: /cgn2\_6/ptodata/2/pna/US6046\_COMB.seq.\*  
102: /cgn2\_6/ptodata/2/pna/US6047\_COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	DB Length	ID	Description
1	1679.6	100.0	1680	PCT-US99-10344-2	Sequence 2, Appl1
2	1679.6	100.0	1680	PCT-US99-10344-2	Sequence 2, Appl1
3	1679.6	100.0	1680	US-09-700-770-2	Sequence 2, Appl1
4	1679.2	100.0	1680	US-09-788-990-1	Sequence 1, Appl1

```
5 1668.6 99.3 1683 15 US-09-092-330-13 Sequence 13, Appl
6 1668.6 99.3 1698 75 US-60-213-359-3023 Sequence 3023, Ap
7 1667 99.2 1702 71 US-60-172-373-9387 Sequence 9387, Ap
8 1667 99.2 1707 32 US-09-720-530-12 Sequence 12, Appl
9 1667 99.2 1707 32 US-09-720-530-12 Sequence 12, Appl
10 1667 99.2 1707 63 US-60-091-677-15 Sequence 15, Appl
11 1656.2 98.6 2036 33 US-09-788-990-5 Sequence 5, Appl1
12 1646.6 98.0 1661 15 US-09-092-330-12 Sequence 12, Appl
13 1627 96.8 1651 47 US-10-170-235-27385 Sequence 27385, A
14 1617 96.2 1636 40 US-09-946-374-127 Sequence 127, App
15 1617 96.2 1636 44 US-10-006-041A-127 Sequence 127, App
16 1617 96.2 1636 44 US-10-006-063A-127 Sequence 127, App
17 1617 96.2 1636 44 US-10-006-116A-127 Sequence 127, App
18 1617 96.2 1636 44 US-10-006-117A-127 Sequence 127, App
19 1617 96.2 1636 44 US-10-006-130A-127 Sequence 127, App
20 1617 96.2 1636 44 US-10-006-172A-127 Sequence 127, App
21 1617 96.2 1636 44 US-10-006-485A-127 Sequence 127, App
22 1617 96.2 1636 44 US-10-006-746A-127 Sequence 127, App
23 1617 96.2 1636 44 US-10-006-818A-127 Sequence 127, App
24 1617 96.2 1636 44 US-10-006-856A-127 Sequence 127, App
25 1617 96.2 1636 44 US-10-006-867-77 Sequence 77, Appl
26 1617 96.2 1636 44 US-10-007-194A-127 Sequence 127, App
27 1617 96.2 1636 44 US-10-007-236A-127 Sequence 127, App
28 1617 96.2 1636 44 US-10-011-671A-127 Sequence 127, App
29 1617 96.2 1636 44 US-10-011-692A-127 Sequence 127, App
30 1617 96.2 1636 44 US-10-011-795A-127 Sequence 127, App
31 1617 96.2 1636 44 US-10-011-795B-127 Sequence 127, App
32 1617 96.2 1636 44 US-10-011-833A-127 Sequence 127, App
33 1617 96.2 1636 44 US-10-012-064A-127 Sequence 127, App
34 1617 96.2 1636 44 US-10-012-101B-127 Sequence 127, App
35 1617 96.2 1636 44 US-10-012-121A-127 Sequence 127, App
36 1617 96.2 1636 44 US-10-012-137A-127 Sequence 127, App
37 1617 96.2 1636 44 US-10-012-149A-127 Sequence 127, App
38 1617 96.2 1636 44 US-10-012-231A-127 Sequence 127, App
39 1617 96.2 1636 44 US-10-012-237A-127 Sequence 127, App
40 1617 96.2 1636 44 US-10-012-752A-127 Sequence 127, App
41 1617 96.2 1636 44 US-10-012-753A-127 Sequence 127, App
42 1617 96.2 1636 44 US-10-012-754A-127 Sequence 127, App
43 1617 96.2 1636 44 US-10-012-755A-127 Sequence 127, App
44 1617 96.2 1636 44 US-10-012-755A-127 Sequence 127, App
45 1617 96.2 1636 44 US-10-013-430A-127 Sequence 127, App
```

## ALIGNMENTS

```
RESULT 1
PCT-US99-10344-2
; Sequence 2, Application PC/TUS9910344
; GENERAL INFORMATION:
; APPLICANT: Yang, Fel
; APPLICANT: Macina, Roberto A.
; APPLICANT: Sun, Yongsang
; TITLE OF INVENTION: A Novel Method of Diagnosing, Monitoring and Staging
; FILE REFERENCE: DEX-0036
; CURRENT APPLICATION NUMBER: PCT/US99/10344
; CURRENT FILING DATE: 1999-05-12
; EARLIER APPLICATION NUMBER: 60/086,212
; EARLIER FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1680
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US99-10344-2
```

```
Query Match 100.0%; Score 1679.6; DB 1; Length 1680;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1680; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GGTGTGACGATTAATGAAGTGTGACTTCAGACCCAGCTCCGCGAGAGAGAGCGGG 60
```

```
Db 1 GGTGTGACGATTAATGAAGTGTGACTTCAGACCCAGCTCCGCGAGAGAGAGCGGG 60
61 CCGAGGACCTCCAGCGTCCAGGCTTGACATCTCTGACACTTGCGCCCTGACACCTGGG 120
61 CCGAGGACCTCCAGCGTCCAGGCTTGACATCTCTGACACTTGCGCCCTGACACCTGGG 120
121 AAGATGGCGCGCGCGTGGACCTTACCCCTTCTGTGGTTTGTGGAGCCACCTTGATC 180
121 AAGATGGCGCGCGCGTGGACCTTACCCCTTCTGTGGTTTGTGGAGCCACCTTGATC 180
121 AAGATGGCGCGCGCGTGGACCTTACCCCTTCTGTGGTTTGTGGAGCCACCTTGATC 180
181 CAAGCACCTCTAGTCCACATGCAATTCATCTGGGCGCCAAATCATCAAGAAAG 240
181 CAAGCACCTCTAGTCCACATGCAATTCATCTGGGCGCCAAATCATCAAGAAAG 240
181 CAAGCACCTCTAGTCCACATGCAATTCATCTGGGCGCCAAATCATCAAGAAAG 240
241 CTGACACAGAGAGCTGAAGACCAACAGCCACAGCATCTGACAGCTGCGCGTCTC 300
241 CTGACACAGAGAGCTGAAGACCAACAGCCACAGCATCTGACAGCTGCGCGTCTC 300
301 AGTGCATCGGGGAAAAAGCCAGCGGAGATCCTGTGGGAGCCTGTGAACACCG 360
301 AGTGCATCGGGGAAAAAGCCAGCGGAGATCCTGTGGGAGCCTGTGAACACCG 360
361 TCTGAAAGCATATCATCTGGTGAAGTCAATCAAGCTAATCTCCAGCTGCAAGTGA 420
361 TCTGAAAGCATATCATCTGGTGAAGTCAATCAAGCTAATCTCCAGCTGCAAGTGA 420
421 AGCCCTCGGCCATATGACAGAGCTGTAGTCAAGATCCCTGTGACATGTGGTGGAT 480
421 AGCCCTCGGCCATATGACAGAGCTGTAGTCAAGATCCCTGTGACATGTGGTGGAT 480
481 TCAACAGCGCCCTGGTCAAGACATCGTGAATTCATCAATGACATGAGGCCAAGCA 540
481 TCAACAGCGCCCTGGTCAAGACATCGTGAATTCATCAATGACATGAGGCCAAGCA 540
541 CCATCCGATGAGACACCAAGTGAAGTGGCCCGCCGCTGCTCATGACTGTGCA 600
541 CCATCCGATGAGACACCAAGTGAAGTGGCCCGCCGCTGCTCATGACTGTGCA 600
601 CCAGCATGGGGGCGCGGCGCATCCAACTGCTGATCAATGCTCTCTGTGTAAGCGCT 660
601 CCAGCATGGGGGCGCGGCGCATCCAACTGCTGATCAATGCTCTCTGTGTAAGCGCT 660
661 TAGCTAAGCATGATGAACCTCTAGTGCCATCCCTGCCAATGATGTAAGAAACCGC 720
661 TAGCTAAGCATGATGAACCTCTAGTGCCATCCCTGCCAATGATGTAAGAAACCGC 720
721 TGTGTCCCGTATGAGGCTTCTTCAATGATGATGACAGCTCTGAGCTGTGA 780
721 TGTGTCCCGTATGAGGCTTCTTCAATGATGATGACAGCTCTGAGCTGTGA 780
781 AGGTGCCATTTCCCTCAGCATGACGTGTGGAGTTGACCTTGTATCTCCATCA 840
781 AGGTGCCATTTCCCTCAGCATGACGTGTGGAGTTGACCTTGTATCTCCATCA 840
841 AGGTGACACCATTCAGCTTACCTGAGGGGCGCAAGTTGAGACTCAGAGAAAGTGA 900
841 AGGTGACACCATTCAGCTTACCTGAGGGGCGCAAGTTGAGACTCAGAGAAAGTGA 900
841 AGGTGACACCATTCAGCTTACCTGAGGGGCGCAAGTTGAGACTCAGAGAAAGTGA 900
901 CCAAGTGGTCAATTAATCTCTGACCTTCCCGAATGCGCCACCTTGACAAATCCCGT 960
901 CCAAGTGGTCAATTAATCTCTGACCTTCCCGAATGCGCCACCTTGACAAATCCCGT 960
961 TCAGCTCATGATGATGAGAGCTGGGAAAGCTGAGTGGCGCTGCTCTCTCAG 1020
961 TCAGCTCATGATGATGAGAGCTGGGAAAGCTGAGTGGCGCTGCTCTCTCAG 1020
1021 AAGATTCATGCTCTGTGACTGTGCTTCTGAGAGTGGCCATGAGCTGAAGTCAA 1080
1021 AAGATTCATGCTCTGTGACTGTGCTTCTGAGAGTGGCCATGAGCTGAAGTCAA 1080
1081 GCATCGGGGCTGATTAATGAAGGCTGACATTAAGCTGGATCTACCCAGATGCTGAAGA 1140
GCATCGGGGCTGATTAATGAAGGCTGACATTAAGCTGGATCTACCCAGATGCTGAAGA 1140
```

Db 1081 GCATCGGGGCTGATCATGTAAGAAAAGCTGCAGATAAGCTGGGATCTACCCAGATCTGTGAAGA 1140  
QY 1141 TCTTAAGTCAAGAGACATCCCGAGTTTATATAGACCAAGGCCATGCGAAGGTGGCCCAAC 1200  
Db 1141 TCTTAAGTCAAGAGACATCCCGAGTTTATATAGACCAAGGCCATGCGAAGGTGGCCCAAC 1200  
QY 1201 TGAATCGGTGGAAGTGTTCCTCCCAAGTGAAGCCCTCCGCTTGTGTCACTGAGGCA 1260  
Db 1201 TGAATCGGTGGAAGTGTTCCTCCCAAGTGAAGCCCTCCGCTTGTGTCACTGAGGCA 1260  
QY 1261 TCGAAGCCAGCTGGAAGTCAAGTTTATACACCAAGGTGACCAATATATCACTGGA 1320  
Db 1261 TCGAAGCCAGCTGGAAGTCAAGTTTATACACCAAGGTGACCAATATATCACTGGA 1320  
QY 1321 ATAAACATCAGCTCTGATCGGATCCAGCTGATGAATCTGGAATTTGGCTGTCCCACTG 1380  
Db 1321 ATAAACATCAGCTCTGATCGGATCCAGCTGATGAATCTGGAATTTGGCTGTCCCACTG 1380  
QY 1381 ATGTTCGAAAAACATATATCATGATGATCATCCACTCTCATCTGCTGCGCAACGAAATG 1440  
Db 1381 ATGTTCGAAAAACATATATCATGATGATCATCCACTCTCATCTGCTGCGCAACGAAATG 1440  
QY 1441 GCAATTAAGATCGGGGCTCCAGTGTCTATGTTGGTGAAGGCTTGGGATTTGGAGGACGCTG 1500  
Db 1441 GCAATTAAGATCGGGGCTCCAGTGTCTATGTTGGTGAAGGCTTGGGATTTGGAGGACGCTG 1500  
QY 1501 AGTCCCTACGACCAAGGATGCGCTTGTGCTACTCCAGCTCTCTTGTGGAACCCAGCT 1560  
Db 1501 AGTCCCTACGACCAAGGATGCGCTTGTGCTACTCCAGCTCTCTTGTGGAACCCAGCT 1560  
QY 1561 CTCTCTCTCCCACTGAAAGTGTGATGAGGACCATTAAGGAAAGGCTGGGTCCAGCTGG 1620  
Db 1561 CTCTCTCTCCCACTGAAAGTGTGATGAGGACCATTAAGGAAAGGCTGGGTCCAGCTGG 1620  
QY 1621 GAGTATGGGTGTGAGCTCTATAGACCAATCCCTCTGCAATCAATAAACACTTGCCTGTG 1680  
Db 1621 GAGTATGGGTGTGAGCTCTATAGACCAATCCCTCTGCAATCAATAAACACTTGCCTGTG 1680

RESULT 2  
PCT-US99-10344-2  
; Sequence 2, Application pc/TUS9910344  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Fel  
; APPLICANT: Machine, Roberto A.  
; APPLICANT: Sun, Yongming  
; TITLE OF INVENTION: A Novel Method of Diagnosing, Monitoring and Staging  
; TITLE OF INVENTION: Lung Cancer  
; FILE REFERENCE: DEX-0036  
; CURRENT APPLICATION NUMBER: PCT/US99/10344  
; CURRENT FILING DATE: 1999-05-12  
; EARLIER APPLICATION NUMBER: 60/086,212  
; EARLIER FILING DATE: 1998-05-21  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1680  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
PCT-US99-10344-2

Query Match 100.0%; Score 1679.6; DB 2; Length 1680;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1680; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGTGAGATATTAAGTTGAGCTTCAGACCCACTGCGGGAGAGAGGAGGAGGG 60  
Db 1 GGTGTGAGATATTAAGTTGAGCTTCAGACCCACTGCGGGAGAGAGGAGGAGGG 60  
QY 61 CCGAGGACTCCAGGCTCCAGGCTGTCGATCTCTGCACTTGTCCCTTGACACCTGG 120  
Db 61 CCGAGGACTCCAGGCTCCAGGCTGTCGATCTCTGCACTTGTCCCTTGACACCTGG 120

QY 121 AAGATGCGCGGCCGCTGGACCTTACCCCTCTCTGTGTGTTGCTGCGACGACCACTTGATC 180  
Db 121 AAGATGCGCGGCCGCTGGACCTTACCCCTCTCTGTGTGTTGCTGCGACGACCACTTGATC 180  
QY 181 CAAGCCACCCCTGATCCCATGCAAGTTCATCTCTGCGGCCCAAAAGTATCAAAAGAAAG 240  
Db 181 CAAGCCACCCCTGATCCCATGCAAGTTCATCTCTGCGGCCCAAAAGTATCAAAAGAAAG 240  
QY 241 CTGACACAGGAGCTGAAGGACACACAGCCACAGATCCCTGACAGCTGCCCTGCTC 300  
Db 241 CTGACACAGGAGCTGAAGGAGACACAGCCACAGATCCCTGACAGCTGCCCTGCTC 300  
QY 301 AGTCCATTCGGGGAAAAAGCCAGCCGAGAGATCCCTGTCTGGGACCTGGTGAACCG 360  
Db 301 AGTCCATTCGGGGAAAAAGCCAGCCGAGAGATCCCTGTCTGGGACCTGGTGAACCG 360  
QY 361 TCTGGAAGCATATATCTGGCTGAAGGTTCATCAGTAACTATCTCAGCTGCAAGGTGA 420  
Db 361 TCTGGAAGCATATATCTGGCTGAAGGTTCATCAGTAACTATCTCAGCTGCAAGGTGA 420  
QY 421 AGCCCTGGGCAATGACAGAGAGCTGTGATGCAAGATCCCTGGACATGGTGGCTGAT 480  
Db 421 AGCCCTGGGCAATGACAGAGAGAGCTGTGATGCAAGATCCCTGGACATGGTGGCTGAT 480  
QY 481 TCAACAGCCCTGCTGTGCAAGACCATGCTGATGATTCACATGACGATGAGGCCAAGCCA 540  
Db 481 TCAACAGCCCTGCTGTGCAAGACCATGCTGATGATTCACATGACGATGAGGCCAAGCCA 540  
QY 541 CCATCCGATGGAACACAGTGAAGTGGCCCAAGCCCTGCTGCTGATGATGATGATGATG 600  
Db 541 CCATCCGATGGAACACAGTGAAGTGGCCCAAGCCCTGCTGCTGATGATGATGATGATG 600  
QY 601 CCAGCCATGGGAGGCTCGCATCCAGTGTGATGATGATGATGATGATGATGATGATG 660  
Db 601 CCAGCCATGGGAGGCTCGCATCCAGTGTGATGATGATGATGATGATGATGATGATG 660  
QY 661 TAGCTAAGAGGTATGAACTCTTGTGATGATGATGATGATGATGATGATGATGATG 720  
Db 661 TAGCTAAGAGGTATGAACTCTTGTGATGATGATGATGATGATGATGATGATGATG 720  
QY 721 TGTGTCCGATGATGAGGCTTCTCAATGATGATGATGATGATGATGATGATGATGATG 780  
Db 721 TGTGTCCGATGATGAGGCTTCTCAATGATGATGATGATGATGATGATGATGATGATG 780  
QY 781 AGGTGCCATTTTCCCTGACAGATGATGATGATGATGATGATGATGATGATGATGATG 840  
Db 781 AGGTGCCATTTTCCCTGACAGATGATGATGATGATGATGATGATGATGATGATGATG 840  
QY 841 AGGTGACACCATTCAGCTTACTGAGGAGCCAAAGTTGTGAGTCAACAGGAAAGTGA 900  
Db 841 AGGTGACACCATTCAGCTTACTGAGGAGCCAAAGTTGTGAGTCAACAGGAAAGTGA 900  
QY 901 CCAAGTGTTCATTAACCTGACCTTCCGCAAGATGATGATGATGATGATGATGATGATG 960  
Db 901 CCAAGTGTTCATTAACCTGACCTTCCGCAAGATGATGATGATGATGATGATGATGATG 960  
QY 961 TCAAGCTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020  
Db 961 TCAAGCTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020  
QY 1021 AAGAAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080  
Db 1021 AAGAAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080  
QY 1081 GCATCGGGGCTGATTAAGTGAAGGCTGATGATGATGATGATGATGATGATGATGATG 1140  
Db 1081 GCATCGGGGCTGATTAAGTGAAGGCTGATGATGATGATGATGATGATGATGATGATG 1140  
QY 1141 TCTTAAGTCAAGGACATCCCGAGTTTATATAGACCAAGGCTGATGATGATGATGATG 1200  
Db 1141 TCTTAAGTCAAGGACATCCCGAGTTTATATAGACCAAGGCTGATGATGATGATGATG 1200  
QY 1201 TGAATCGGTGGAAGTGTTCCTCCCAAGTGAAGCCCTCCGCTTGTTCACCTGGGCA 1260

## US-09-700-770-2

```

1  INVENTION:
2  ORGANISM:
3  APPLICANT: Yang, Fei
4  APPLICANT: Macina, Roberto A.
5  APPLICANT: Sun, Yongming
6  TITLE OF INVENTION: A Novel Method of Diagnosing, Monitoring and Staging Lung Cancer
7  FILE REFERENCE: DEX-0036
8  CURRENT APPLICATION NUMBER: US/09/7700,770
9  CURRENT FILING DATE: 2000-11-20
10 PRIOR APPLICATION NUMBER: 60/086,212
11 PRIOR FILING DATE: 1998-05-21
12 NUMBER OF SEQ ID NOS: 9
13 SOFTWARE: PatentIn Ver. 2.0
14 SEQ ID NO 2
15 LENGTH: 1680
16 TYPE: DNA
17 ORGANISM: Homo sapiens
18 US-09-700-770-2

```

QY 1 GGTGTGCGAGGATTAATAGGTGGATCTTCCACAAACCCACTCTGCCCGAGAGAGAGGACGGG 60  
 |||||  
 DDb 1 GGTGTGACAGGATTAATAGGTGTGACTTCCAAACCCACTCTGCCCGAGAGAGAGGACGGG 60  
 |||||  
 QY 61 CCGAGGACTCCAGCGTGCCTCCAGGTCTGGCATCTCTGACTTGGTGGCCCTCTGACACTGGG 120  
 |||||  
 DDb 61 CCGAGGACTCCAGCGTGCCTCCAGGTCTGGCATCTCTGACTTGGTGGCCCTCTGACACTGGG 120  
 |||||  
 QY 121 AAGATGGCGCGGCGCGGAGACCTTACCCCTTCTCTGTGTGTGGTCTGGACCCACTTGTATC 180  
 |||||  
 DDb 121 AAGATGGCGCGGCGCGGAGACCTTACCCCTTCTCTGTGTGTGGTCTGGACCCACTTGTATC 180  
 |||||  
 QY 181 CAAGCCACCCCTCAGTCCCACTGCACTTCTCATCTCTGTGGCCCAAAAGTATCAAAAGAAAG 240  
 |||||  
 DDb 181 CAAGCCACCCCTCAGTCCCACTGCACTTCTCATCTCTGTGGCCCAAAAGTATCAAAAGAAAG 240  
 |||||

QY	241	CTGACACGAGGCGTGAAGAGACCAACAAGCCACCCAGCATCTCTGCACAGACTCCCGTCTC	3000
Dp	241	CTGACACGAGGCGTGAAGAGACCAACAAGCCACCCAGCATCTCTGCACAGACTCCCGTCTC	3000
QY	301	AGTGCATGCGGGAAAAAGCCAGCCGAGAGATCCCTGTGCTGGGGAGCTGTGTAAACCG	360
Dp	301	AGTGCATGCGGGAAAAAGCCAGCCGAGAGATCCCTGTGCTGGGGAGCTGTGTAAACCG	360
QY	361	TCCGAAGCCATCATCTGTGGCTGAAGTCAATCAAGCTAAACATCTTCAGACTCAGGTGA	420
Dp	361	TCCGAAGCCATCATCTGTGGCTGAAGTCAATCAAGCTAAACATCTTCAGACTCAGGTGA	420
QY	421	AGCCCTGGCCAAATGACACGAGAGCTGGTATATCAAGATCCCCCGAGACATAGTGGCTGAT	480
Dp	421	AGCCCTGGCCAAATGACACGAGAGCTGGTATATCAAGATCCCCCGAGACATAGTGGCTGAT	480
QY	481	TCAACAGCCCTGTGCTCAGACCATGTGGAGTTCCACATGACGACTGAGGCCCAAGCA	540
Dp	481	TCAACAGCCCTGTGCTCAGACCATGTGGAGTTCCACATGACGACTGAGGCCCAAGCA	540
QY	541	CCATCGGCATGAGACACAGTGCAGAGTGGGCCCAACCGCGCTGGTCTCATGTACTGTGCCA	600
Dp	541	CCATCGGCATGAGACACAGTGCAGAGTGGGCCCAACCGCGCTGGTCTCATGTACTGTGCCA	600
QY	601	CCAGGCATGGGAGCCTGCGCATCAACTGCTGATTAAGTCTCTCTTCCTGGAGAACGCTT	660
Dp	601	CCAGGCATGGGAGCCTGCGCATCAACTGCTGATTAAGTCTCTCTTCCTGGAGAACGCTT	660
QY	661	TAGCTAAGAGGTCATGAACCTCTCATGTGCATCCCTGCCCATCTAAGTAAAAACAAGC	720

QY	721	TGTGTC	CCGTGATGCGAGGCTTCCTTAATGSGCATGTATGCAGACCTCCTGCAGCTGATGA	780
Db	721	TGTGTC	CCGTGATGCGAGGCTTCCTTAATGSGCATGTATGCAGACCTCCTGCAGCTGATGA	780
QY	781	AGGTGCCAT	TTCCCTCAGACATTTGACCCGCTGGAATTGGACCTCTGTATCCTGCATCA	840
Db	781	AGGTGCCAT	TTCCCTCAGACATTTGACCCGCTGGAATTGGACCTCTGTATCCTGCATCA	840
QY	841	AGGGGACACCA	CTTATAGCTCTTACCTGGGGGCCCAAGTTGGAGCTCACAGGAAAGGTGA	900
Db	841	AGGGGACACCA	CTTATAGCTCTTACCTGGGGGCCCAAGTTGGAGCTCACAGGAAAGGTGA	900
QY	901	CCAAATGGTTCA	TTAACTCTCAGCTTCCTCGACAAATCCCAACCTGAGCAACATCCCGT	960
Db	901	CCAAATGGTTCA	TTAACTCTCAGCTTCCTCGACAAATCCCAACCTGAGCAACATCCCGT	960
QY	961	TCAGCGCTATG	TAGTACAGACGTGGTGAAAGCTGCAGTGGCTGCTGTCTCTCCAG	1020
Db	961	TCAGCGCTATG	TAGTACAGACGTGGTGAAAGCTGCAGTGGCTGCTGTCTCTCCAG	1020
QY	1021	AAGAATTCATG	GTCTGTGGACTCTGTCTCTCTGAGAGTGGCCATCGGCTGAAAGTCA	1080
Db	1021	AAGAATTCATG	GTCTGTGGACTCTGTCTCTCTGAGAGTGGCCATCGGCTGAAAGTCA	1080
QY	1081	GCATCGGGGCTG	ATTAATGAAGAGCTCAGATTAAGCTGGCATCTAACCCAGATCGTGAAGA	1140
Db	1081	GCATCGGGGCTG	ATTAATGAAGAGCTCAGATTAAGCTGGCATCTAACCCAGATCGTGAAGA	1140
QY	1141	TCCTTA	CTCAGACACTCCGAGTTTTTTATAGACCAAGGCCAATGGCAAGTGGCCCAAC	1200
Db	1141	TCCTTA	CTCAGACACTCCGAGTTTTTTATAGACCAAGGCCAATGGCAAGTGGCCCAAC	1200
QY	1201	TGATCGT	CGTGAAGTCTTCCTCCAGTGAAGCCCTCGGCCCTTGTGTTACACCTGGGCA	1260
Db	1201	TGATCGT	CGTGAAGTCTTCCTCCAGTGAAGCCCTCGGCCCTTGTGTTACACCTGGGCA	1260
QY	1261	TCGAAGC	CAGACTGGGAAGCTCACTTTTAAACCCAAAGGTACCAACTTAATATGCACTTGA	1320
Db	1261	TCGAAGC	CAGACTGGGAAGCTCACTTTTAAACCCAAAGGTACCAACTTAATATGCACTTGA	1320
QY	1321	ATTAACAT	CAGCTCTGATCGGATTCAGCTGATGAACCTCTGGGATGGCTGGTTTCAACCTGA	1380



|||||  
Db 1321 ATAAACACACCTCTGATCGGATCCAGCTGATGAAGTGGATGGCTGTCTCAACCTG 1380  
|||  
Qy 1381 ATGTTTGAAGAAACATCATGATGATCATTCACCTCATCTCTGCTCCGACAGATG 1440  
|||  
Db 1381 ATGTTTGAAGAAACATCATGATGATCATTCACCTCATCTCTGCTCCGACAGATG 1440  
|||  
Qy 1441 GCAAAATTAAGATCTGGGGTCCAGTGTCTATGTTGTAAGAGCTTGGATGAGGACAGT 1500  
|||  
Db 1441 GCAAAATTAAGATCTGGGGTCCAGTGTCTATGTTGTAAGAGCTTGGATGAGGACAGT 1500  
|||  
Qy 1501 AGTCTCTACTGACCAAGATGAGCTTGTCTTACTTCAAGCTCTTGTGAAACCAAGCT 1560  
|||  
Db 1501 AGTCTCTACTGACCAAGATGAGCTTGTCTTACTTCAAGCTCTTGTGAAACCAAGCT 1560  
|||  
Qy 1561 CTCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAGGAGAGGAGCTGGGCTCCAGCTG 1620  
|||  
Db 1561 CTCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAGGAGAGGAGCTGGGCTCCAGCTG 1620  
|||  
Qy 1621 GAGTATGGTGTGAGCTCTATAGACATCCCTCTCTGCAATCAATAAACCTTGCCTGTG 1680  
|||  
Db 1621 GAGTATGGTGTGAGCTCTATAGACATCCCTCTCTGCAATCAATAAACCTTGCCTGTG 1680  
|||

## RESULT 4

US-09-788-990-1  
; Sequence 1, Application US/09788990  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Sei Yu  
; APPLICANT: Sun, Yongming  
; APPLICANT: Maolina, Roberto  
; TITLE OF INVENTION: Method of Diagnosing, Monitoring, Staging, Imaging and  
; FILE OF INVENTION: Treating Lung Cancer  
; FILE REFERENCE: DEX-0140  
; CURRENT APPLICATION NUMBER: US/09/788,990  
; PRIOR FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: 60/183,188  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Patent Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1680  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-788-990-1

Query Match 100.0%; Score 1679.2; DB 33; Length 1680;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1678; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGTGAGATATTAAGTTGAGCTTCCAGACCCACTGCCCCGGAGAGAGRGAGCGCG 60  
|||  
Db 1 GGTGTGAGATATTAAGTTGAGCTTCCAGACCCACTGCCCCGGAGAGAGRGAGCGCG 60  
|||  
Qy 61 CCGAGGACTCTCAGCGTGTCCAGAGTCTGCAATCTGCACTTGTGCTCTGACACTGGG 120  
|||  
Db 61 CCGAGGACTCTCAGCGTGTCCAGAGTCTGCAATCTGCACTTGTGCTCTGACACTGGG 120  
|||  
Qy 121 AAGATGCGCGCGCGGAGGAGCTTCAACCTCTCTGTTGGTGGGAGGAGGACACTTATC 180  
|||  
Db 121 AAGATGCGCGCGCGGAGGAGCTTCAACCTCTCTGTTGGTGGGAGGAGGACACTTATC 180  
|||  
Qy 181 CAAGCCACCTCTCAGTCCACTGCACTGCTATCTATCTCTGCGCCAAAAGTCAATCAAGAAAG 240  
|||  
Db 181 CAAGCCACCTCTCAGTCCACTGCACTGCTATCTATCTCTGCGCCAAAAGTCAATCAAGAAAG 240  
|||  
Qy 241 CTGACACAGAGAGCTGAAGAGACACACAGCCACAGCATCTGACAGAGCTGCGCTGCTC 300  
|||  
Db 241 CTGACACAGAGAGCTGAAGAGACACACAGCCACAGCATCTGACAGAGCTGCGCTGCTC 300  
|||  
Qy 301 AGTCCATGCGGGGAAAAAGCCAGCGGAGAGATCCCTGCTGGGAGAGCTGGTGAACACCG 360  
|||  
Db 301 AGTCCATGCGGGGAAAAAGCCAGCGGAGAGATCCCTGCTGGGAGAGCTGGTGAACACCG 360  
|||

Qy 361 TCCTGAAGCAATCATCTGGCTGAAGTCAATCAACAGTAACATCTCCAGCTGAGGTGA 420  
|||  
Db 361 TCCTGAAGCAATCATCTGGCTGAAGTCAATCAACAGTAACATCTCCAGCTGAGGTGA 420  
|||  
Qy 421 AGCCCTGGCCCAATGACCAAGAGAGCTGCTAGTCAAGATCCCTGGAGACATGGTGGAT 480  
|||  
Db 421 AGCCCTGGCCCAATGACCAAGAGAGCTGCTAGTCAAGATCCCTGGAGACATGGTGGAT 480  
|||  
Qy 481 TCACACAGCCCTGGTGAAGCAATCTGCTGAAGTTCACATGACACAGAGGAGGAGGAGG 540  
|||  
Db 481 TCACACAGCCCTGGTGAAGCAATCTGCTGAAGTTCACATGACACAGAGGAGGAGGAGG 540  
|||  
Qy 541 CCATCCCATGAGACACAGTGAAGTGGAGCCACCCGCTGGTCTGAGTACTGAGTGA 600  
|||  
Db 541 CCATCCCATGAGACACAGTGAAGTGGAGCCACCCGCTGGTCTGAGTACTGAGTGA 600  
|||  
Qy 601 CCAGCCATGGAGAGCTGCGCATCCCACTGCTGATTAAGTCTCTCTGCTGGTGAAGGCT 660  
|||  
Db 601 CCAGCCATGGAGAGCTGCGCATCCCACTGCTGATTAAGTCTCTCTGCTGGTGAAGGCT 660  
|||  
Qy 661 TAGCTTAAGCAGGTGATGACCTCTAGTGGCATCCGCGCAATCTAGTGAAGAACAGC 720  
|||  
Db 661 TAGCTTAAGCAGGTGATGACCTCTAGTGGCATCCGCGCAATCTAGTGAAGAACAGC 720  
|||  
Qy 721 TGTGTCCCGTATGAGAGGCTTCTTCAATGAGCATGTATGACAGACCTCTGAGCTGAGTGA 780  
|||  
Db 721 TGTGTCCCGTATGAGAGGCTTCTTCAATGAGCATGTATGACAGACCTCTGAGCTGAGTGA 780  
|||  
Qy 781 AGTGGCCCATTTTCCCTGAGCATGACGCTGTGAGAGTTGACCTTCTGATCTGCATCA 840  
|||  
Db 781 AGTGGCCCATTTTCCCTGAGCATGACGCTGTGAGAGTTGACCTTCTGATCTGCATCA 840  
|||  
Qy 841 AGGTGACACCATTCAGCTTACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900  
|||  
Db 841 AGGTGACACCATTCAGCTTACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900  
|||  
Qy 901 CCAAGTGGTTCATTAATCTGACAGCTTCCCTGACATGACCCAGCCCTGGACAAATCCCGT 960  
|||  
Db 901 CCAAGTGGTTCATTAATCTGACAGCTTCCCTGACATGACCCAGCCCTGGACAAATCCCGT 960  
|||  
Qy 961 TCAGCTCATCTGATGATGACAGAGAGCTGTGAAGAGTGAAGTGTGCTGTCTCTCAG 1020  
|||  
Db 961 TCAGCTCATCTGATGATGACAGAGAGCTGTGAAGAGTGAAGTGTGCTGTCTCTCAG 1020  
|||  
Qy 1021 AAGAATTCAGGCTCTGTTGAGACCTGCTGCTCTGAGAGGAGGAGGAGGAGGAGGAGG 1080  
|||  
Db 1021 AAGAATTCAGGCTCTGTTGAGACCTGCTGCTCTGAGAGGAGGAGGAGGAGGAGGAGG 1080  
|||  
Qy 1081 GCATCGGAGCTGATCAATGAAAAGAGCTGAGTAAGTGGAGATCTACCAAGTCTGAGA 1140  
|||  
Db 1081 GCATCGGAGCTGATCAATGAAAAGAGCTGAGTAAGTGGAGATCTACCAAGTCTGAGA 1140  
|||  
Qy 1141 TCCTTAATCTGAGACACTCCGAGTCTTATAGACCAAGGACATGCCAAGGTGGCCAAAC 1200  
|||  
Db 1141 TCCTTAATCTGAGACACTCCGAGTCTTATAGACCAAGGACATGCCAAGGTGGCCAAAC 1200  
|||  
Qy 1201 TGATCGTGGTGGAGTGTTCCTCCAGTGAAGGCTCCGCGCTTGTTCACCTTGAGCA 1260  
|||  
Db 1201 TGATCGTGGTGGAGTGTTCCTCCAGTGAAGGCTCCGCGCTTGTTCACCTTGAGCA 1260  
|||  
Qy 1261 TCGAAGCCAGCTCGGAAGCTCAGTTTACACCAAGGTGACCAATTAATCAACTTGA 1320  
|||  
Db 1261 TCGAAGCCAGCTCGGAAGCTCAGTTTACACCAAGGTGACCAATTAATCAACTTGA 1320  
|||  
Qy 1321 ATTAACATCAGCTCTGATCGGATCCAGTGAATGAACTTGGATGGCTGGTCTCAACTG 1380  
|||  
Db 1321 ATTAACATCAGCTCTGATCGGATCCAGTGAATGAACTTGGATGGCTGGTCTCAACTG 1380  
|||  
Qy 1381 ATGTTTGAAGAAACATCATCACTGATGATCACTCCATCTCTGCTCCGACAGATG 1440  
|||  
Db 1381 ATGTTTGAAGAAACATCATCACTGATGATCACTCCATCTCTGCTCCGACAGATG 1440  
|||

QY 1441 GCATTAATGATGTGGGGTCCAGTGTCAATGGTGAAGGCTTGGGATTCGAGGCACTG 1500  
DB 1441 GCAATTAATGATGTGGGGTCCAGTGTCAATGGTGAAGGCTTGGGATTCGAGGCACTG 1500  
QY 1501 AGTCTCAGTGAAGGATGCGCTTGTCTACTGCTTGTGCTTGTGGAAGCCAGCT 1560  
DB 1501 AGTCTCAGTGAAGGATGCGCTTGTCTACTGCTTGTGCTTGTGGAAGCCAGCT 1560  
QY 1561 CTCTCTCTCCAGTGAAGCTTGTGATGCGAGCCATCAAGGAGGCTGGTCCAGCTG 1620  
DB 1561 CTCTCTCTCCAGTGAAGCTTGTGATGCGAGCCATCAAGGAGGCTGGTCCAGCTG 1620  
QY 1621 GAGTATGGTGTGAGTCTATAGACCATCTCTCTGCAATCAATTAACACTTGGCTGTG 1680  
DB 1621 GAGTATGGTGTGAGTCTATAGACCATCTCTCTGCAATCAATTAACACTTGGCTGTG 1680

RESULT 5  
US-09-092-330-13

Sequence 13, Application US/09092330  
GENERAL INFORMATION:  
APPLICANT: BILLING-MEDEL, PATRICIA  
APPLICANT: COHEN, MAURICE  
APPLICANT: COLPITTS, TRACEY L.  
APPLICANT: FRIEDMAN, PAULA N.  
APPLICANT: KLAAS, MICHAEL R.  
APPLICANT: RUSSELL, JOHN C.  
APPLICANT: STROUPE, STEPHEN D.  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: Fastseq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/092,330  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/048,838  
FILING DATE: 06-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 6108.US.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1683 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-092-330-13

Query Match 99.3%; Score 1668.6; DB 15; Length 1683;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1679; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGTGGGAGATATTAAGGTTGAGCTTCCAGACCCAGTGGCCGGAGAGAGAGGAGCGGG 60  
DB 1 GGTGGGAGATATTAAGGTTGAGCTTCCAGACCCAGTGGCCGGAGAGAGAGAGGAGCGGG 60

QY 61 CCGAGATCCAGCGGTGCCAGGTCGATCCTGCACTTGTGCTGACCTGAG 120  
DB 61 CCGAGATCCAGCGGTGCCAGGTCGATCCTGCACTTGTGCTGACCTGAG 120  
QY 121 AAGATGCGCGCCCGTGGAGCTTCAACCTTCTGTGTGTTGCTGGCAGCACTTGATC 180  
DB 121 AAGATGCGCGCCCGTGGAGCTTCAACCTTCTGTGTGTTGCTGGCAGCACTTGATC 180  
QY 181 CAAAGCCACCCGTCAGTCCATGCAATGCTTCCTGCGCCCAAAAGTCATCAAGAAAG 240  
DB 181 CAAAGCCACCCGTCAGTCCATGCAATGCTTCCTGCGCCCAAAAGTCATCAAGAAAG 240  
QY 241 CTGACACAGAGAGCTGAAGACCAACAGCCACAGCATCTGAGAGAGTGGCTGCTC 300  
DB 241 CTGACACAGAGAGCTGAAGACCAACAGCCACAGCATCTGAGAGAGTGGCTGCTC 300  
QY 301 AGTGCATGGGGGAAAAGCCAGCCGAGG-ATGCCCTGTGTGGGAGCCGTGTAACAC 359  
DB 301 AGTGCATGGGGGAAAAGCCAGCCGAGGATGCCCTGTGTGGGAGCCGTGTAACAC 359  
QY 360 GTCCCTGAAGCACATCATCTGCTGAAGGTCATCAGAGCAATATCTCCAGCTGAGGTG 419  
DB 360 GTCCCTGAAGCACATCATCTGCTGAAGGTCATCAGAGCAATATCTCCAGCTGAGGTG 419  
QY 420 AAGCCCTGGCCCAATGACCAAGAGCTGCTAGTCAAGATCCCTGAGACATGATGGCTGGA 479  
DB 420 AAGCCCTGGCCCAATGACCAAGAGCTGCTAGTCAAGATCCCTGAGACATGATGGCTGGA 479  
QY 480 TTCAACAGCCCTGCTGTGAAGCCATCTGTGAGTTCCACATGACGACTGAGGCCAAAGCC 539  
DB 480 TTCAACAGCCCTGCTGTGAAGCCATCTGTGAGTTCCACATGACGACTGAGGCCAAAGCC 539  
QY 540 ACCATCCGATGAGACACCAAGTGAAGTGGCCCAACCCGCTGTGCTCAGTGAATGAGCC 599  
DB 540 ACCATCCGATGAGACACCAAGTGAAGTGGCCCAACCCGCTGTGCTCAGTGAATGAGCC 599  
QY 541 ACCATCCGATGAGACACCAAGTGAAGTGGCCCAACCCGCTGTGCTCAGTGAATGAGCC 600  
DB 541 ACCATCCGATGAGACACCAAGTGAAGTGGCCCAACCCGCTGTGCTCAGTGAATGAGCC 600  
QY 600 ACCAGCCATGGGAGAGCTGCGCATCCACTGCTGATTAAGCTCTCTCTGATGAAGGCC 659  
DB 600 ACCAGCCATGGGAGAGCTGCGCATCCACTGCTGATTAAGCTCTCTCTGATGAAGGCC 659  
QY 660 TTAGCTAAGCAGGTGATGAACCTCTAGTGCATCCCTGCGCAATCAAGGAAAACCAAG 719  
DB 660 TTAGCTAAGCAGGTGATGAACCTCTAGTGCATCCCTGCGCAATCAAGGAAAACCAAG 719  
QY 720 CTGTGTCCTGATGAGGCTTCTCTTAATGCAATGATGATGACAGCTCTGACGCTGTG 779  
DB 720 CTGTGTCCTGATGAGGCTTCTCTTAATGCAATGATGATGACAGCTCTGACGCTGTG 779  
QY 780 AAGGTGCCATTTCCCTCAGCATTTGACCGCTGAGAGTTGACCTTGTATCTGTCGATC 839  
DB 780 AAGGTGCCATTTCCCTCAGCATTTGACCGCTGAGAGTTGACCTTGTATCTGTCGATC 839  
QY 840 AAGGTGCCATTTCCCTCAGCATTTGACCGCTGAGAGTTGACCTTGTATCTGTCGATC 840  
DB 840 AAGGTGCCATTTCCCTCAGCATTTGACCGCTGAGAGTTGACCTTGTATCTGTCGATC 840  
QY 841 AAGGTGCCATTTCCCTCAGCATTTGACCGCTGAGAGTTGACCTTGTATCTGTCGATC 899  
DB 841 AAGGTGCCATTTCCCTCAGCATTTGACCGCTGAGAGTTGACCTTGTATCTGTCGATC 899  
QY 900 ACCAAGTGTTCATTAATCTGAGAGCTTCCCTGACAAAGCCACCTGAGCAACATCCCG 959  
DB 900 ACCAAGTGTTCATTAATCTGAGAGCTTCCCTGACAAAGCCACCTGAGCAACATCCCG 959  
QY 960 TTACAGCTCATGCTGATGAGAGAGCTGTTGAAGCTGACAGTGGCTGTGCTCTCTCA 1019  
DB 960 TTACAGCTCATGCTGATGAGAGAGCTGTTGAAGCTGACAGTGGCTGTGCTCTCTCA 1019  
QY 1020 GAAGAAATTCATGCTCTGTGAGTCTGTGCTTCTGAGAGTGGCCATGCGCTGAAGTCA 1079  
DB 1020 GAAGAAATTCATGCTCTGTGAGTCTGTGCTTCTGAGAGTGGCCATGCGCTGAAGTCA 1079  
QY 1080 AAGATCGGCTGATCAATGAAGAGCTCAGATTAAGCTGAGATCAACAGATGTGAAG 1139  
DB 1080 AAGATCGGCTGATCAATGAAGAGCTCAGATTAAGCTGAGATCAACAGATGTGAAG 1139  
QY 1081 AACATCGGCTGATCAATGAAGAGCTCAGATTAAGCTGAGATCAACAGATGTGAAG 1140  
DB 1081 AACATCGGCTGATCAATGAAGAGCTCAGATTAAGCTGAGATCAACAGATGTGAAG 1140

OY	1140	ATCCTAATCTGAGGACACTCCCGAGTTTATTATACCAAGGCCATGCCAAGTGGCCAA	1139
OY	1140		
Db	1141	ATCCTAATCTGAGGACACTCCCGAGTTTATTATACCAAGGCCATGCCAAGTGGCCAA	1200
OY	1200	CTGATTCGTCGGGAAGTGTTCCTCCAGTAGAAGCCCTCCGCCCTTTGTACCCCTGGGC	1259
OY	1200		
Db	1201	CTGATTCGTCGGGAAGTGTTCCTCCAGTAGAAGCCCTCCGCCCTTTGTACCCCTGGGC	1260
OY	1260	ATCGAAGCCAGCTCGGAAGCTCAGTCTTATACACAAAGGTGACCAACTTATACTCAACTTG	1319
OY	1261	ATCGAAGCCAGCTCGGAAGCTCAGTCTTATACACAAAGGTGACCAACTTATACTCAACTTG	1320
OY	1320	AATTAACATCAGCTCGATCGGATCGAGTCGATGAACTCTGGATTGGCTGGTTCCAACT	1379
Db	1321	AATTAACATCAGCTCGATCGGATCGAGTCGATGAACTCTGGATTGGCTGGTTCCAACT	1380
OY	1380	GATGTTCTGAAAAAATCATCATCATGAGATCATCCACTCATCTGCTGCCAGACAGAT	1439
Db	1381	GATGTTCTGAAAAAATCATCATCATGAGATCATCCACTCATCTGCTGCCAGACAGAT	1440
OY	1440	GGCAAAATTAAGATCTGGGGTCCCACTGTCATGTGTGAAGGCCCTTGGGATTCGAGGCACT	1499
Db	1441	GGCAAAATTAAGATCTGGGGTCCCACTGTCATGTGTGAAGGCCCTTGGGATTCGAGGCACT	1500
OY	1500	GAGTCTCTACAGCAGCAAGGATGCCCTGTGCTTACTCCAGCCTCCTTGTGGAAACCCAGC	1559
Db	1501	GAGTCTCTACAGCAGCAAGGATGCCCTGTGCTTACTCCAGCCTCCTTGTGGAAACCCAGC	1560
OY	1560	TCTCCTGTCTCCAGTAGAAGACTTGATGCGCAGCCATCAGGGAAGGCTGSGTCCAGCTG	1619
Db	1561	TCTCCTGTCTCCAGTAGAAGACTTGATGCGCAGCCATCAGGGAAGGCTGSGTCCAGCTG	1620
OY	1620	GGAGTATGGGGTGTAGCTCTATAGACCATCCCTCTGCGCAATCAATAACACTTGCCCTGT	1679
Db	1621	GGAGTATGGGGTGTAGCTCTATAGACCATCCCTCTCTGCAATCAATAACACTTGCCCTGT	1680
OY	1680	G	
Db	1681	G	
RESULT 6			
US-60-213-359-3023			
: Sequence 3023, Application US/60213359			
: GENERAL INFORMATION:			
: APPLICANT: Morris, MacDonald			
: APPLICANT: Lal, Preeti			
: TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using			
: TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor			
: FILE REFERENCE: GX-0015 P			
: CURRENT APPLICATION NUMBER: US/60/213,359			
: CURRENT FILING DATE: 2000-06-21			
: NUMBER OF SEQ ID NOS: 7924			
: SOFTWARE: PERL Program			
: SEQ ID NO 3023			
: LENGTH: 1698			
: TYPE: DNA			
: ORGANISM: Homo sapiens			
: FEATURE:			
: NAME/KEY: misc_feature			
: OTHER INFORMATION: Incyte ID No: 026723.3			
US-60-213-359-3023			

Query Match	99.3%	Score 1668.6;	DB 75;	Length 1698;
Best Local Similarly	99.9%;			
Matches 1679; Conservative	1;	Mismatches	0;	Indels 1; Gaps 1.

Oy 1 GGTGTGCAGGATATTAAGTTGGACTTCCAGACCACTGCCCGGGAGAGAGRGAGCGGG 60  
 |||||  
 Db 18 GGTGTGCAGGATATTAAGTTGGACTTCCAGACCACTGCCCGGGAGAGAGAGAGCGGG 77

[illegible]

Db 81 CCGAGACTCCACGCTGCCAGGCTCTGGCATCTGACATTTGCTGCTCCCTGTGACACCTGGG 140

QY 121 AAGATGGCCGGCCCGCTGGACCTTCAACCTTCTGCTGGTTTGCTGGGAGCCACCTTGATC 180

Db 141 AAGATGGCCGGCCCGCTGGACCTTCAACCTTCTGCTGGTTTGCTGGGAGCCACCTTGATC 200

QY 181 CAAGCACCCTTCAGTCCCATCTGACAGTTCATCTCTGGGCCCAAAAGATCAAAAGAAAAG 240

Db 201 CAAGCACCCTTCAGTCCCATCTGACAGTTCATCTCTGGGCCCAAAAGATCAAAAGAAAAG 260

QY 241 CTGACACAGGAGCTGAAGAGACACAAAGCCACACAGCATCTCTGACAGAGTCCGCTGTC 300

Db 261 CTGACACAGGAGCTGAAGAGACACAAAGCCACACAGCATCTCTGACAGAGTCCGCTGTC 320

QY 301 AGTGCATGCGGGAAAAAGCCAGCCGGAGG-ATCCCTGCTGCTGGGACGCTGGTGAACAC 359

Db 321 AGTGCATGCGGGAAAAAGCCAGCCGGAGGAGCATCCCTGCTGCTGGGACGCTGGTGAACAC 380

QY 360 GTCCCTGAAGACATCATCTGGCTGAAGAGTATACAGATCTCTCAAGCTGACAGGTG 419

Db 381 GTCCCTGAAGACATCATCTGGCTGAAGAGTATACAGATCTCTCAAGCTGACAGGTG 440

QY 420 AAGCCCTCGGCCCATATGACAGAGGCTGTAGTCAAGATCCCTCGACATGTGTGCTGGA 479

Db 441 AAGCCCTCGGCCCATATGACAGAGGCTGTAGTCAAGATCCCTCGACATGTGTGCTGGA 500

QY 480 TTCAACAGCGCCCTTGTCGAAGACATCTGGAGTTCTCATATGACACTGAGGCCCAAGCC 539

Db 501 TTCAACAGCGCCCTTGTCGAAGACATCTGGAGTTCTCATATGACACTGAGGCCCAAGCC 560

QY 540 ACCATCCGATGAGACACCAAGTGCATGTGGCCCCACCGCGCTGTCTTAGTGAAGTGTGCC 599

Db 561 ACCATCCGATGAGACACCAAGTGCATGTGGCCCCACCGCGCTGTCTTAGTGAAGTGTGCC 620

QY 600 ACCAGCATGTGGAGGCTGGGCATCCAACTGCTGCATTAAGCTTCTCTTCTGGTGAAGGCC 659

Db 621 ACCAGCATGTGGAGGCTGGGCATCCAACTGCTGCATTAAGCTTCTCTTCTGGTGAAGGCC 659

QY	880	TTAGGTAAAGCAGGTCATGAACCTCTCTAGTGCCTCAATCCCGCCCAATCTGTGAAAAACACG	713
Db	681	TTAGGTAAAGCAGGTCATGAACCTCTCTAGTGCATCCCTCCCAATCTGTGAAAAACACG	740
QY	720	CTGTGTCCCGTGATCGAGGCTTCCTCTCAATGGCATGTATGACGACCTCTCTGACGTGGTG	779
Db	741	CTGTGTCCCGTGATCGAGGCTTCCTCTCAATGGCATGTATGACGACCTCTCTGACGTGGTG	800
QY	780	AAGGTGCCAATTTCCCTCAGACATTGACCGCTGTGAGTTTGACCTTCTGTATCTCGCATC	839
Db	801	AAGGTGCCAATTTCCCTCAGACATTGACCGCTGTGAGTTTGACCTTCTGTATCTCGCATC	866
QY	840	AAAGGTACACCAATTGACGTCTACCTCGGGGGCCAAAGTTGTGGACTCAGACAGGAAAAGTG	899
Db	861	AAAGGTACACCAATTGACGTCTACCTCGGGGGCCAAAGTTGTGGACTCAGACAGGAAAAGTG	920
QY	900	ACCAAGTGGTTCAATTAACCTCGAGCTTCCCTGCAATGCGCCACCGCTGGACAAACATCCCG	959
Db	921	ACCAAGTGGTTCAATTAACCTCGAGCTTCCCTGCAATGCGCCACCGCTGGACAAACATCCCG	980
QY	960	TTAGGCTCATCTGTAGTCAAGGACCTGGTGAAGCTGACGAGTGGCTGTGTCTCTCTCA	1011
Db	981	TTAGGCTCATCTGTAGTCAAGGACCTGGTGAAGCTGACGAGTGGCTGTGTCTCTCTCTCA	

Accession	Sequence	Position
QY	1020 GAAGAAATTCATGGTCCCTGTTGGACCTCTGCTCTCCAGAGTGCCCATCGGCTGAAGTGA	107
Db	1041 GAAGAAATTCATGGTCCCTGTTGGACCTCTGCTCTCCAGAGTGCCCATCGGCTGAAGTGA	1107
QY	1080 AGCATTGGGCGCTCATTAATGAAGAAAGCGTCGAGATTAAGCTGGGATCTTCCAGATCTGGAAG	1137
Db	1101 AGCATTGGGCGCTCATTAATGAAGAAAGCGTCGAGATTAAGCTGGGATCTTCCAGATCTGGAAG	1167
QY	1140 ATCCCTAATCAGAGAACATCCCGAGATTTTATTAAGCCAGAGCCCATCCAAAGGTGGCCCAA	1199
Db	1161 ATCCCTAATCAGAGAACATCCCGAGATTTTATTAAGCCAGAGCCCATCCAAAGGTGGCCCAA	1229

QY	1200	CTGATCGTGC	TGGAAGTCTTTCCTCCAGTAAAGCCTCCGCCCTTTTGTACCCCTGGGC	1239
Db	1221	CTGATCGTGC	TGGAAGTCTTTCCTCCAGTAAAGCCTCCGCCCTTTTGTACCCCTGGGC	1280
QY	1260	ATCGAAGCAGCTCG	GAAGTCAAGTTTACACCAAGAGTGACCAACTATACCACTG	1319
Db	1281	ATCGAAGCAGCTCG	GAAGTCAAGTTTACACCAAGAGTGACCAACTATACCACTG	1340
QY	1320	AATAACATCAGCTCTG	ATCGGATCCAGCTGTAAGACTCTGGGATTGGCTGGTCCAACT	1379
Db	1341	AATAACATCAGCTCTG	ATCGGATCCAGCTGTAAGACTCTGGGATTGGCTGGTCCAACT	1400
QY	1380	GATGTTCTGAAAAACATCATC	AGATTCATCCATCCATCCATCCGTCGTCGCCAACCAGAT	1439
Db	1401	GATGTTCTGAAAAACATCATC	AGATTCATCCATCCATCCATCCGTCGTCGCCAACCAGAT	1460
QY	1440	GGCAAAATTAAGTCTG	GGGTCCTCCAGTGCATTTGGTGAAGGCCCTTGGATTGAGGACGCT	1499
Db	1461	GGCAAAATTAAGTCTG	GGGTCCTCCAGTGCATTTGGTGAAGGCCCTTGGATTGAGGACGCT	1520
QY	1500	GAGTCTTCAC	TGACCAAGATGCCCTTGTGCTTACTCCAGCCTCCTTGTGGAACCCAGC	1559
Db	1521	GAGTCTTCAC	TGACCAAGATGCCCTTGTGCTTACTCCAGCCTCCTTGTGGAACCCAGC	1580
QY	1560	TCTCCTGCTCCCAAGTGA	AGACTTGGATGGAGCATATGGGAAGAGCGGTGCCAAGCTG	1619
Db	1581	TCTCCTGCTCCCAAGTGA	AGACTTGGATGGAGCATATGGGAAGAGCGGTGCCAAGCTG	1640
QY	1620	GGAGTATGGTGTG	TAGCTCTATAGCAATCCCTCTCTGCATCATATAAACACTTGCCCTGT	1679
Db	1641	GGAGTATGGTGTG	TAGCTCTATAGCAATCCCTCTCTGCATCATATAAACACTTGCCCTGT	1700
QY	1680	G	1680	
Db	1701	G	1701	
RESULT 8				
US-09-720-530-12				
; Sequence 12, Application US/09720530				
; GENERAL INFORMATION:				
; APPLICANT: INCYTE PHARMACEUTICALS, INC.				
; APPLICANT: LAL, Preeti				
; APPLICANT: TANG, Y. Tom				
; APPLICANT: YUE, Henry				
; APPLICANT: CORLEY, Neil C.				
; APPLICANT: GUESLER, Karl J.				
; APPLICANT: GORGONE, Gina A.				
; APPLICANT: BAUSHN, Mariah R.				
; APPLICANT: PATTERSON, Chandra				
; TITLE OF INVENTION: NEUROTRANSMISSION ASSOCIATED PROTEINS				
; FILE REFERENCE: PF-0551 PCT				
; CURRENT APPLICATION NUMBER: US/09/720,530				
; CURRENT FILING DATE: 2002-08-26				
; PRIOR APPLICATION NUMBER: 60/091,667				
; PRIOR FILING DATE: 1998-07-02				
; NUMBER OF SEQ ID NOS: 12				
; SOFTWARE: PERL Program				
; SEQ ID NO 12				
; LENGTH: 1707				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
; FEATURE:				
; NAME/KEY: misc_feature				
; OTHER INFORMATION: Incyte Clone No: 2799056				
US-09-720-530-12				
Query Match 99.2%; Score 1667; DB 32; Length 1707;				
Best Local Similarity 99.8%; Pred. No. 0;				
Matches 1678; Conservative 1; Mismatches 1; Indels 1; Gaps 1;				
1 GCGTGCAGATATTAAGTTTGGACTTCCAGACCCACTCCGGGAGAGAGRNGACGCGG 60				

[illegible]

Db	1081	AGCATGGGGCTGATTCATATGAAAAGCTGCAGATTAAGCTGGAGTCTAACCATCATGCTGTGAAG	1140
QY	1140	ATCTTAAGTACGAGACACTCCGAGTCTTTTATATAGACCAAGGCCATGCGAAGTGGCCCA	1199
Db	1141	ATCTTAAGTACGAGACACTCCGAGTCTTTTATATAGACCAAGGCCATGCGAAGTGGCCCA	1200
QY	1200	CTGATGTCCTGGAAAGTCTTTTCCCTCCAGTGAAGCCCTCCGCCCTTTGTCACCCCTGGAG	1259
Db	1201	CTGATGTCCTGGAAAGTCTTTTCCCTCCAGTGAAGCCCTCCGCCCTTTGTCACCCCTGGAG	1260
QY	1260	ATCGAAGCCAGCTCGAAGCTCAGTTTATACACCAAGGTGACCAACTATATCTCAACTTG	1319
Db	1261	ATCGAAGCCAGCTCGAAGCTCAGTTTATACACCAAGGTGACCAACTATATCTCAACTTG	1320
QY	1320	AATTAACATCAGCTCTGATCGAGTCCAGCTGATGAACTGCGAGTTGGCTGGTTCACACT	1379
Db	1321	AATTAACATCAGCTCTGATCGAGTCCAGCTGATGAACTCTGGAGTTGGCTGGTTCACACT	1380
QY	1380	GATGTCCTGGAAAAACATATCATCTAGATTCATCCATCCATCTCTGTCGCCGAACAGAAAT	1439
Db	1381	GATGTCCTGGAAAAACATATCATCTAGATTCATCCATCCATCTCTGTCGCCGAACAGAAAT	1440
QY	1440	GGCATAATTAAGATCTGGGGTCCCAAGTGCATGTTGTAAGGCTTTGGATTTCGAGGCAGCT	1499
Db	1441	GGCATAATTAAGATCTGGGGTCCCAAGTGCATGTTGTAAGGCTTTGGATTTCGAGGCAGCT	1500
QY	1500	GAGTCTCTACTGACCAAGAGATGCCCTGTGCTTACTCCAGCTCCCTGTTGGAAAACCCAGC	1559
Db	1501	GAGTCTCTACTGACCAAGAGATGCCCTGTGCTTACTCCAGCTCCCTGTTGGAAAACCCAGC	1560
QY	1560	TCTCTGTCTCCCAAGTGAACCTTTGGATGGCAGCCATCAGGAAGGCTGGGTCCCAAGTTG	1619
Db	1561	TCTCTGTCTCCCAAGTGAACCTTTGGATGGCAGCCATCAGGAAGGCTGGGTCCCAAGTTG	1620
QY	1620	GGAGTATGGGTGAGCTTATAGACCATCCCTCTGCAATTAATTAACACTTGGCTGT	1679
Db	1621	GGAGTATGGGTGAGCTTATAGACCATCCCTCTGCAATTAATTAACACTTGGCTGT	1680
QY	1680	G	1680
Db	1681	G	1681

```

US-09-720-530A-12
: Sequence 12, Application US/09720530A
: GENERAL INFORMATION:
: APPLICANT: INCYTE PHARMACEUTICALS, INC.
: APPLICANT: IAL, Preci1
: APPLICANT: TANG, Y. Tom
: APPLICANT: YDE, Henry
: APPLICANT: CORLEY, Neil C.
: APPLICANT: GUEGLER, Karl J.
: APPLICANT: GORGONE, Gina A.
: APPLICANT: BAUGHN, Mariah R.
: APPLICANT: PATTERSON, Chandra
: TITLE OF INVENTION: NEUTROTRANSMISSION ASSOCIATED PROTEINSS
: FILE REFERENCE: PF-0551 PCT
: CURRENT APPLICATION NUMBER: US/09/720,530A
: CURRENT FILING DATE: 2000-12-19
: PRIOR APPLICATION NUMBER: 60/091,667
: PRIOR FILING DATE: 1998-07-02
: NUMBER OF SEQ. ID NOS: 12
: SOFTWARE: PERL Program
: SEQ ID NO 12
:
: LENGTH: 1707
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte Clone No: 279056
US-09-720-530A-12

```

Query Match	99.24%	Score 1667	DB 32	Length 1707
Best Local Similarity	99.88%	Pred. No. 0		
Matches 1678	Conservative 1	Mismatches 1	Indels 1	Gaps 1
QY	1	GGGTGACAGATATATAGGTGGACCTTCCACACCACCTGCCCGGGAGAGAGAGACGGG	60	
Db	1	GGGTGACAGATATATAGGTGGACCTTCCACACCACCTGCCCGGGAGAGAGAGACGGG	60	
QY	61	CCGAGGACTCCAGGTTGCCCAAGGCTGCGCATCTGACATGTCCTTGACACCTTGGG	120	
Db	61	CCGAGGACTCCAGGTTGCCCAAGGCTGCGCATCTGACATGTCCTTGACACCTTGGG	120	
QY	121	AAGATGGCCCGGCGGTGGACCTTCCACCCCTTCTGTGGTTTCTGTGGACACCTTATC	180	
Db	121	AAGATGGCCCGGCGGTGGACCTTCCACCCCTTCTGTGGTTTCTGTGGACACCTTATC	180	
QY	181	CAAGCCACCTCAGTCCCACTGCATGATTCATCTCTGGCCCAAAAGATATCAAAAGAAAG	240	
Db	181	CAAGCCACCTCAGTCCCACTGCATGATTCATCTCTGGCCCAAAAGATATCAAAAGAAAG	240	
QY	241	CTGACACAGAGAGCTGTAAGGACCAACAGCCACACAGATCTTGACAGCTCCGCTGTC	300	
Db	241	CTGACACAGAGAGCTGTAAGGACCAACAGCCACACAGATCTTGACAGCTCCGCTGTC	300	
QY	301	AGTGGCATCGGGGAAAGCCAGCCGAGG - ATCCCTGTGGTGGGAGACCTGGTAGAACCC	359	
Db	301	AGTGGCATCGGGGAAAGCCAGCCGAGGATCCCTGTGCTGGGAGACCTGGTAGAACCC	360	
QY	360	GTCCTTAACACATCATCTCTGGGTGAAGGATACACAGTAACATCTTCCAGCTCAGAGT	419	
Db	361	GTCCTTAACACATCATCTCTGGGTGAAGGATACACAGTAACATCTTCCAGCTCAGAGT	420	
QY	420	AAGCCTCGGCAATGACCCAGGAGCTGTAGTCAAGATCCCTCGGACATGGTGGCGGA	479	
Db	421	AAGCCTCGGCAATGACCCAGGAGCTGTAGTCAAGATCCCTCGGACATGGTGGCGGA	480	
QY	480	TTCAACACAGCCCTCTGGTCAAGCATCTGGAGTTCCATGATGACGACTGAGGCCAAGCC	539	
Db	481	TTCAACACAGCCCTCTGGTCAAGCATCTGGAGTTCCATGATGACGACTGAGGCCAAGCC	540	
QY	540	ACCATCCGCATGACACCAAGTGAAGTGGCCCAACCCGCTGGTCCCTCACTGATCTGGCC	599	
Db	541	ACCATCCGCATGACACCAAGTGAAGTGGCCCAACCCGCTGGTCCCTCACTGATCTGGCC	600	
QY	600	ACCAGCATGGGAGGCTCGCATCACTGCTGCATATAGCTCTCTCTGCTGTAAGGCC	659	
Db	601	ACCAGCATGGGAGGCTCGCATCACTGCTGCATATAGCTCTCTCTGCTGTAAGGCC	660	
QY	660	TTAGCTTAAGCAGGTATGAACCTCTCTAGTGCATCCCTGCCCAATGTAGTGAAGAAACG	719	
Db	661	TTAGCTTAAGCAGGTATGAACCTCTCTAGTGCATCCCTGCCCAATGTAGTGAAGAAACG	720	
QY	720	CTGTGTCCCGGATGACGAGCTCTCTTAATGGCATGTATGCAGACCTCTGACGTGGTG	779	
Db	721	CTGTGTCCCGGATGACGAGCTCTCTTAATGGCATGTATGCAGACCTCTGACGTGGTG	780	
QY	780	AAGGTGCCATTTCCCTCAGCATTTGACCGCTGAGATTTTGAGCTTGTATCTCTGCATC	839	
Db	781	AAGGTGCCATTTCCCTCAGCATTTGACCGCTGAGATTTTGAGCTTGTATCTCTGCATC	840	
QY	840	AAGGTGACACCATTTACGCTCTACCTGTGGGGGCCAAGTTTGGAGCTACAGGAAAGATG	899	
Db	841	AAGGTGACACCATTTACGCTCTACCTGTGGGGGCCAAGTTTGGAGCTACAGGAAAGATG	900	
QY	900	ACCAAGGTGTTCAATATCTGTGAGTTCTCCGTGACAAATCCCAACCTTGACAAATCCCG	959	
Db	901	ACCAAGGTGTTCAATATCTGTGAGTTCTCCGTGACAAATCCCAACCTTGACAAATCCCG	960	
QY	960	TTTAACTCATGTGTGATGACGACGTGTGAAGGTGACAGTGGTCTGTGCTCTTCCA	1019	
Db	961	TTTAACTCATGTGTGATGACGACGTGTGAAGGTGACAGTGGTCTGTGCTCTTCCA	1020	
QY	1020	GAGCAATTAATGCTCTGTGGACATCTGTGCTCTCTGAGATGGCCCATGGCTGAAGTCA	1079	



```
Db 1021 GAGAAATTCATGGTCCGTGGAGCTGTGCTTCCTAGAGTGCCTGCGCTGAAGTCA 1080
QY 1080 AGCATCGGGCGTGCATCAATGAAAAAGGCTGCAGATTAAGCTGGAGATCTACCCAGATCTGAAG 1139
Db 1081 AGCATCGGGCGTGCATCAATGAAAAAGGCTGCAGATTAAGCTGGAGATCTACCCAGATCTGAAG 1140
QY 1140 ATCTTAATCAAGAGACTCCCGAGTTTATTAATAGACCAAGGCCATGCGCAAGGTCGCCAA 1199
Db 1141 ATCTTAATCAAGAGACTCCCGAGTTTATTAATAGACCAAGGCCATGCGCAAGGTCGCCAA 1200
QY 1200 CTGATCGTGTGGAAGGTTCCTCCAGTGAAGCCCTCGCCCTTGTTCACCTTGCGC 1259
Db 1201 CTGATCGTGTGGAAGGTTCCTCCAGTGAAGCCCTCGCCCTTGTTCACCTTGCGC 1260
QY 1260 ATCGAAGCCAGCTCGAAGCTCAGTTTATACCAAAAGTGAACCACTTATACCACTTG 1319
Db 1261 ATCGAAGCCAGCTCGAAGCTCAGTTTATACCAAAAGTGAACCACTTATACCACTTG 1320
QY 1320 AATTAACATCAGCTCTGATCGGATCCAGCTGATGAATCTGGGATTTGGCTGGTCCAACT 1379
Db 1321 AATTAACATCAGCTCTGATCGGATCCAGCTGATGAATCTGGGATTTGGCTGGTCCAACT 1380
QY 1380 GATGTTCTGAAAAAATCATCATCTGAGATATCATCTCCATCTGCTGCTGCCGAACCAAT 1439
Db 1381 GATGTTCTGAAAAAATCATCATCTGAGATATCATCTCCATCTGCTGCTGCCGAACCAAT 1440
QY 1440 GGCATAATTAAGATCTGGGGTCCAGTGTCAATTTGGTGAAGCCCTTGGGATTCGAGGACGT 1499
Db 1441 GGCATAATTAAGATCTGGGGTCCAGTGTCAATTTGGTGAAGCCCTTGGGATTCGAGGACGT 1500
QY 1500 GAGTCTCTACTGACCAAGATGCCCTTGTGCTTACTCTACCTGCTGCTGCTGCTGCTGCTGCT 1559
Db 1501 GAGTCTCTACTGACCAAGATGCCCTTGTGCTTACTCTACCTGCTGCTGCTGCTGCTGCTGCT 1560
QY 1560 TCTCCCTCTCTCCAGTGAACCTTGAATGTCGACGATCAGGAGAGGCTGGGTCCACTG 1619
Db 1561 TCTCCCTCTCTCCAGTGAACCTTGAATGTCGACGATCAGGAGAGGCTGGGTCCACTG 1620
QY 1620 GGAATATGGGTGTGAGCTCTATAGACCATCCCTCTGCAATCAATTAACACTTGGCTGT 1679
Db 1621 GGAATATGGGTGTGAGCTCTATAGACCATCCCTCTGCAATCAATTAACACTTGGCTGT 1680
QY 1680 G 1680
Db 1681 G 1681
```

```
RESULT 10
US-60-091-677-15
; Sequence 15, Application US/60091677
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Gorgone, Gina
; APPLICANT: Baugh, Mariah R.
; APPLICANT: Pateson, Chandra
; TITLE OF INVENTION: NEUTROTRANSMISSION ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0551 P
; CURRENT APPLICATION NUMBER: US/60/091,677
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 1707
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
; FEATURE:
; OTHER INFORMATION: 2799056, NP01NOT01
```

```
US-60-091-677-15
Query Match 99.2%; Score 1667; DB 63; Length 1707;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1678; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 GGTGTGAGAGATATTAAGTTTGAGCTTCAGACCCACTGCCCGGAGAGAGAGGAGCGGG 60
Db 1 GGTGTGAGAGATATTAAGTTTGAGCTTCAGACCCACTGCCCGGAGAGAGAGAGGAGCGGG 60
QY 61 CCGAGGACCTCAGGAGTCCAGGCTGCGGATCCGTCGACCTTGTCCCTCTGACACTGGG 120
Db 61 CCGAGGACCTCAGGAGTCCAGGCTGCGGATCCGTCGACCTTGTCCCTCTGACACTGGG 120
QY 121 AAGATGGCCGCGCCGCTGAGCTTTCACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 121 AAGATGGCCGCGCCGCTGAGCTTTCACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 181 CAAGCCACCTCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCC 240
Db 181 CAAGCCACCTCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCC 240
QY 241 CTGACACAGAGAGCTGAAGAGACACCAAGCCACAGCTCCTGACAGAGCTGCGCTCTC 300
Db 241 CTGACACAGAGAGCTGAAGAGACACCAAGCCACAGCTCCTGACAGAGCTGCGCTCTC 300
QY 301 AGTGCATATGGCGGAAAAAGCCAGCCGAGAG-ATCCCTGCTGGGAGCCTGCTGCTGCTGCT 359
Db 301 AGTGCATATGGCGGAAAAAGCCAGCCGAGAGAGCTCCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 360 GTCTGAGAGCATCATCTGCTGAGGATCATCAGACCTTAACATCTCCAGCTGACAGT 419
Db 361 GTCTGAGAGCATCATCTGCTGAGGATCATCAGACCTTAACATCTCCAGCTGACAGT 420
QY 420 AAGCCCTGCGCCATGACACAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 479
Db 421 AAGCCCTGCGCCATGACACAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 480 TTCAACAGCCCGCTGCTGCAAGACCATGCTGAGTTCACATGACAGTGAAGGCCCAAGCC 539
Db 481 TTCAACAGCCCGCTGCTGCAAGACCATGCTGAGTTCACATGACAGTGAAGGCCCAAGCC 540
QY 540 ACCATCCGATGACACCAAGTGAAGTGGCCCAAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 599
Db 541 ACCATCCGATGACACCAAGTGAAGTGGCCCAAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 600 ACCAGCCATGGAGAGCTGCGCATCCATCTGATATAGCTCTCTCTGCTGCTGCTGCTGCT 659
Db 601 ACCAGCCATGGAGAGCTGCGCATCCATCTGATATAGCTCTCTCTGCTGCTGCTGCTGCTGCT 660
QY 660 TTAGCTAAGCAGGTCATGACCTCTAGTGCATCCCTGCGCAATCTAGTGAAGAAACAG 719
Db 661 TTAGCTAAGCAGGTCATGACCTCTAGTGCATCCCTGCGCAATCTAGTGAAGAAACAG 720
QY 720 CTGTGTCGCTGATGAGGCTTCCTTCATGATGATGATGATGATGATGATGATGATGATGATG 779
Db 721 CTGTGTCGCTGATGAGGCTTCCTTCATGATGATGATGATGATGATGATGATGATGATGATG 780
QY 780 AAGGTGCCAATTCCTGACATGACCTGAGTGAAGTTGACCTTCTGATTCGCTGATC 839
Db 781 AAGGTGCCAATTCCTGACATGACCTGAGTGAAGTTGACCTTCTGATTCGCTGATC 840
QY 840 AAGGTGACACCATTCAGCTCTACTGGGGCCAAAGTTGTTGATGATGATGATGATGATGATGAT 899
Db 841 AAGGTGACACCATTCAGCTCTACTGGGGCCAAAGTTGTTGATGATGATGATGATGATGATGAT 900
QY 900 ACCAAGTGTTCATTAATCTGACGCTTCCCTGCAATGCGCCACCTGGAACAATCCG 959
Db 901 ACCAAGTGTTCATTAATCTGACGCTTCCCTGCAATGCGCCACCTGGAACAATCCG 960
QY 960 TTGAGCTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1019
Db 961 TTGAGCTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
```



QY	1020	GAGAAATTGATGTCCTGTTGGACATCTGTCCTTCTTGAGAGTGGCCCATGGGCTGAAGTCA	1079
Db	1021	GAAGAATTATAGTCTCTGTTGGACATCTGTGCTTCTTGAGAGTGGCCCATGGGCTGAAGTCA	
QY	1080	AGCATCGGGCTGATCATTAATGAAAAGGCTGAGATTAAGTGGGATCTACCAACATGCTGAAG	1139
Db	1081	AGCATCGGGCTGATCATTAATGAAAAGGCTGAGATTAAGTGGGATCTACCAACATGCTGAAG	1140
QY	1140	ATCCTTAACTCAGAGACACTCCGAGTTTATATAGCCAAAGGCCATGCCAAGGTGGCCCA	1199
Db	1141	ATCCTTAACTCAGAGACACTCCGAGTTTATATAGCCAAAGGCCATGCCAAGGTGGCCCA	1200
QY	1200	CTGATCGTCTGGAAGTGTTCCTCCACAGTGAAGCCCGCGCCCTTGTACCTGGGC	1239
Db	1201	CTGATCGTCTGGAAGTGTTCCTCCACAGTGAAGCCCGCGCCCTTGTACCTGGGC	1260
QY	1260	ATCGAAGCCAGCTCGGAAGCTCAGTTTACACCAAAAGGTGACCAATTATCTCAACTTG	1319
Db	1261	ATCGAAGCCAGCTCGGAAGCTCAGTTTACACCAAAAGGTGACCAATTATCTCAACTTG	1320
QY	1320	AATTAACATCAGCTCTGATCGGATCCAGTGAATCGATGGGATTTGGCTGGTCCAACT	1379
Db	1321	AATTAACATCAGCTCTGATCGGATCCAGTGAATCGATGGGATTTGGCTGGTCCAACT	1380
QY	1380	GATGTTCTGAAAAACATCATCATCTGAGATTCATCCACTCCAGTCCGTGCGCAACAGAAAT	1439
Db	1381	GATGTTCTGAAAAACATCATCATCTGAGATTCATCCACTCCAGTCCGTGCGCAACAGAAAT	1440
QY	1440	GGCAAAATTAAGTCTGGGGTCCCAAGTGTCAATTTGGTGAAGGCTTGGGATTCGAGGCACT	1499
Db	1441	GGCAAAATTAAGTCTGGGGTCCCAAGTGTCAATTTGGTGAAGGCTTGGGATTCGAGGCACT	1500
QY	1500	GAGTCCCTCAGTACCAAGATGCCCTGTGCTACTCAGGCTCCTTGTGGAACCCAGC	1559
Db	1501	GAGTCCCTCAGTACCAAGATGCCCTGTGCTACTCAGGCTCCTTGTGGAACCCAGC	1560
QY	1560	TCTCTGCTCCCAAGTGAAGACTTGGATGGCAGCCATCAGGAAAGCTGGGTCCCAAGCTG	1619
Db	1561	TCTCTGCTCCCAAGTGAAGACTTGGATGGCAGCCATCAGGAAAGCTGGGTCCCAAGCTG	1620
QY	1620	GGAGTATGGGTGAGCTCTATTAGACCATCCCTCTGCAATCAATTAACATCTGGCTGT	1679
Db	1621	GGAGTATGGGTGAGCTCTATTAGACCATCCCTCTGCAATCAATTAACATCTGGCTGT	1680
QY	1680	G	1680
Db	1681	G	1681

```

: RESULT 11
: US-09-788-990-5
: Sequence 5, Application US/09788990
: GENERAL INFORMATION:
: APPLICANT: Chen, Sei Yu
: APPLICANT: Sun, Yongming
: APPLICANT: Maqina, Roberto
: TITLE OF INVENTION: Method of Diagnosing
: TITLE OF INVENTION: Treating Lung Cancer
: FILE REFERENCE: DEX-0140
: CURRENT APPLICATION NUMBER: US/09/788, 990
: CURRENT FILING DATE: 2001-02-20
: PRIOR APPLICATION NUMBER: 60/183,188
: PRIOR FILING DATE: 2000-02-17
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 5
: LENGTH: 2036
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-788-990-5

```

Query Match	98.68;	Score 1656.2;	DB 33;	Length 2036;
-------------	--------	---------------	--------	--------------

Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1678; Conservative 2; Mismatches 0; Indels 3; Gaps 2

OY	1	GGTGTGAGGATATAAAGTTTGGACTTCACAGCCACTGCCGGGAGAG - GAGRGAGCG	58
Db	38	GGTGTGAGGATATAAAGTTTGGACTTCACAGCCACTGCCGGGAGAGAGGAGCG	97
OY	59	GGCCGAGAGACTCCAGCCGTGCCAGGTGTGGCATCTTCACCTGTGGTTCGTCGACACCTG	118
Db	98	GGCCGAGAGACTCCAGCCGTGCCAGGTGTGGCATCTTCACCTGTGGTTCGTCGACACCTG	157
OY	119	GGAGATATGGCGCGCCCTGGACCTTCACCTCTCTGTGGTTCGTCGACACCTTGA	178
Db	158	GGAGATATGGCGCGCCCTGGACCTTCACCTCTCTGTGGTTCGTCGACACCTTGA	217
OY	179	TCCAAAGCCACCTTCAGTCCCACTGCAATTCCTCCGCCCCAAAAGTATCAAAAGAA	238
Db	218	TCCAAAGCCACCTTCAGTCCCACTGCAATTCCTCCGCCCCAAAAGTATCAAAAGAA	277
OY	239	AGCGAACAAGAGAGCTGAAGGACCAACGCCACACAGACTCTTCGACAGAGCTCCGCTGC	298
Db	278	AGCTGACACAGAGAGCTGAAGGACCAACGCCACACAGACTCTTCGACAGAGCTCCGCTGC	337
OY	299	TCAATGCCATCGCGGAAAAACCCAGCCGGAGG - ATCCCTGTGCTGGGGAGCTGGTAACA	357
Db	338	TCAGTGCATCGCGGAAAAACCCAGCCGGAGGATCCCTGTGTGGTGGCAGCTGTAAACA	397
OY	358	CCGTCTCGAAGCAATCATCTGGCTGAAGTCAACAAGCTAATCTTCACAGCTCAGG	417
Db	398	CCGTCTCGAAGCAATCATCTGGCTGAAGTCAACAAGCTAATCTTCACAGCTCAGG	457
OY	418	TGAAGCCCTCGGCCAATGACACAGAGACTGCTAATCAAGATCCCCCGGAGCATGTGGCG	477
Db	458	TGAAGCCCTCGGCCAATGACACAGAGACTGCTAATCAAGATCCCCCGGAGCATGTGGCG	517
OY	478	GATTCAACAACGCCCTCGGTCAAGACCATGTGGAGTTCCACATGACAGACTGAGGCCAAG	537
Db	518	GATTCAACAACGCCCTCGGTCAAGACCATGTGGAGTTCCACATGACAGACTGAGGCCAAG	577
OY	538	CCACCATCGCATGAGACACAGTGCMAAGTGGCCCCACCGCGTGGTCCCAATGACACTGG	597
Db	578	CCACCATCGCATGAGACACAGTGCMAAGTGGCCCCACCGCGTGGTCCCAATGACACTGG	637
OY	598	CCACCAAGCCATGGAGACCTGCCCATTCCAACTGCTGCATTAAGCTCTTCCTCGGTGAACG	657
Db	638	CCACCAAGCCATGGAGACCTGCCCATTCCAACTGCTGCATTAAGCTCTTCCTCGGTGAACG	697
OY	658	CCTTAGCTAAGCAGTGAAGCTCCCTGATGCCATCCCTGGCCATCTAGTGAAGAAACC	717
Db	698	CCTTAGCTAAGCAGTGAAGCTCCCTGATGCCATCCCTGGCCATCTAGTGAAGAAACC	757
OY	718	ACCTGTGTCCCTGATCGAGGCTCTCTTCATGGCATGTATGACAGACCTCTGCAGCTGG	777
Db	758	ACCTGTGTCCCTGATCGAGGCTCTCTTCATGGCATGTATGACAGACCTCTGCAGCTGG	817
OY	778	TGAAGGTGCCATTTCCCTCCAGCATTTGAACCGCTGAGATTGAGACTTCTGTATCTGCCA	837
Db	818	TGAAGGTGCCATTTCCCTCCAGCATTTGAACCGCTGAGATTGAGACTTCTGTATCTGCCA	877
OY	838	TCAAGGTTGACACACATTCAGTCTACCTGGGGGCCAAGTTGTTGACTCAACAGGAAAGG	897
Db	878	TCAAGGTTGACACACATTCAGTCTACCTGGGGGCCAAGTTGTTGACTCAACAGGAAAGG	937
OY	898	TGACCAATGGTTCATTAACCTGTGAGCTTCCCTGACAAATCCCAACCTTGACAACAATCC	957
Db	938	TGACCAATGGTTCATTAACCTGTGAGCTTCCCTGACAAATCCCAACCTTGACAACAATCC	997
OY	958	CGTTACGCTCATCGTGAATCAGACAGCTGTGAAAGCTGCAAGTGGCTCTGTGCTCTC	1017
Db	998	CGTTACGCTCATCGTGAATCAGACAGCTGTGAAAGCTGCAAGTGGCTCTGTGCTCTC	1057
OY	1018	CAGAAAGATTATGTGCTCTGTGGACCTCTGTGCTCTGAGAGTCCCATCGGCTGAAGT	1077

```

Db 1058 CAGAGAAATTCAGTCTCTGTTGACACTGTGCTTCTCTGAGAGTGGCCCATCGCTGAAGT 1117
QY 1078 CAAGCATCGGGCTGATCAATGAAAAAGGCTGCAGATAGCTGGAGTCTACCCAGATCGTGA 1137
Db 1118 CAAGCATCGGGCTGATCAATGAAAAAGGCTGCAGATAGCTGGAGTCTACCCAGATCGTGA 1177
QY 1138 AGATCTTAAGTCAAGACACTCCGAGTCTTATATAGACCAAGGCCATGACCAAGGTGCCCC 1197
Db 1178 AGATCTTAAGTCAAGACACTCCGAGTCTTATATAGACCAAGGCCATGACCAAGGTGCCCC 1237
QY 1198 AACTGATGCTGCTGGAAGTCTTCCCTCCAGTGAAGCCCTCCGCTTGTCTACCCCTGG 1257
Db 1238 AACTGATGCTGCTGGAAGTCTTCCCTCCAGTGAAGCCCTCCGCTTGTCTACCCCTGG 1297
QY 1258 GCATCGAAGCCAGCTCGGAAGCTCAGTTTATACCAAGAGTGACCAATTATACCTAAT 1317
Db 1298 GCATCGAAGCCAGCTCGGAAGCTCAGTTTATACCAAGAGTGACCAATTATACCTAAT 1357
QY 1318 TGAATTAACATCAGCTCTGATCGATCCAGCTGATGAACCTCTGGATTGGCTGTTCCAAC 1377
Db 1358 TGAATTAACATCAGCTCTGATCGATCCAGCTGATGAACCTCTGGATTGGCTGTTCCAAC 1417
QY 1378 CTGATGTTCTGAAAAAATCATCATCATGAGATCACTCCATCCATCCCTGCTGCCAGACAGA 1437
Db 1418 CTGATGTTCTGAAAAAATCATCATCATGAGATCACTCCATCCATCCCTGCTGCCAGACAGA 1477
QY 1438 ATGCAAAATTAAGATCTGGGGTCCAGTGTCTGATGTGAAGGCTTGGGATTCAGGACAG 1497
Db 1478 ATGCAAAATTAAGATCTGGGGTCCAGTGTCTGATGTGAAGGCTTGGGATTCAGGACAG 1537
QY 1498 CTGATGCTCTGACAGCAAGAGTCCCTTGTCTTACTCCAGCCCTTGTGGAACCCA 1557
Db 1538 CTGATGCTCTGACAGCAAGAGTCCCTTGTCTTACTCCAGCCCTTGTGGAACCCA 1597
QY 1558 GCTCTCTGCTCCAGTGAAGACTGGATGGAGCCATCAGGAGGAGGAGGAGGAGGAGGAGG 1617
Db 1598 GCTCTCTGCTCCAGTGAAGACTGGATGGAGCCATCAGGAGGAGGAGGAGGAGGAGGAGG 1657
QY 1618 TGGAGATGAGGAGTGTGAGTCTATAGACCAATCCCTCTGCAATCAATTAACACTTGGCT 1677
Db 1658 TGGAGATGAGGAGTGTGAGTCTATAGACCAATCCCTCTGCAATCAATTAACACTTGGCT 1717
QY 1678 GTG 1680
Db 1718 GTG 1720

```

RESULT 12  
US-09-330-12

; Sequence 12, Application US/09092330

; GENERAL INFORMATION:

; APPLICANT: BILLING-MEDEL, PATRICIA

; APPLICANT: COHEN, MAURICE

; APPLICANT: COLETTIS, TRACEY L.

; APPLICANT: FRIEDMAN, PAULA N.

; APPLICANT: KLAAS, MICHAEL R.

; APPLICANT: RUSSELL, JOHN C.

; APPLICANT: STROUPE, STEPHEN D.

; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL

; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Abbott Laboratories

; STREET: 100 Abbott Park Road

; CITY: Abbott Park

; STATE: IL

; COUNTRY: USA

; ZIP: 60064-3500

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092.330
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,838
; FILING DATE: 06-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6108, US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1661 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-092-330-12

```

```

Query Match 98.0%; Score 1646.6; DB 15; Length 1661;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1657; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

```

```

QY 23 ACTTCAGACCCATGCGCCGGAGAGAGRGAGCGGCGAGGAGCTCCAGCGTCCGAG 82
Db 1 ACTTCAGACCCATGCGCCGGAGAGAGRGAGCGGCGAGGAGCTCCAGCGTCCGAG 60
QY 83 GTCGAGCATCTGACATGCTGCTGCTGACACCTGGGAAAGATGGCGCGCTGAGACT 142
Db 61 GTCGAGCATCTGACATGCTGCTGCTGACACCTGGGAAAGATGGCGCGCTGAGACT 120
QY 143 TCACCTCTTCTGTGTTGCTGTGAGCAGCACCTTGATCCAGCCAGCTCCACTG 202
Db 121 TCACCTCTTCTGTGTTGCTGTGAGCAGCACCTTGATCCAGCCAGCTCCACTG 180
QY 203 CAGTTTCATCTGCGGCCCAAAAGTCATCAAAAGAGCTGACAGAGAGTGAAGAAC 262
Db 181 CAGTTTCATCTGCGGCCCAAAAGTCATCAAAAGAGCTGACAGAGAGTGAAGAAC 240
QY 263 ACAAGGCGACAGCATCTGCGAGCAGCTGCGCTGCTCAGTGCCATGCGGAGGAGGAG 322
Db 241 ACAAGGCGACAGCATCTGCGAGCAGCTGCGCTGCTCAGTGCCATGCGGAGGAGGAG 300
QY 323 CCGGAGG-ATCCCTGTGCTGGGAGCAGCTGTGTAACACCGTCTGAAGCATATCTGGC 381
Db 301 CCGGAGGATCCCTGTGCTGGGAGCAGCTGTGTAACACCGTCTGAAGCATATCTGGC 360
QY 382 TGAAGGTCATCAGCATCAATCTCCAGCAGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 441
Db 361 TGAAGGTCATCAGCATCAATCTCCAGCAGTGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
QY 442 AGTGTAGTCAATATCCCTTGAGCATAGTGGGTGATTAACAGCGCCCTGGTCAAGA 501
Db 421 AGTGTAGTCAATATCCCTTGAGCATAGTGGGTGATTAACAGCGCCCTGGTCAAGA 480
QY 502 CCATGTGAGATTCACATGACGACTGAGGCGCAAGCCAGCATCCGATGGAGACCAAGTG 561
Db 481 CCATGTGAGATTCACATGACGACTGAGGCGCAAGCCAGCATCCGATGGAGACCAAGTG 540
QY 562 CAATGTGCGCCACCGCGCTGCTCTCACTGATGCTGTCACACGACGACGAGGAGGAGGAG 621
Db 541 CAATGTGCGCCACCGCGCTGCTCTCACTGATGCTGTCACACGACGAGGAGGAGGAGGAG 600
QY 622 TCCAACTGTCATAGCTCTCTTCCGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 681
Db 601 TCCAACTGTCATAGCTCTCTTCCGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
QY 682 TCCTAGTCCATCCCTGCGCAATCTAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 741

```

Db	661	TTCTTAGTGCATCCCTGCCAACTAGTGAATAAACCAAGCTGTGTCCCGTATCGAGGCTT	720
QY	742	CCTTCATATGCATGATAGACAGCTCTGACAGCTGGTGAAGGTGCCATTTCCACACA	801
Db	721	CCTTCATATGCATGATAGACAGCTCTGACAGCTGGTGAAGGTGCCATTTCCACACA	780
QY	802	TTGACCGCTGAGAGTTTGAACCTCTGTATTCCTGCCATCAAGGCTACACCAATTCAGCTCT	861
Db	781	TTGACCGCTGAGAGTTTGAACCTCTGTATTCCTGCCATCAAGGCTACACCAATTCAGCTCT	840
QY	862	ACCTGGGGGCCAAGTTGTTGGACATCCAGGGGAAAGGTACCAAGTGTTCATTAACCTCTG	921
Db	841	ACCTGGGGGCCAAGTTGTTGGACATCCAGGGGAAAGGTACCAAGTGTTCATTAACCTCTG	900
QY	922	CAGCTTCCCTTCACAATGCCACCTGAGCAACATCCCTTACAGCTCATTCGTGAGTCAAG	981
Db	901	CAGCTTCCCTTCACAATGCCACCTGAGCAACATCCCTTACAGCTCATTCGTGAGTCAAG	960
QY	982	ACGATGTAAGGCGAGATGGCTGTGTGTCTCTCCAGAAAGAAATTCATGGTCTGTG	1041
Db	961	ACGATGTAAGGCGAGATGGCTGTGTGTCTCTCCAGAAAGAAATTCATGGTCTGTG	1020
QY	1042	ACTCTGTGCTTCCGAGAGTCCCATCGGCTGGAAGTCAAGCATGGGCTGATCATATAA	1101
Db	1021	ACTCTGTGCTTCCGAGAGTCCCATCGGCTGGAAGTCAAGCATGGGCTGATCATATAA	1080
QY	1102	AGGTCGAGATTAAGCTGGGATCTTACCAGATCGTGAAGATCTTAATCAGAGACCTCCG	1161
Db	1081	AGGTCGAGATTAAGCTGGGATCTTACCAGATCGTGAAGATCTTAATCAGAGACCTCCG	1140
QY	1162	AGTTTTTATATAGACCAAGGCCATGCGCAAGGTGGCCCAACATGATCTGTGGAAGTGTTC	1221
Db	1141	AGTTTTTATATAGACCAAGGCCATGCGCAAGGTGGCCCAACATGATCTGTGGAAGTGTTC	1200
QY	1222	CGTCCAGTGAAGCCCTCCGCCCTTGTGTCACCTGGGCATCGAAGCAGTCGGGAAGCTC	1281
Db	1201	CGTCCAGTGAAGCCCTCCGCCCTTGTGTCACCTGGGCATCGAAGCAGTCGGGAAGCTC	1260
QY	1282	AGTTTTACACCAAGGTGACCAACTTATACTCAAGTTGAATTAACATCAGCTCGATCGGA	1341
Db	1261	AGTTTTACACCAAGGTGACCAACTTATACTCAAGTTGAATTAACATCAGCTCGATCGGA	1320
QY	1342	TCCAGCTGATGAACCTGGGATTTGGCTGGTTCACACTATGTTCGAAAAACATCATCA	1401
Db	1321	TCCAGCTGATGAACCTGGGATTTGGCTGGTTCACACTATGTTCGAAAAACATCATCA	1380
QY	1402	CTGAGATTCATCCATCTCCATCTGTGCTGCCAGAACAGATGGCAAAATTAAGTCGGGGTCC	1461
Db	1381	CTGAGATTCATCCATCTCCATCTGTGCTGCCAGAACAGATGGCAAAATTAAGTCGGGGTCC	1440
QY	1462	CAGTGTCAATTTGGTGAAGGCTTTGGGATTTGAGAGCAGCTGATCTCCTCACTGACCAAGATG	1521
Db	1441	CAGTGTCAATTTGGTGAAGGCTTTGGGATTTGAGAGCAGCTGATCTCCTCACTGACCAAGATG	1500
QY	1522	CCCTTGTGCTTACTCCAGCTCTCTTGTGGAAACCAGCTCTCTGTCCTCCAGTGAATAC	1581
Db	1501	CCCTTGTGCTTACTCCAGCTCTCTTGTGGAAACCAGCTCTCTGTCCTCCAGTGAATAC	1560
QY	1582	TTGGATGGCAAGCATCAGGGAAAGCTGGGCTCCAGCTGGGATATGGTGTGAGCTCAT	1641
Db	1561	TTGGATGGCAAGCATCAGGGAAAGCTGGGCTCCAGCTGGGATATGGTGTGAGCTCAT	1620
QY	1642	AGACCATCCCTCTCTGCAATCAATTAACATTCGCTGTG	1680
Db	1621	AGACCATCCCTCTCTGCAATCAATTAACATTCGCTGTG	1659

```

; TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
; FILE REFERENCE: CL001380
; CURRENT APPLICATION NUMBER: US/10/170,235
; CURRENT FILING DATE: 2003-03-17
; NUMBER OF SEQ ID NOS: 42514
; SEQ ID NO 27385
; LENGTH: 1651
; TYPE: DNA
; ORGANISM: HUMAN
US-10-170-235-27385

```

Query Match	96.8%;	Score 1627;	DB 47;	Length 1651;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 1638; Conservative	1;	Mismatches	1;	Indels 1;

	Index	1	Gaps
QY	41	CGGAGAGGAGRGAGCGGGCCGAGACTCCAGCGTGGCCAGGTCMGACCTCCGCACTT	100
Db	1	CGGAGAGGAGAGGAGCGGGCCGAGAGACTCCAGCGTGGCCAGGTCMGACCTCCGCACTT	60
QY	101	GCTGCCCTTGACACCTGGGAGATGGCGGCCCGTGGACCTTCACCCCTTCTGTGGTT	160
Db	61	GCTGCCCTTGACACCTGGGAGATGGCGGCCCGTGGACCTTCACCCCTTCTGTGGTT	120
QY	161	TGCTGGGAGCCACCTTGATCCAAAGCCACCTCAGTCCACTCAGTTCTCATCTCGGGC	220
Db	121	TGCTGGGAGCCACCTTGATCCAAAGCCACCTCAGTCCACTCAGTTCTCATCTCGGGC	180
QY	221	CAAAAGTCATCAAGAAAAGCTACACAGAGAGCTGAAGACCAACAGCCACAGACATCC	280
Db	181	CAAAAGTCATCAAGAAAAGCTACACAGAGAGCTGAAGACCAACAGCCACAGACATCC	240
QY	281	TGCAGCAGCTGCCGCTGCTCACTGTCATGCGCATCGGGAAAAGCAGCCCGGAGG - ATCCCTGTGC	339
Db	241	TGCAGCAGCTGCCGCTGCTCACTGTCATGCGCATCGGGAAAAGCAGCCCGGAGGATCCCTGTGC	300
QY	340	TGGGCGAGCTTGGTGAACACCGTCTCGAAGACATATATCTGGCTGAAGTCAATCAGACTA	399
Db	301	TGGGCGAGCTTGGTGAACACCGTCTCGAAGACATATATCTGGCTGAAGTCAATCAGACTA	360
QY	400	ACATCTCTCCAGTGCAGAGTGAAGCCCTCGGCCAATGACACAGAGCTGCTATCAAGATCC	459
Db	361	ACATCTCTCCAGTGCAGAGTGAAGCCCTCGGCCAATGACACAGAGCTGCTATCAAGATCC	420
QY	460	CCCTGGACATGGTGGCTGGATTCACACAGCCCTGTGGTAAAGACATGTGGAGTTCCACA	519
Db	421	CCCTGGACATGGTGGCTGGATTCACACAGCCCTGTGGTAAAGACATGTGGAGTTCCACA	480
QY	520	TGAGCACTGAGGCCCAAGCCACATCCGCATGAGACACAGTGCAGAAAGTGGCCCAACCCGCC	579
Db	481	TGAGCACTGAGGCCCAAGCCACATCCGCATGAGACACAGTGCAGAAAGTGGCCCAACCCGCC	540
QY	580	TGGTCTCAGTGAACGTGTCACACAGCCATGGGAGCCTGGCCATCCAACTCTGCATTAAGC	639
Db	541	TGGTCTCAGTGAACGTGTCACACAGCCATGGGAGCCTGGCCATCCAACTCTGCATTAAGC	600
QY	640	TCTCCTTCTGTGAGCCTTACTTAAGCAGGTGCATGAACCTCTCATGTGTCATTCCTTCG	699
Db	601	TCTCCTTCTGTGAGCCTTACTTAAGCAGGTGCATGAACCTCTCATGTGTCATTCCTTCG	660
QY	700	CCATTCATGTAAAAAACAGCTGTGTCCGTGATCGAGGCTTCTCAATGAGCATATATG	759
Db	661	CCATTCATGTAAAAAACAGCTGTGTCCGTGATCGAGGCTTCTCAATGAGCATATATG	720
QY	760	CAGACCTTCGACAGCTGGTGAAGTGGCCATTCCTCCAGCATTTGACCGCTGTGGAGTTTG	819
Db	721	CAGACCTTCGACAGCTGGTGAAGTGGCCATTCCTCCAGCATTTGACCGCTGTGGAGTTTG	780
QY	820	ACCTTCTGTATCCTGCCATCAAGGGTGAACACATTCAGCTACCTACCTGGGGGCCAAGTTGT	879
Db	781	ACCTTCTGTATCCTGCCATCAAGGGTGAACACATTCAGCTACCTACCTGGGGGCCAAGTTGT	840
QY	880	TGGACTCAGAGGGAAGGTACCAATGGTTCAATTAATCTCGACGTTCCCTGACAAATGC	939

DB 841 TGAATCAGAGGAAAGCTGACCAAGTGTTCATTAAGTCTGACGCTTCCCTGACAAATGC 900  
OY 940 CCACCTGGAGAACATCCGGTTCAGCCCTCATCGTAGTCAAGAGCTGGTGAAGCTGCAG 999  
DB 901 CCACCTGGAGAACATCCGGTTCAGCCCTCATCGTAGTCAAGAGCTGGTGAAGCTGCAG 960  
OY 1000 TGGCTGCTGCTCTCTCTCCAGAAAGATTCATGATGCTCTCTGAGCTCTGCTCTCTGAGA 1059  
DB 961 TGGCTGCTGCTCTCTCTCCAGAAAGATTCATGATGCTCTCTGAGCTCTGCTCTCTGAGA 1020  
OY 1060 GTGCCATCGGCTGAGTCAAGCATCGGGCTGATCATATGAAAGGCTCAGATTAAGCTGG 1119  
DB 1021 GTGCCATCGGCTGAGTCAAGCATCGGGCTGATCATATGAAAGGCTCAGATTAAGCTGG 1080  
OY 1120 GATCTACCCAGATCGTGAAGATCTCTAATCAAGACACTCCGAGTTTTTTATAGCAAG 1179  
DB 1081 GATCTACCCAGATCGTGAAGATCTCTAATCAAGACACTCCGAGTTTTTTATAGCAAG 1140  
OY 1180 GCCATGCCAAGGTGGCCCACTGATCGTCTGGAAGTGTTCCTCCAGTGAAGCCCTCC 1239  
DB 1141 GCCATGCCAAGGTGGCCCACTGATCGTCTGGAAGTGTTCCTCCAGTGAAGCCCTCC 1200  
OY 1240 GCCCTTTGTACCCCTGGGCAATCGAAGCCAGCTGGGAAGCTCAGTTTTACACCAAGGTG 1299  
DB 1201 GCCCTTTGTACCCCTGGGCAATCGAAGCCAGCTGGGAAGCTCAGTTTTACACCAAGGTG 1260  
OY 1300 ACCAATTAATCACTTAATCAATCAATCACTGATCGATCGATCGATCGATCGATCGATCG 1359  
DB 1261 ACCAATTAATCACTTAATCAATCAATCACTGATCGATCGATCGATCGATCGATCGATCG 1320  
OY 1360 GGATTTGGTGTTCACACCTGATGTTCGAAAACATATATACATGAGATATCATCCATCCCA 1419  
DB 1321 GGATTTGGTGTTCACACCTGATGTTCGAAAACATATATACATGAGATATCATCCATCCCA 1380  
OY 1420 TCCTGCTCCCAACAGATGGAATTAAGATCTGGGCTCCAGTGCATTTGGAGAG 1479  
DB 1381 TCCTGCTCCCAACAGATGGAATTAAGATCTGGGCTCCAGTGCATTTGGAGAG 1440  
OY 1480 CTTTGGATTCGAGGACAGTCTGCTCACTGACCAAGATGCCCTTGTGTTACTCCAG 1539  
DB 1441 CTTTGGATTCGAGGACAGTCTGCTCACTGACCAAGATGCCCTTGTGTTACTCCAG 1500  
OY 1540 CTTCTTTTGGAAACCCAGCTCTCTGCTCTCCAGTGAAGCTTGGATGGCAGCCATCAG 1599  
DB 1501 CTTCTTTTGGAAACCCAGCTCTCTGCTCTCCAGTGAAGCTTGGATGGCAGCCATCAG 1560  
OY 1600 GGAAGGCTGGGTCACAGCTGGGAGATGGGTGTGAGCTCTATAGACATCCCTCTCTGCA 1659  
DB 1561 GGAAGGCTGGGTCACAGCTGGGAGATGGGTGTGAGCTCTATAGACATCCCTCTCTGCA 1620  
OY 1660 ATCAATAAACACTTGCTGTG 1680  
DB 1621 ATCAATAAACACTTGCTGTG 1641

RESULT 14  
US-09-946-374-127  
Sequence 127, Application US/0946374

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Botsch, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830P1C1  
CURRENT APPLICATION NUMBER: US/09/946,374  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098803  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098821  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098843  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/099536  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099596  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099598  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099602  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099642  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099741  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099754  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099763  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099792  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099808  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099812  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099815  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099816  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100385  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100388  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100390  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100584  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100661  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100662  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100664  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100683  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100684  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100710

1	PRIOR FILING DATE: 1998-09-17	1	PRIOR APPLICATION NUMBER: 60/100711
2	PRIOR APPLICATION NUMBER: 60/100711	2	PRIOR FILING DATE: 1998-09-17
3	PRIOR FILING DATE: 1998-09-17	3	PRIOR APPLICATION NUMBER: 60/100846
4	PRIOR APPLICATION NUMBER: 60/100846	4	PRIOR FILING DATE: 1998-09-18
5	PRIOR FILING DATE: 1998-09-18	5	PRIOR APPLICATION NUMBER: 60/100845
6	PRIOR APPLICATION NUMBER: 60/100845	6	PRIOR FILING DATE: 1998-09-18
7	PRIOR FILING DATE: 1998-09-18	7	PRIOR APPLICATION NUMBER: 60/100919
8	PRIOR APPLICATION NUMBER: 60/100919	8	PRIOR FILING DATE: 1998-09-17
9	PRIOR FILING DATE: 1998-09-17	9	PRIOR APPLICATION NUMBER: 60/100930
10	PRIOR APPLICATION NUMBER: 60/101014	10	PRIOR FILING DATE: 1998-09-17
11	PRIOR FILING DATE: 1998-09-18	11	PRIOR APPLICATION NUMBER: 60/101068
12	PRIOR APPLICATION NUMBER: 60/101068	12	PRIOR FILING DATE: 1998-09-18
13	PRIOR FILING DATE: 1998-09-18	13	PRIOR APPLICATION NUMBER: 60/101071
14	PRIOR APPLICATION NUMBER: 60/101071	14	PRIOR FILING DATE: 1998-09-18
15	PRIOR FILING DATE: 1998-09-18	15	PRIOR APPLICATION NUMBER: 60/101279
16	PRIOR APPLICATION NUMBER: 60/101279	16	PRIOR FILING DATE: 1998-09-22
17	PRIOR FILING DATE: 1998-09-22	17	PRIOR APPLICATION NUMBER: 60/101471
18	PRIOR APPLICATION NUMBER: 60/101471	18	PRIOR FILING DATE: 1998-09-23
19	PRIOR FILING DATE: 1998-09-23	19	PRIOR APPLICATION NUMBER: 60/101475
20	PRIOR APPLICATION NUMBER: 60/101475	20	PRIOR FILING DATE: 1998-09-23
21	PRIOR FILING DATE: 1998-09-23	21	PRIOR APPLICATION NUMBER: 60/101476
22	PRIOR APPLICATION NUMBER: 60/101476	22	PRIOR FILING DATE: 1998-09-23
23	PRIOR FILING DATE: 1998-09-23	23	PRIOR APPLICATION NUMBER: 60/101477
24	PRIOR APPLICATION NUMBER: 60/101479	24	PRIOR FILING DATE: 1998-09-23
25	PRIOR FILING DATE: 1998-09-23	25	PRIOR APPLICATION NUMBER: 60/101738
26	PRIOR APPLICATION NUMBER: 60/101738	26	PRIOR FILING DATE: 1998-09-24
27	PRIOR FILING DATE: 1998-09-24	27	PRIOR APPLICATION NUMBER: 60/101741
28	PRIOR APPLICATION NUMBER: 60/101741	28	PRIOR FILING DATE: 1998-09-24
29	PRIOR FILING DATE: 1998-09-24	29	PRIOR APPLICATION NUMBER: 60/101743
30	PRIOR APPLICATION NUMBER: 60/101915	30	PRIOR FILING DATE: 1998-09-24
31	PRIOR FILING DATE: 1998-09-24	31	PRIOR APPLICATION NUMBER: 60/101916
32	PRIOR APPLICATION NUMBER: 60/101916	32	PRIOR FILING DATE: 1998-09-24
33	PRIOR FILING DATE: 1998-09-24	33	PRIOR APPLICATION NUMBER: 60/102207
34	PRIOR APPLICATION NUMBER: 60/102240	34	PRIOR FILING DATE: 1998-09-29
35	PRIOR FILING DATE: 1998-09-29	35	PRIOR APPLICATION NUMBER: 60/102307
36	PRIOR APPLICATION NUMBER: 60/102307	36	PRIOR FILING DATE: 1998-09-29
37	PRIOR FILING DATE: 1998-09-29	37	PRIOR APPLICATION NUMBER: 60/102330
38	PRIOR APPLICATION NUMBER: 60/102331	38	PRIOR FILING DATE: 1998-09-29
39	PRIOR FILING DATE: 1998-09-29	39	PRIOR APPLICATION NUMBER: 60/102484
40	PRIOR APPLICATION NUMBER: 60/102484	40	PRIOR FILING DATE: 1998-09-30
41	PRIOR FILING DATE: 1998-09-30	41	PRIOR APPLICATION NUMBER: 60/102487
42	PRIOR APPLICATION NUMBER: 60/102487	42	PRIOR FILING DATE: 1998-09-30
43	PRIOR FILING DATE: 1998-09-30	43	PRIOR APPLICATION NUMBER: 60/102570
44	PRIOR APPLICATION NUMBER: 60/102571	44	PRIOR FILING DATE: 1998-09-30
45	PRIOR FILING DATE: 1998-09-30	45	PRIOR APPLICATION NUMBER: 60/102684
46	PRIOR APPLICATION NUMBER: 60/102684	46	PRIOR FILING DATE: 1998-10-01
47	PRIOR FILING DATE: 1998-10-01	47	PRIOR APPLICATION NUMBER: 60/102687
48	PRIOR APPLICATION NUMBER: 60/102965	48	PRIOR FILING DATE: 1998-10-01
49	PRIOR FILING DATE: 1998-10-02	49	PRIOR APPLICATION NUMBER: 60/103258
50	PRIOR APPLICATION NUMBER: 60/103258	50	PRIOR FILING DATE: 1998-10-06
51	PRIOR FILING DATE: 1998-10-06	51	PRIOR APPLICATION NUMBER: 60/103314
52	PRIOR APPLICATION NUMBER: 60/103315	52	PRIOR FILING DATE: 1998-10-07
53	PRIOR FILING DATE: 1998-10-07	53	PRIOR APPLICATION NUMBER: 60/103315
54	PRIOR APPLICATION NUMBER: 60/103315	54	PRIOR FILING DATE: 1998-10-07

```

1  PRIOR APPLICATION NUMBER: 60/103328
2  PRIOR FILING DATE: 1998-10-07
3  PRIOR APPLICATION NUMBER: 60/103395
4  PRIOR FILING DATE: 1998-10-07
5  PRIOR APPLICATION NUMBER: 60/103396
6  PRIOR FILING DATE: 1998-10-07
7  PRIOR APPLICATION NUMBER: 60/103401
8  PRIOR FILING DATE: 1998-10-07
9  PRIOR APPLICATION NUMBER: 60/103449
10 PRIOR FILING DATE: 1998-10-06
11 PRIOR APPLICATION NUMBER: 60/103633
12 PRIOR FILING DATE: 1998-10-08
13 PRIOR APPLICATION NUMBER: 60/103678
14 PRIOR FILING DATE: 1998-10-08
15 PRIOR APPLICATION NUMBER: 60/103679
16 PRIOR FILING DATE: 1998-10-08
17 PRIOR APPLICATION NUMBER: 60/103711
18 PRIOR FILING DATE: 1998-10-08
19 PRIOR APPLICATION NUMBER: 60/104257
20 PRIOR FILING DATE: 1998-10-14
21 PRIOR APPLICATION NUMBER: 60/104887
22 PRIOR FILING DATE: 1998-10-20
23 PRIOR APPLICATION NUMBER: 60/105000
24 PRIOR FILING DATE: 1998-10-20
25 PRIOR APPLICATION NUMBER: 60/105002
26 PRIOR FILING DATE: 1998-10-20
27 PRIOR APPLICATION NUMBER: 60/105104
28 PRIOR FILING DATE: 1998-10-21
29 PRIOR APPLICATION NUMBER: 60/105169
30 PRIOR FILING DATE: 1998-10-22
31 PRIOR APPLICATION NUMBER: 60/105266
32 PRIOR FILING DATE: 1998-10-22
33 PRIOR APPLICATION NUMBER: 60/105693
34 PRIOR FILING DATE: 1998-10-26
35 PRIOR APPLICATION NUMBER: 60/105694
36 PRIOR FILING DATE: 1998-10-26
37 PRIOR APPLICATION NUMBER: 60/105807
38 PRIOR FILING DATE: 1998-10-27

```

Query Match	96.28;	Score 1617;	DB 40;	Length 1636;
Best Local Similarity	99.88;	Pred. No. 0;		
Matches 1628;	Conservative	1;	Mismatches	1;
			Indels	1;
			Gaps	1;

[illegible]

Db 421 GGTGGCTGATTCACAGCCGCCCTGTCAGAACCATCTGTGAGTTCCACATGACGACTGA 480  
QY 530 GGCCCAAGCCACCATCCGATGACACACAGTGAAGTGGCCCCACCCGCTGTGCTCAG 589  
|||||  
Db 481 GGCCCAAGCCACCATCCGATGACACACAGTGAAGTGGCCCCACCCGCTGTGCTCAG 540  
QY 590 TGAATGTGACCAACGACCATGGAGCTGGCGATCCAACTGCTGATTAAGTCTCTCTCT 649  
|||||  
Db 541 TGAATGTGACCAACGACCATGGAGCTGGCGATCCAACTGCTGATTAAGTCTCTCTCT 600  
QY 650 GGTGAAGCGCTTGAAGGAGGTGAACGCTGCTGAGCCATCCCTGGCCCATCTAGT 709  
|||||  
Db 601 GGTGAAGCGCTTGAAGGAGGTGAACGCTGCTGAGCCATCCCTGGCCCATCTAGT 660  
QY 710 GAAAAACACAGCTGTGCTCCGTGATGAGGCTTCCCTCAATGAGATGAGAGACTCT 769  
|||||  
Db 661 GAAAAACACAGCTGTGCTCCGTGATGAGGCTTCCCTCAATGAGATGAGAGACTCT 720  
QY 770 GCAAGCTGTGAAGGTGCTCCATTTCCCTCAGCATTTGACCTGTGAGTGA 829  
|||||  
Db 721 GCAAGCTGTGAAGGTGCTCCATTTCCCTCAGCATTTGACCTGTGAGTGA 780  
QY 830 TCCGCGCATGAGGGGTGACACATTTGAGCTTACCTGAGGGGCCAAGTTGGAGCTGACA 889  
|||||  
Db 781 TCCGCGCATGAGGGGTGACACATTTGAGCTTACCTGAGGGGCCAAGTTGGAGCTGACA 840  
QY 890 GGGAAAGGTGACCAAGTGTGTCATTAATCTGACAGTTCCTCTGACATGGCCACCTGGA 949  
|||||  
Db 841 GGGAAAGGTGACCAAGTGTGTCATTAATCTGACAGTTCCTCTGACATGGCCACCTGGA 900  
QY 950 CAACATCCCTGTCAGCCTCATCGAGTCAAGAGTGTGTAAGCTCAGTGGCTGTGT 1009  
|||||  
Db 901 CAACATCCCTGTCAGCCTCATCGAGTCAAGAGTGTGTAAGCTCAGTGGCTGTGT 960  
QY 1010 GCTCTCTCCAGAAATTTCAATGCTGCTGTTGAGACTGTGCTGCTGAGAGTGGCCATCG 1069  
|||||  
Db 961 GCTCTCTCCAGAAATTTCAATGCTGCTGTTGAGACTGTGCTGCTGAGAGTGGCCATCG 1020  
QY 1070 GCTGAACTCAAGCATCGGGCTGATCAATGAAAAGGTGACAGTAAAGCTGGGATACCCA 1129  
|||||  
Db 1021 GCTGAACTCAAGCATCGGGCTGATCAATGAAAAGGTGACAGTAAAGCTGGGATACCCA 1080  
QY 1130 GATGTGTAAGATCTTAATCACTGAGACACTCCGAGTCTTTTATAGACCAAGGCCATGCCAA 1189  
|||||  
Db 1081 GATGTGTAAGATCTTAATCACTGAGACACTCCGAGTCTTTTATAGACCAAGGCCATGCCAA 1140  
QY 1190 GGTGGGCCAATGATGCTGCTGGAAGTGTTCCTCCAGTGAAGCCCTCCGCCCTTGT 1249  
|||||  
Db 1141 GGTGGGCCAATGATGCTGCTGGAAGTGTTCCTCCAGTGAAGCCCTCCGCCCTTGT 1200  
QY 1250 CACCTGGGATCGAAGCCAGCTGGAAGTCAATTTTACACAAAGGTGACCAACTAT 1309  
|||||  
Db 1201 CACCTGGGATCGAAGCCAGCTGGAAGTCAATTTTACACAAAGGTGACCAACTAT 1260  
QY 1310 ACTCACTTGAATTAACATCACTGCTGTGATCGGATCAGCTGATGAATCTGGGATGGCTG 1369  
|||||  
Db 1261 ACTCACTTGAATTAACATCACTGCTGTGATCGGATCAGCTGATGAATCTGGGATGGCTG 1320  
QY 1370 GTTCCAACTGATGCTGGAAGAAATCATCATGATGATCATGATCCATCCATCCGCTGCC 1429  
|||||  
Db 1321 GTTCCAACTGATGCTGGAAGAAATCATCATGATGATCATGATCCATCCATCCGCTGCC 1380  
QY 1430 GAACCAAGATGGAATTAAGATCTGGGGTCCAGTGTCAATTTGGTGAAGGCTTGGGAT 1489  
|||||  
Db 1381 GAACCAAGATGGAATTAAGATCTGGGGTCCAGTGTCAATTTGGTGAAGGCTTGGGAT 1440  
QY 1490 CGAGGAGCTGATGCTCACTGACCAAGATGCCCTGTGTACTCTCAGGCTCTCTGTG 1549  
|||||  
Db 1441 CGAGGAGCTGATGCTCACTGACCAAGATGCCCTGTGTACTCTCAGGCTCTCTGTG 1500  
QY 1550 GAAACCCAGCTGCTGCTGCTCCAGTGAAGACTTGGATGGCAGCCATCAGGAAAGGCTGG 1609  
|||||  
Db 1501 GAAACCCAGCTGCTGCTGCTCCAGTGAAGACTTGGATGGCAGCCATCAGGAAAGGCTGG 1560

QY 1610 GTCCACCTGGGAGTATGGTGTGAGCTATAGACCATCCCTCTCTGCAATCAATAAAC 1669  
|||||  
Db 1561 GTCCACCTGGGAGTATGGTGTGAGCTATAGACCATCCCTCTCTGCAATCAATAAAC 1620  
QY 1670 ACTTGCTGTG 1680  
|||||  
Db 1621 ACTTGCTGTG 1631

RESULT 15  
US-10-006-041A-127  
Sequence 127, Application US/10006041A  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan I.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas P.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2830P18  
CURRENT FILING DATE: 2001-12-06  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 477  
SEQ ID NO 127  
LENGTH: 1636  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-006-041A-127

Query Match 96.2%; Score 1617; DB 44; Length 1636;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1628; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 51 GRGAGGGGGCGGAGACTCCAGGCTGCCAGGCTGGCAATCCCTGCACTTCTCCTCT 110  
|:|||||  
Db 1 GAGAGGGGGCGGAGACTCCAGGCTGCCAGGCTGGCAATCCCTGCACTTCTCCTCT 60  
QY 111 GACACTGGGAAATGAGCGGCGCGGTGACCTTCACTTCTGTGGTTGTGGAGC 170  
|||||  
Db 61 GACACTGGGAAATGAGCGGCGCGGTGACCTTCACTTCTGTGGTTGTGGAGC 120  
QY 171 CACCTTGATCCAGCCACCTCACTGCTGACGTTCTCATCTCGGCGCCAAAGTCAT 230  
|||||  
Db 121 CACCTTGATCCAGCCACCTCACTGCTGACGTTCTCATCTCGGCGCCAAAGTCAT 180  
QY 231 CAAAGAAAGCTGACAGAGCTGAAGGAGACACAGCCACAGCAATCTCGACGACT 290  
|||||  
Db 181 CAAAGAAAGCTGACAGAGCTGAAGGAGACACAGCCACAGCAATCTCGACGACT 240  
QY 291 GCCGCTGCTAGTGCATGCGGGAAGAGCCAGCGGAGG-ATCCCTGTGCTGGGAGCT 349  
|||||  
Db 241 GCCGCTGCTAGTGCATGCGGGAAGAGCCAGCGGAGGATCCCTGTGCTGGGAGCT 300  
QY 350 GGTGAACCGTCTGTAAGCATCATCTGCTGAAGGTCAATCAAGTAAATCTCTCA 409  
|||||  
Db 301 GGTGAACCGTCTGTAAGCATCATCTGCTGAAGGTCAATCAAGTAAATCTCTCA 360  
QY 410 GCTGAGGTGAAGGCTCGGCGCATGACAGAGACTGTATCAAGATCCCTCGAGAT 469  
|||||  
Db 361 GCTGAGGTGAAGGCTCGGCGCATGACAGAGACTGTATCAAGATCCCTCGAGAT 420





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2003, 13:21:47 : Search time 2169.15 seconds

(without alignments)  
10028.129 Million cell updates/sec

Title: US-09-700-770-5

Perfect score: 895

Sequence: 1 ctaatcgttcacgtaacagc.....ataaataatttaaatgtc 895

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

EST:\*

1: em\_estba:\*  
2: em\_estchum:\*  
3: em\_estcin:\*  
4: em\_estmu:\*  
5: em\_estrov:\*  
6: em\_estropl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hrc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vr1:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	707	79.0	748	14	CB242167 UI-CF-FNO
2	677	75.6	677	12	BM769732 K-EST0053
3	672.2	75.1	820	12	BT770944
4	671	75.0	671	13	BX102380

Result No.	Score	Query Match	Length	DB ID	Description
5	667.8	74.6	715	12	BM982101 UI-CF-EN1
6	666	74.4	756	12	BM831028 K-EST0104
7	664.8	74.3	663	12	BM978124 UI-CF-RC1
8	664	74.2	664	12	BM854000 K-EST0136
9	615	68.7	615	12	BM766904 K-EST0048
10	607.2	67.8	628	12	BM746867 K-EST0021
11	587	65.6	587	12	BM766900 K-EST0048
12	582.6	65.1	613	12	BM536626 K-EST0048
13	575.6	64.3	594	12	BM743525 K-EST0016
14	572.4	64.0	592	12	BM682452 UI-CF-RC1
15	557.4	62.3	578	12	BM979898 UI-CF-EN1
16	546	61.0	580	13	BM684368 UI-CF-ENO
17	510.6	57.1	667	9	AM471176
18	509.2	56.9	526	13	BM951534
19	497	55.5	498	10	BM196945
20	488.4	54.6	491	9	BM1340056
21	487.2	54.4	504	9	BM1809681
22	471	52.6	491	9	BM1830551
23	465.2	52.0	482	10	BM061539
24	464	51.8	477	9	BM142875
25	451.2	50.4	457	12	BM856234
26	451	50.4	451	12	BM766526
27	431.8	48.2	438	13	BM951285
28	427.6	47.8	461	9	BM1276107
29	426	47.6	426	9	BM148882
30	414.8	46.3	419	9	BM4430487
31	409	45.7	429	9	BM298444
32	408.4	45.6	434	14	CB241301
33	405	45.3	431	9	BM1079465
34	397	44.4	397	9	BM481852
35	394.4	44.1	404	12	BM687291
36	376.4	42.1	378	14	BM4946289
37	375.2	41.9	404	10	BM745581
38	374	41.8	374	12	BM768531
39	372	41.6	372	12	BM769069
40	365	40.8	392	9	BM4433968
41	363	38.3	366	13	BM674071
42	341.2	38.1	356	9	BM770737
43	339.4	37.9	409	10	BM073132
44	333	37.2	611	14	CB420858
45					

## ALIGNMENTS

RESULT 1  
LOCUS CB242167/c 748 bp mRNA  
DEFINITION UI-CF-FNO-aggd-f-19-0-UI-s1 UI-CF-FNO Homo sapiens  
ACCESSION CB242167  
VERSION CB242167.1 GI:28363811  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 748)  
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
TITLES Normalization and subtraction: two approaches to facilitate gene discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 97044477  
PUBMED 8889548

COMMENT  
Contact: McCray, PB  
McCray Lab  
University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171  
Email: paul-mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa









The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transfection of the remaining DNA into competent cells E. coli Top10<sup>+</sup> with electroporation method."

```

BASE COUNT      172 a      139 g      159 t
ORIGIN
Query Match      74.4% Score 666; DB 12; Length 666;
Best Local Similarity 100.0%; Pred. No. 1.7e-161;
Matches 666; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 CTGACCTGAGTCATCCCGAGGATCCAGAGCCTCCAGAGGAACTTCATATATATCT 163
    |||||
Db 1 CTGACCTGAGTCATCCCGAGGATCCAGAGCCTCCAGAGGAACTTCATATATATCT 60
    |||||

QY 164 TCAAGCACTTAAGCTGACCGACAGTCCGATGAAAGTTCTATCTCTCCCTCC 223
    |||||
Db 61 TCAAGCACTTAAGCTGACCGACAGTCCGATGAAAGTTCTATCTCTCCCTCC 120
    |||||

QY 224 TGTTCGTCACATATGCTGATGTCATGCTCTGACACCTCGAATCCAGGGGTGCCA 283
    |||||
Db 121 TGTTCGTCACATATGCTGATGTCATGCTCTGACACCTCGAATCCAGGGGTGCCA 180
    |||||

QY 284 GAGGCCACAGGAGCCAGGCGGAGCTTTCAGAGATGCTCCAGAGGCGCCAGAAAT 343
    |||||
Db 181 GAGGCCACAGGAGCCAGGCGGAGCTTTCAGAGATGCTCCAGAGGCGCCAGAAAT 240
    |||||

QY 344 GTGAGTGCAGAAAGTTGGTTCCTAGAGCCCGCGAGAAATTCATGACAGTCTGGGC 403
    |||||
Db 241 GTGAGTGCAGAAAGTTGGTTCCTAGAGCCCGCGAGAAATTCATGACAGTCTGGGC 300
    |||||

QY 404 TGCAGAGAGAGAGTCCCTGTCATTCATTCAGAGGCAATGAGAGAAACAGACACC 463
    |||||
Db 301 TGCAGAGAGAGAGTCCCTGTCATTCATTCAGAGGCAATGAGAGAAACAGACACC 360
    |||||

QY 464 AAGAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 523
    |||||
Db 361 AAGAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
    |||||

QY 524 GTCAGAGTAAAGCTTGTGCTGCTTTAGAGAGCTGAGAGCCCACTCTCCAAATTA 583
    |||||
Db 421 GTCAGAGTAAAGCTTGTGCTGCTTTAGAGAGCTGAGAGCCCACTCTCCAAATTA 480
    |||||

QY 584 AACATTTTCAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 643
    |||||
Db 481 AACATTTTCAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
    |||||

QY 644 ACTCTCCACGTGTACCCACCCCTTAATATTCATTCAGATGCTCTAAAGAGAGTTTTC 703
    |||||
Db 541 ACTCTCCACGTGTACCCACCCCTTAATATTCATTCAGATGCTCTAAAGAGAGTTTTC 600
    |||||

QY 704 GATCATTTTGTGTTGTGCTCTAGTGTCTTCTCTCTGCTGCTTACGCTTACGCTG 763
    |||||
Db 601 GATCATTTTGTGTTGTGCTCTAGTGTCTTCTCTCTGCTGCTTACGCTTACGCTG 660
    |||||

QY 764 CTCGCC 769
    |||||
Db 661 CTCGCC 666
    |||||

```

RESULT 7  
BM978124/c

LOCUS BM978124 753 bp mRNA linear EST 21-FEB-2003  
 DEFINITION UI-CF-ECL1-aeb-a-22-0-UI.s1 UI-CF-ECL1 Homo sapiens cDNA clone  
 ACCESSION UI-CF-ECL1-aeb-a-22-0-UI 3', mRNA sequence.  
 VERSION BM978124  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 753)  
 AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996).  
 MEDLINE 97044477  
 PUBMED 8889548  
 COMMENT Contact: McCray, PB  
 McCray Lab  
 University of Iowa  
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
 Tel: 319 356 4866  
 Fax: 319 356 7171  
 Email: paul-mccray@uiowa.edu  
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Genome Distribution: Researchers may obtain clones from Research  
 Genetics (www.reagen.com) or from Open Biosystems  
 (www.openbiosystems.com).  
 Seq primer: M13 FORWARD  
 POLY-A=yes.

#### FEATURES

source Location/Qualifiers  
 1..753  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-CF-ECL1-aeb-a-22-0-UI"  
 /tissue\_type="lung"  
 /dev\_stage="Adult and Fetal"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_lib="UI-CF-ECL1"  
 /note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a  
 modified polylinker; Site 1: EcoR I; Site 2: Not I;  
 UI-CF-ECL1 is a normalized cDNA library containing the  
 following tissue(s): Normal lung from adult and from fetal  
 day 64, day 87, week 19 and week 42. The library was  
 constructed according to Bonaldo, Lennon and Soares,  
 Genome Research, 6:791-806, 1996. First strand cDNA  
 synthesis was primed with an oligo-dT primer containing a  
 Not I site. Double stranded cDNA was ligated to an EcoR I  
 adaptor, digested with Not I, and cloned directionally  
 into p773-Pac vector. The oligonucleotide used to prime  
 the synthesis of first-strand cDNA contains a library tag  
 sequence that is located between the Not I site and the  
 (dT)18 tail. The sequence tag for this library is  
 AAGTCTTAC.  
 TAG\_LIB=UI-CF-ECL1  
 TAG\_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371  
 and 380-383  
 TAG\_SEQ=AAAGTCTTAC"  
 BASE COUNT 183 a 149 c 201 g 219 t 1 others  
 ORIGIN

```

Query Match      74.3% Score 664.8; DB 12; Length 753;
Best Local Similarity 97.0%; Pred. No. 3.6e-161;
Matches 713; Conservative 0; Mismatches 3; Indels 19; Gaps 3;

QY 176 CAGCTGACGACGAGTGCATGATGAAGTTCAATCTGCTCCCTCCCTGCTGCGAC 235
    |||||
Db 753 CAGCTGACGACGACGAGTGCATGATGAAG-TCTAATCTCTCCCTCCCTGCTGCGAC 696
    |||||

```

```

QY 236 TATGCTGATGTCATGCTCTCTAGACGCTGTAATCCAGGGGTCGCCAAGGCCACAGGG 295
    |||
Db 695 TATGCTGATGTCATGCTCTCTAGACGCTGTAATCCAGGGGTCGCCAAGGCCACAGGG 636
QY 296 ACCGAGGCCAGGCTTTAGAGATGGCTCCAGAAAGCGGCCCAAGATGAGTGGAA-- 353
    |||
Db 635 ACCGAGGCCAGGCTTTAGAGATGGCTCCAGAAAGCGGCCCAAGATGAGTGGAAAG 576
QY 354 -----AGATTGGTTCTCTGAGAGCCCGAGAGAAATTCATGACAGTGC 398
    |||
Db 575 CAATGCTGTTGTTCCAGATTGGTTGTTCTGAGAGCCCGAGAGAAATTCATGACAGTGC 516
QY 399 TGGGCTGCCAAGAAAGCACTGCCCTGTATCATCTTTCAAAGGCAATGTGAAGAAACAG 458
    |||
Db 515 TGGGCTGCCAAGAAAGCACTGCCCTGTATCATCTTTCAAAGGCAATGTGAAGAAACAG 456
QY 459 ACACCAAGGCAACACAGAAAGCAAGCAAGCATTCAGAGCCTGCGACGAATTTGCCAA 518
    |||
Db 455 ACACCAAGGCAACACAGAAAGCAAGCAAGCATTCAGAGCCTGCGACGAATTTGCCAA 396
QY 519 ACAATGTCAGTAAGAAAGCTTGTCTGCTGCTTGTGAGAGCTCTGAGCGCCCACTCTCC 578
    |||
Db 395 ACAATGTCAGTAAGAAAGCTTGTCTGCTGCTTGTGAGAGCTCTGAGCGCCCACTCTCC 336
QY 579 AATTAAACATTTCTCAGCCCAAGAAAGACAGTACACCTACACAGACACTCTTCTCC 638
    |||
Db 335 AATTAAACATTTCTCAGCCCAAGAAAGACAGTACACCTACACAGACACTCTTCTCC 276
QY 639 ACCTCATCTCCACAGTACACCAACCCCTTAATCATTCAGTGTCTCAAAAGCATGTT 698
    |||
Db 275 ACCTCATCTCCACAGTACACCAACCCCTTAATCATTCAGTGTCTCAAAAGCATGTT 216
QY 699 TTCAAGATCATTTTGTGTTGTCCTCTAGTGTCTTCTCTCTCTCTCTCTCTCTCTCT 758
    |||
Db 215 TTCAAGATCATTTTGTGTTGTCCTCTAGTGTCTTCTCTCTCTCTCTCTCTCTCTCT 156
QY 759 GTGCCCTCCCTTACCAGGCTTAACTTAACTGAAAGATTCAGAAACCTGAC 818
    |||
Db 155 GTGCCCTCCCTTACCAGGCTTAACTTAACTGAAAGATTCAGAAACCTGAC 96
QY 819 TTCTGATGATGTCATTTAACCTTAATGCAATCAGAAAGTAAAGCAAGTCAAT 878
    |||
Db 95 TTCTGATGATGTCATTTAACCTTAATGCAATCAGAAAGTAAAGCAAGTCAAT 36
QY 879 AATATTTTAAATGTC 895
    |||
Db 35 AATATTTTAAATGTC 19

```

**RESULT 8**  
**BM854000**  
**LOCUS** 664 bp mRNA linear EST 06-MAR-2002  
**DEFINITION** K-EST0136291 S14K402 Homo sapiens cDNA clone S14K402-37-E04 5',  
**ACCESSION** BM854000  
**VERSION** BM854000.1 GI:19210399  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
**REFERENCE** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
**AUTHORS** 1 (bases 1 to 664)  
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
 Kim,Y.S.  
**TITLE** 21C Frontlter Korean EST Project 2001  
**JOURNAL** Unpublished  
**COMMENT** Contact: Kim YS  
 Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409

```

FEATURES
    source
        Email: yongsung@mail.kribb.re.kr
        Plate: 37 row: E column: 04
        High quality sequence stop: 664.
        Location/Qualifiers
            1..664
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="S14K402-37-E04"
                /cell_line="K402"
                /lab_host="top10F"
                /clone_lib="S14K402"
                /note="Organ: Stomach; Vector: pTZ19Rp1; site:1: EcoRI;
                site:2: NotI; The poly (A)+ RNA was dephosphorylated with
                bacterial alkaline phosphatase (BAP) and then deacapped
                with tabacco acid pyrophosphatase (TAP). The deacapped
                intact mRNA was ligated with DNA-RNA linker including EcoR
                I site by treatment of T4 RNA ligase and the first strand
                cDNA was synthesized from oligo dt-selected mRNA by
                priming with dt-tailed vector. The dt-tailed vector was
                adjusted to have about 60nt. The cDNA vector was
                circularized with E. coli DNA ligase after digestion of
                EcoRI which site is also included in vector. An RNA strand
                converted to a DNA strand by Okayama-Berg method. The
                obtained cDNA vectors were used for transformation of
                competent cells E. coli Top10F by electroporation method.
                The cDNA libraries constructed by this method are
                full-length enriched cDNA library."
BASE COUNT      172 a      194 c      139 g      159 t
ORIGIN
Query Match      74.2%; Score 664; DB 12; Length 664;
Best Local Similarity 100.0%; Pred. No. 5.6e-161;
Matches 664; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 104 CTGACCTGAGTATCCCGAGGATCAGAGACCTCCAGAGGAACTTCATTATATCT 163
    |||
Db 1 CTGACCTGAGTATCCCGAGGATCAGAGACCTCCAGAGGAACTTCATTATATCT 60
QY 164 TCAGACACTTACAGTGCACGACAGTTCGATGTAAGTTCAATCTCCCTCCCTCC 223
    |||
Db 61 TCAGACACTTACAGTGCACGACAGTTCGATGTAAGTTCAATCTCCCTCCCTCC 120
QY 224 TGTGTGTCACATATGCTGATGTCATGATGTCCTAGACGCTGAATTCAGGGGTGCCA 283
    |||
Db 121 TGTGTGTCACATATGCTGATGTCATGATGTCCTAGACGCTGAATTCAGGGGTGCCA 180
QY 284 GAGGCCACAGGGACCGAGGCCAGGCTTCTNAGAGATGCTCCAGAAAGCGGCCAAGAT 343
    |||
Db 181 GAGGCCACAGGGACCGAGGCCAGGCTTCTNAGAGATGCTCCAGAAAGCGGCCAAGAT 240
QY 344 GTGAGTGCAAAGTTGGTTCCTGAGAGCCCGGAGAAATTCATGACAGTCTGGGC 403
    |||
Db 241 GTGAGTGCAAAGTTGGTTCCTGAGAGCCCGGAGAAATTCATGACAGTCTGGGC 300
QY 404 TGCCAAAGAAAGCAGTCCCTCTGATCATTTCAAGGGCAATGGAAGAAACAAGACACC 463
    |||
Db 301 TGCCAAAGAAAGCAGTCCCTCTGATCATTTCAAGGGCAATGGAAGAAACAAGACACC 360
QY 464 AAAGGCAACACAGAAAGCCAAACACAGATTCAGAGGCTGCCAGCAATTTCTCAACAT 523
    |||
Db 361 AAAGGCAACACAGAAAGCCAAACACAGATTCAGAGGCTGCCAGCAATTTCTCAACAT 420
QY 524 GTGAGTGAAGACTTGTGCTGCTCTTGTGAGAGAGCTGAGAGGCCCACTCTCAATTA 583
    |||
Db 421 GTGAGTGAAGACTTGTGCTGCTCTTGTGAGAGAGCTGAGAGGCCCACTCTCAATTA 480
QY 584 AACATTCAGCCCAAGAAAGACAGTACACACCTACAGACACTCTCTCTCCACCTC 643
    |||
Db 481 AACATTCAGCCCAAGAAAGACAGTACACACCTACAGACACTCTCTCTCCACCTC 540
QY 644 ACTCTCCACTGTACCCACCCTTAATCATTCAGTGTCTCAAAAAGCATGTTTTCAA 703
    |||

```



Db 541 ACCTGCCACTGATACCCACCCCTAATCATTCAGTCTCTCAAAAAGCATGTTTTTCAA 600

QY 704 GATCATTTTGTGTGCTCTCTAGTGTCTTCTCTCTGTCAGTCTTAGCCTGTGCC 763  
|||||

Db 601 GATCATTTTGTGTGCTCTCTAGTGTCTTCTCTCTGTCAGTCTTAGCCTGTGCC 660  
|||||

QY 764 CTCCT 767  
|||||

Db 661 CTCCT 664

RESULT 9  
BM766904  
LOCUS  
DEFINITION K-EST0048888 S6SNU620s1 Homo sapiens cDNA S6SNU620s1-10-G04  
5', mRNA sequence.  
ACCESSION BM766904 GI:19096519  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 615)  
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
Kim,Y.S.  
21C Frontier Korean EST Project 2001  
Unpublished

TITLE  
JOURNAL  
COMMENT Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Boseun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 10 row: 6 column: 04  
High quality sequence stop: 615.  
Location/Qualifiers  
1. 615

FEATURES  
source  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="S6SNU620s1-10-G04"  
/sex="F"  
/tissue\_type="Scaltes"  
/cell\_type="Scattering floating"  
/cell\_line="SNU-620"  
/lab\_host="Top10F"  
/clone\_lib="S6SNU620s1"  
/note="Organ: Stomach; Vector: pcms; Site:1. EcoRI;  
Site:2. NotI. The poly (A)+ RNA was dephosphorylated with  
bacterial alkaline phosphatase (BAP) and then decapped  
with tabacco acid pyrophosphatase (TAP). The decapped  
intact mRNA was ligated with DNA-RNA linker including EcoR  
I site by treatment of T4 RNA ligase and the first strand  
cDNA was synthesized from oligo dt-selected mRNA by  
priming with dt-tailed vector. The dt-tailed mRNA was  
adjusted to have about 60nt. The cDNA vector was  
circularized with E. coli DNA ligase after digestion of  
EcoRI which site is also included in vector. An RNA strand  
converted to a DNA strand by Okayama-Bery method. The  
obtained cDNA vectors were used for transformation of  
competent cells E. coli Top10F by electroporation method.  
The cDNA libraries constructed by this method are  
full-length enriched cDNA library. After analyzing and  
sequencing about 2,000 ~ 3,000 colonies in original cDNA  
library, the abundant cDNAs were selected and amplified by  
PCR reaction using vector region primer including T7  
promotor as 5' primer and N(dt)14 as 3' primer. The PCR  
products were used as template for synthesis of  
biotinylated single stranded RNA by in vitro transcription  
reaction. The synthesized RNA probes were hybridized with

Query Match 68.7%; Score 615; DB 12; Length 615;  
Best Local Similarity 100.0%; Pred. No. 2,7e-148;  
Matches 615; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

antisease single stranded cDNAs prepared from original  
library and incubated with avidin-gel. After removing  
DNA-RNA hybrids by centrifuge, the subtracted cDNA  
libraries were constructed by transformation of the  
remaining DNA into competent cells E. coli Top10F with  
electroporation method."

BASE COUNT 173 a 172 c 146 g 124 t

ORIGIN

QY 8 GTTACGTAACAGACAGAGGTCACCCACCTGTTCTCGCCCTCAATGGAACGCTGG 67  
|||||

Db 1 GTTACGTAACAGACAGAGGTCACCCACCTGTTCTCGCCCTCAATGGAACGCTGG 60  
|||||

QY 68 CCGGGACTAAAGCATAGACACACAGGCTGAGTATCCGACCTGAGTCATCCCGAGGAT 127  
|||||

Db 61 CCGGGACTAAAGCATAGACACACAGGCTGAGTATCCGACCTGAGTCATCCCGAGGAT 120  
|||||

QY 128 CAGAGAGCTCCAGAGGAGAACCTTCATATATCTTCAAGCACTTACAGCTGCACCGA 187  
|||||

Db 121 CAGAGAGCTCCAGAGGAGAACCTTCATATATCTTCAAGCACTTACAGCTGCACCGA 180  
|||||

QY 188 CAGTGGCATGAAGTTCTATCTCTCCGTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 247  
|||||

Db 181 CAGTGGCATGAAGTTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTGAT 240  
|||||

QY 248 CCATGCTCTAGACAGCTGATTCAGAGGAGGTCGACAGGACAGGAGGAGGAGGAGG 307  
|||||

Db 241 CCATGCTCTAGACAGCTGATTCAGAGGAGGTCGACAGGAGGAGGAGGAGGAGGAGG 300  
|||||

QY 308 CTTCTAGAGATGGCTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 367  
|||||

Db 301 CTTCTAGAGATGGCTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360  
|||||

QY 368 GAGCCCGAG 427  
|||||

Db 361 GAGCCCGAG 420  
|||||

QY 428 ATCATTTCAAGGGCAATGTGAAGAAACAAGACACCAAGGACACAGAGAGAGAGAG 487  
|||||

Db 421 ATCATTTCAAGGGCAATGTGAAGAAACAAGACACCAAGGACACAGAGAGAGAGAG 480  
|||||

QY 488 AGCATTCAGAGGCTGAG 547  
|||||

Db 481 AGCATTCAGAGGCTGAG 540  
|||||

QY 548 CTTTGTAGAGAGCTGAG 607  
|||||

Db 541 CTTTGTAGAGAGCTGAG 600  
|||||

QY 608 GAGCACACCTACACAG 622  
|||||

Db 601 GAGCACACCTACACAG 615  
|||||

RESULT 10  
BM746867  
LOCUS  
DEFINITION K-EST0021326 S6SNU620s1 Homo sapiens cDNA S6SNU620s1-4-A11  
5', mRNA sequence.  
ACCESSION BM746867  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 628)  
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

TITLE  
JOURNAL  
COMMENT

Kim, Y.S.  
21C Frontier Korean EST Project 2001  
Unpublished  
Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 4 row: A column: 11  
High quality sequence stop: 628.  
Location/Qualifiers

FEATURES  
source

1. 628  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="S6SNU620s1-4-F11"  
/sex="F"  
/tissue\_type="Asclites"  
/cell\_type="Scattering floating"  
/cell\_line="SNU-620"  
/lab\_host="Top10F"  
/clone\_lib="S6SNU620s1"  
/note="Organ: Stomach; Vector: pcNS; Site:1: EcoRI; Site:2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okazama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli Top10F with electroporation method"

BASE COUNT 175 a 185 c 133 g 134 t 1 others  
ORIGIN

Query Match 67.8%; Score 607.2; DB 12; Length 628;  
Best Local Similarity 98.6%; Pred. No. 2.9e-146;  
Matches 612; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 79 AGCATAGACCAAGGCTGAGTATCTGACCTGATCATCCCGAGATCAGAGCCCTCC 138  
DB 1 AGCATAGACCAAGGCTGAGTATCTGACCTGATCATCCCGAGATCAGAGCCCTCC 60  
QY 139 AGCAGGGAACCTCATATATCTTCAAGCAACTTACAGCTGCACCGACAGTTCCGATG 198  
DB 61 AGCAGGGAACCTCATATATCTTCAAGCAACTTACAGCTGCACCGACAGTTCCGATG 120  
QY 199 AAAGTTCAATCTTCCCTCCTCTGTTGTCGACATAAGTATGATGTCATGTCCT 258  
DB 121 AAAGTTCAATCTTCCCTCCTCTGTTGTCGACATAAGTATGATGTCATGTCCT 180  
QY 259 AGCAGCTGAATCCAGGGGTGCCACAGAGCCACAGGACCGAGGCTTTCTAGAGAGA 318

DB 181 AGCAGCTGAATCCAGGGGTGCCACAGAGCCACAGGACCGGAGGCTTTCTAGAGAGA 240  
QY 319 TGGCTCCAGGAAGGCGGCCAAGAAATGTGATGTCAAAGATTGGTCTTGAGACCCCGAGA 378  
DB 241 TGGCTCCAGGAAGGCGGCCAAGAAATGTGATGTCAAAGATTGGTCTTGAGACCCCGAGA 300  
QY 379 AGAAATTCATGACAGTGTCTGGGCTGCCAAGAGCAGTGGCCCTGTGATCATTTTCAAG 438  
DB 301 AGAAATTCATGACAGTGTCTGGGCTGCCAAGAGCAGTGGCCCTGTGATCATTTTCAAG 360  
QY 439 GGCATGTGAGAGAAAACAAGACACCAAGGCGACACAGAAAGCCAAACAGATTCCAGA 498  
DB 361 GGCATGTGAGAGAAAACAAGACACCAAGGCGACACAGAAAGCCAAACAGATTCCAGA 420  
QY 499 GCCTGCCAGCAATTTCTCAACAAATGTGACGATTAAGGTTGCTGCTTTGAGAGG 558  
DB 421 GCCTGCCAGCAATTTCTCAACAAATGTGACGATTAAGGTTGCTGCTTTGAGAGG 480  
QY 559 CTCTGAGGCGCCACTCTTCCATTAATTAACATTTCTCAGCCAGAGACAGTACACACCTA 618  
DB 481 CTCTGAGGCGCCACTCTTCCATTAATTAACATTTCTCAGCCAGAGACAGTACACACCTA 540  
QY 619 CCAGACACTCTTCTTCTGCGACACTCTCTCCACTGTACCCACCCCTAATCATTCAG 678  
DB 541 CCAGACACTCTTCTTCTGCGACACTCTCTCCACTGTACCCACCCCTAATCATTCAG 600  
QY 679 TGCCTCAAAAAGCATGTTT 699  
DB 601 TGCCTCTCAAAAAGCCTGTTT 621

RESULT 11  
BM766900 587 bp mRNA linear EST 04-MAR-2002  
LOCUS BM766900  
DEFINITION K-EST0048883 S6SNU620s1 Homo sapiens cDNA clone S6SNU620s1-10-F11  
5', mRNA sequence.  
ACCESSION BM766900  
VERSION BM766900.1 GI:19096515  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 587)  
Kim, N.S., Bahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, D.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.  
21C Frontier Korean EST Project 2001  
Unpublished  
Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 10 row: F column: 11  
High quality sequence stop: 587.  
Location/Qualifiers

FEATURES  
source

1. 587  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="S6SNU620s1-10-F11"  
/sex="F"  
/tissue\_type="Asclites"  
/cell\_type="Scattering floating"  
/cell\_line="SNU-620"  
/lab\_host="Top10F"  
/clone\_lib="S6SNU620s1"  
/note="Organ: Stomach; Vector: pcNS; Site:1: EcoRI; Site:2: NotI; The poly (A)+ RNA was dephosphorylated with



```

QY 440 GCATGTGAAGAAACAGACACCAAGCCACAGAAAGCCAAAGCATTCAGAG 499
    |||||||
DB 314 GCAATGTGAAGAAACAGACACCAAGCCACAGAAAGCCAAAGCATTCAGAG 373
QY 500 CCTGCCAGCAATTTCTCAACAATGTCACCTAAGAAAGCTTGTGCTCTGTAGAGAC 559
    |||||||
DB 374 CCTGCCAGCAATTTCTCAACAATGTCACCTAAGAAAGCTTGTGCTCTGTAGAGAC 433
QY 560 TCTGAGCGCCGACCTCTCCATTTAAACATTCAGCAAGAAAGACAGTACAGACCTTAC 619
    |||||||
DB 434 TCTGAGCGCCGACCTCTCTCAATTTAAACATTCAGCAAGAAAGACAGTACAGACCTTAC 493
QY 620 CAGACACTCTCTCTCTCCACCTCACTCTCCACCTGACCAACCCCTTAATCATTCAGCT 679
    |||||||
DB 494 CAGACACTCTCTCTCTCCACCTCACTCTCCACCTGACCAACCCCTTAATCATTCAGCT 553
QY 680 GCTCTCAAAAAGCATTTTTCAGAAATCATTTTGTGCTCTCTCTCTCTCTCTCTCTCT 739
    |||||||
DB 554 GCTCTCAAAAAGCATTTTTCAGAAATCATTTTGTGCTCTCTCTCTCTCTCTCTCTCT 612
QY 740 C 740
    |
DB 613 C 613

```

```

RESULT 13
LOCUS BM743525 594 bp mRNA linear EST 01-MAR-2002
DEFINITION K-EST0016660 S6SNU620 Homo sapiens cDNA clone S6SNU620-8-F07 5',
            mRNA sequence.
ACCESSION BM743525
VERSION BM743525.1 GI:19064854
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 594)
Oh,K.N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Kim,Y.S., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
JOURNAL 21C Frontier Korean EST Project 2001
COMMENT Unpublished
CONTACT: Kim YS
GENOME RESEARCH CENTER
Korea Research Institute of Bioscience & Biotechnology
52 Pseun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@email.kribb.re.kr
Plate: 8 row: F column: 07
High quality sequence stop: 594.
Location/Qualifiers
1..594
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S6SNU620-8-F07"
/sex="F"
/tissue_type="Ascltes"
/cell_type="Scattering floating"
/cell_line="SNU-620"
/lab_host="Top10F"
/clone_idb="S6SNU620"

```

```

FEATURES
source
1..594
Site_1: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was

```

adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

```

BASE COUNT 166 a 175 c 130 g 123 t
ORIGIN
Query Match 64.3%; Score 575.6; DB 12; Length 594;
Best Local Similarity 99.2%; Pred. No. 4.4e-138;
Matches 589; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
QY 79 AGCATGAGCACACAGGCTGATTCCTGACCTGAGTCATCCCA-GGGATCAGGACCTC 137
    |||||||
DB 1 AGCATGAGCACACAGGCTGATTCCTGACCTGAGTCATCCCAAGGAGATCAGGACCTC 60
QY 138 CAGCAGGAACCTTCATTATATTCATCAAGCACTTACAGTGCACCGCAGTTCGAT 197
    |||||||
DB 61 CAGCAGGAACCTTCATTATATTCATCAAGCACTTACAGTGCACCGCAGTTCGAT 120
QY 198 GAAAGTTCTAATCTCTTCCCTCCTCTGTTGCTGCCACTAAGCTGAATGTCATG 257
    |||||||
DB 121 GAAAGTTCTAATCTCTTCCCTCCTCTGTTGCTGCCACTAAGCTGAATGTCATG 180
QY 258 TAGCAGCTGAATCCAGGGGGTGGCCAGAGGCCACAGGACCGGAGGCTCTTGGAG 317
    |||||||
DB 181 TAGCAGCTGAATCCAGGGGGTGGCCAGAGGCCACAGGACCGGAGGCTCTTGGAG 240
QY 318 ATGGCTCCAGGAAGGCGGCCAAGAAATGTAGTCAAGATTTGGTCTTGAGAGCCCGAG 377
    |||||||
DB 241 ATGGCTCCAGGAAGGCGGCCAAGAAATGTAGTCAAGATTTGGTCTTGAGAGCCCGAG 300
QY 378 AAGAAATTCATGACAGTGTCTGGGCTGCCAAGAAAGAGTGGCCCTGTGATCATTTCAA 437
    |||||||
DB 301 AAGAAATTCATGACAGTGTCTGGGCTGCCAAGAAAGAGTGGCCCTGTGATCATTTCAA 360
QY 438 GGGCAATGTGAAGAAAGAAAGAACAGCAAGGACCCACAGAAAGCCAAAGCATTCAG 497
    |||||||
DB 361 GGGCAATGTGAAGAAAGAAAGAACAGCAAGGACCCACAGAAAGCCAAAGCATTCAG 420
QY 498 AGCCTGCCAGCAATTTCTCAACAATGTACATTAAGAGTTGCTGCTTGTAGGA 557
    |||||||
DB 421 AGCCTGCCAGCAATTTCTCAACAATGTACATTAAGAGTTGCTGCTTGTAGGA 480
QY 558 GCTCTGAGCGCCGACCTCTTCAATTAACATTCAGCCAGCAAGAGACAGTACACCT 617
    |||||||
DB 481 GCTCTGAGCGCCGACCTCTTCAATTAACATTCAGCCAGCAAGAGACAGTACACCT 540
QY 618 ACCAGACACTCTCTCTCCACCTCACTCTCCACCTGATACCCACCCCTTAATC 671
    |||||||
DB 541 ACCAGACACTCTCTCTCCACCTCACTCTCCACCTGATACCCACCCCTTAATC 594

```

```

RESULT 14
LOCUS BU682452/c 592 bp mRNA linear EST 07-OCT-2002
DEFINITION UI-CF-EC1-acf-e-16-0-UI-s1 UI-CF-EC1 Homo sapiens cDNA clone
            UI-CF-EC1-acf-e-16-0-UI 3', mRNA sequence.
ACCESSION BU682452
VERSION BU682452.1 GI:23533364
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 592)
REFERENCE Bonaldi,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
JOURNAL genome Res. 6 (9), 791-806 (1996)

```

MEDLINE  
PUBMED  
COMMENT

97044477  
8889548  
Contact: McCray, PB  
McCray Lab  
University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171  
Email: paul.mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
Clone Sequencing by: Dr. M. Bento Soares, University of Iowa  
Genetics (www.resgen.com) or from Open Biosystems  
(www.openbiosystems.com).  
Seq primer: M13 FORWARD  
POLY-A=Yes.

FEATURES  
Source

Location/Qualifiers  
1..592  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-CF-EC1-act-e-16-0-UI"  
/tissue\_type="Lung"  
/dev\_stage="Adult and Fetal"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-CF-EC1"  
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site\_1: Ecor I; Site\_2: Not I; UI-CF-EC1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (drr)18 tail. The sequence tag for this library is AAGTGGCTTAC.  
TAG\_LIB=UI-CF-EC1  
TAG\_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383  
TAG\_SEQ=AAGTGGCTTAC"

BASE COUNT 145 a 106 c 155 g 186 t  
ORIGIN  
Query Match 64.0%; Score 572.4; DB 13; Length 592;  
Best Local Similarity 99.8%; Pred. No. 2.9e-137;  
Matches 573; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 322 CTCGAGAGGCGCCAGAAATGTGAGTGAAGAAATGTGCTTCGAGAGCCCGGAGAGA 381  
|||||  
Db 592 CTCGAGAGAGGCGCCAGAAATGTGAGTGAAGAAATGTGCTTCGAGAGCCCGGAGAGA 533  
382 AAATTCATGACAGTGTGGGCTGCGCAAGAAGAGAGTGGCCCGTGTGATTCATTTCAAGGC 441  
|||||  
Db 532 AAATTCATGACAGTGTGGGCTGCGCAAGAAGAGAGTGGCCCGTGTGATTCATTTCAAGGC 473  
442 AATGTGAAGAAACAGACACCAAGGCGACACAGAAAGCCAAACAGCATTCAGAGCC 501  
|||||  
Db 472 AATGTGAAGAAACAGACACCAAGGCGACACAGAAAGCCAAACAGCATTCAGAGCC 413  
502 TGCAGCAATTTTCGAACAATGTGACGTAAAGAGCTTGTCTGCTTGTGTAGAGCTC 561  
|||||  
Db 412 TGCAGCAATTTTCGAACAATGTGACGTAAAGAGCTTGTCTGCTTGTGTAGAGCTC 353  
562 TGAGCGCCCACTTCCCAATTAACATTCACAGCAAGAGAGACAGTACAGACACCTACCA 621  
|||||  
Db 352 TGAGCGCCCACTTCCCAATTAACATTCACAGCAAGAGAGACAGTACAGACACCTACCA 293

QY 622 GACACTCTTCTCCACACCTCCTCCACACTGACCTGACCCACCCCTAAATCATTCACAGTC 681  
|||||  
Db 292 GACACTCTTCTCCACACCTCCTCCACACTGACCTGACCCACCCCTAAATCATTCACAGTC 233  
QY 682 TCTCAAAAGCATGTTTTCGAAGATCATTTGTTGTGTCTCTCTGTGTGTCTCTCT 741  
|||||  
Db 232 TCTCAAAAGCATGTTTTCGAAGATCATTTGTTGTGTCTCTCTGTGTGTCTCTCT 173  
QY 742 CTCGCACTTTAGGCTGTGCTGCTCCCTCCCTACCCAGGCTTATTAATGAGTGAAGA 801  
|||||  
Db 172 CTCGCACTTTAGGCTGTGCTGCTCCCTCCCTACCCAGGCTTATTAATGAGTGAAGA 113  
QY 802 TTCGAGAACTGTAGCTTCTAGTACTGTATTAATGAGTGAAGA 861  
|||||  
Db 112 TTCGAGAACTGTAGCTTCTAGTACTGTATTAATGAGTGAAGA 53  
QY 862 AGCAAAAGAGTCAATTAATATTTTAAATGTC 895  
|||||  
Db 52 AGCAAAAGAGTCAATTAATATTTTAAAGTTC 19

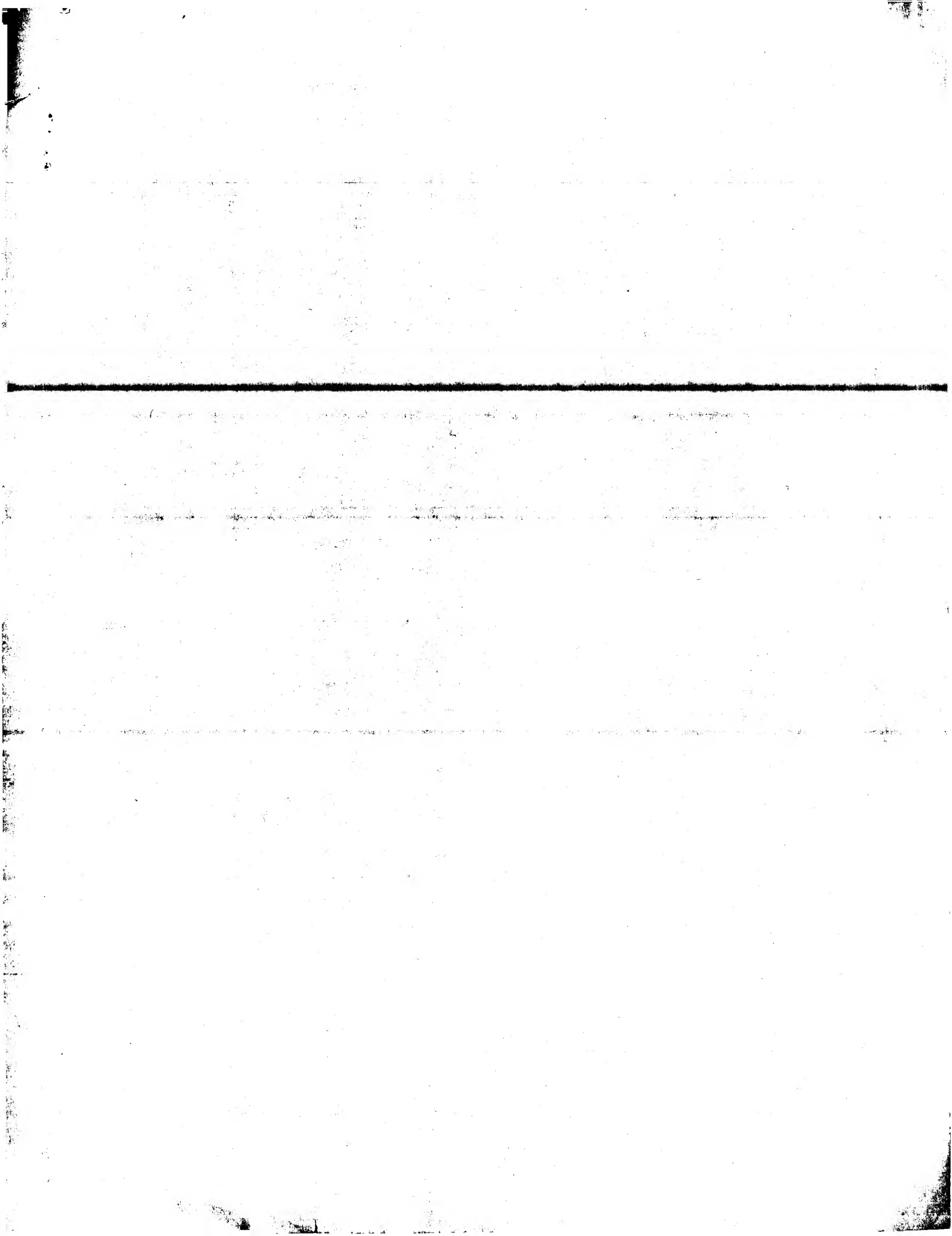
RESULT 15  
BM979898 578 bp mRNA linear EST 21-FEB-2003  
LOCUS  
DEFINITION  
UI-CF-EN1-act-g-08-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone  
BM979898 UI-CF-EN1-act-g-08-0-UI 3', mRNA sequence.  
ACCESSION  
BM979898  
KEYWORDS  
BM979898.1 GI:19600817  
SOURCE  
Homo sapiens (human)  
ORGANISM

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: McCray, PB  
McCray Lab  
University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171  
Email: paul.mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
Clone Sequencing by: Dr. M. Bento Soares, University of Iowa  
Genetics (www.resgen.com) or from Open Biosystems  
(www.openbiosystems.com).  
The following repetitive elements were found in this cDNA  
sequence: 1-39, >AT richlow\_complexity (matched complement)  
Seq primer: M13 FORWARD  
POLY-A=Yes.

FEATURES  
Source

Location/Qualifiers  
1..578  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-CF-EN1-act-g-08-0-UI"  
/tissue\_type="Primary Lung Cystic Fibrosis Epithelial Cells"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-CF-EN1"  
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site\_1: Ecor I; Site\_2: Not I; UI-CF-EN1 is a normalized cDNA library containing the







GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2003, 13:28:11 ; Search time 183.79 Seconds  
(without alignments)  
6801.360 Million cell updates/sec

Title: US-09-700-770-5

Perfect score: 895  
Sequence: 1 ctaactcttactgaacgc.....ataataatttaaatgctc 895

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1776535 seqs, 698337343 residues

Total number of hits satisfying chosen parameters: 3553070

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New:\*  
1: /cgn2\_6/ptodata/1/pna/PCT\_NEW\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/pna/US06\_NEW\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/pna/US07\_NEW\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/pna/US08\_NEW\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/pna/US09\_NEW\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/pna/US10\_NEW\_COMB.seq:\*  
7: /cgn2\_6/ptodata/1/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	445.2	49.7	511	6	US-10-649-857-18
2	39.6	4.4	791	7	US-60-480-590-3106
3	39	4.4	170991	7	US-60-487-610-19426
4	38.2	4.3	71246	7	US-60-495-114-16664
5	38	4.2	961	7	US-60-480-590-2427
6	37.2	4.2	305565	7	US-60-500-337-19019
7	36.6	4.1	443524	7	US-60-500-337-19091
8	36.4	4.1	117	1	PCT-US03-26220-118
9	36.2	4.0	391495	7	US-60-495-114-16368
10	35.8	4.0	201	7	US-60-487-610-62689
11	35.8	4.0	57143	7	US-60-487-610-19698
12	35.6	4.0	13831263	5	US-09-947-914-41
13	35.6	4.0	62546	7	US-60-487-610-19475
14	35.2	3.9	209522	7	US-60-500-315-11484
15	34.8	3.9	440017	7	US-60-485-450-11923
16	34.6	3.9	302222	7	US-60-487-610-19742
17	34.6	3.9	415998	7	US-60-500-315-11917
18	34.2	3.8	121612	7	US-60-495-114-16855
19	34	3.8	201	7	US-60-499-964-10130
20	34	3.8	32702	7	US-60-499-964-4990
21	34	3.8	50396	1	PCT-US02-36071A-235
22	34	3.8	50396	1	PCT-US02-36071A-238
23	34	3.8	4813087	5	US-09-947-914-75
24	33.8	3.8	1309	6	US-10-425-114A-34487
25	33.8	3.8	1396	6	US-10-425-114A-27505
26	33.8	3.8	1701	6	US-10-425-114A-32666

C 27	33.6	3.8	487	5	US-09-540-233D-87861	Sequence 87861, A
28	33.6	3.8	22772	7	US-60-495-114-16338	Sequence 16338, A
29	33.6	3.8	129142	7	US-60-495-114-16833	Sequence 16833, A
C 30	33.4	3.7	28477	7	US-60-500-337-19884	Sequence 19884, A
C 31	33.4	3.7	175829	7	US-60-500-315-11410	Sequence 11410, A
32	33.2	3.7	201	7	US-60-499-964-11481	Sequence 11481, A
33	33.2	3.7	3916	1	PCT-US03-29267-34	Sequence 34, Appl
34	33.2	3.7	77682	7	US-60-499-964-4996	Sequence 4996, Ap
C 35	33.2	3.7	765438	7	US-60-500-315-11549	Sequence 11549, A
36	33	3.7	897	7	US-60-480-590-5470	Sequence 5470, Ap
37	33	3.7	16299	7	US-60-493-007-2987	Sequence 2987, Ap
38	33	3.7	210570	7	US-60-500-315-11637	Sequence 11637, A
C 39	33	3.7	1946141	5	US-09-947-914-42	Sequence 42, Appl
C 40	32.8	3.7	348	5	US-09-540-233D-89064	Sequence 89064, A
41	32.8	3.7	7450	7	US-60-490-890-2084	Sequence 2084, Ap
42	32.8	3.7	20696	7	US-60-499-964-5130	Sequence 5130, Ap
43	32.8	3.7	26715	7	US-60-499-964-4997	Sequence 4997, Ap
C 44	32.8	3.7	221510	7	US-60-487-610-19346	Sequence 19346, A
C 45	32.8	3.7	221510	7	US-60-485-450-11913	Sequence 11913, A

ALIGNMENTS

RESULT 1  
US-10-649-857-18  
; Sequence 18, Application US/10649857  
; GENERAL INFORMATION:  
; APPLICANT: Craig Rosen et al.  
; TITLE OF INVENTION: 20 Human Secreted Proteins  
; FILE REFERENCE: P2005P1  
; CURRENT APPLICATION NUMBER: US/10/649,857  
; PRIOR FILING DATE: 2003-08-28  
; PRIOR APPLICATION NUMBER: US/09/166,780  
; PRIOR FILING DATE: 1998-10-06  
; PRIOR APPLICATION NUMBER: PCT/US98/06801  
; PRIOR FILING DATE: 1998-04-07  
; PRIOR APPLICATION NUMBER: 60/042,726  
; PRIOR FILING DATE: 1997-04-08  
; PRIOR APPLICATION NUMBER: 60/042,727  
; PRIOR FILING DATE: 1997-04-08  
; PRIOR APPLICATION NUMBER: 60/042,728  
; PRIOR FILING DATE: 1997-04-08  
; PRIOR APPLICATION NUMBER: 60/048,068  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: 60/048,070  
; PRIOR FILING DATE: 1997-05-30  
; PRIOR APPLICATION NUMBER: 60/048,184  
; PRIOR FILING DATE: 1997-05-30  
; NUMBER OF SEQ ID NOS: 86  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 511  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (459)  
; OTHER INFORMATION: n equals a,t,g, or c  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (494)  
; OTHER INFORMATION: n equals a,t,g, or c  
; US-10-649-857-18  
Query Match 49.7%; Score 445.2; DB 6; Length 511;  
Best Local Similarity 97.9%; Pred. No. 66133; 4; Indels 2; Gaps 2;  
Matches 466; Conservative

```

OY 1 CTAATCTGTAGTAACAGACAGAGGCTACCTGCTGTCGCGCCCTCAAAATGGGA 60
DB 38 CTAATCTGTAGTAACAGACAGAGGCTACCTGCTGTCGCGCCCTCAAAATGGGA 97
OY 61 ACGCTGGCTGGAGCTAAAGCATAGACACAGGCTGATGTCGACCTGATGTCATCC 120
DB 98 ACGCTGGCTGGAGCTAAAGCATAGACACAGGCTGATGTCGACCTGATGTCATCC 157
OY 121 CAGGATCAGAGGCTCCAGCAGGAGACCTTCATATATATCTTCAAGCAATTACAGCT 180
DB 158 CAGGATCAGAGGCTCCAGCAGGAGACCTTCATATATATCTTCAAGCAATTACAGCT 217
OY 181 GCACGAGAGTGGCAGTGAAGTCTATCTCTCCCTCCCTCTCTCTCTCTCTCTCTCT 240
DB 218 GCACGAGAGTGGCAGTGAAGTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 277
OY 241 CTGATGTCATGTCCTAGCAGGCTGATCCAGAGGCTGCGCAGAGGCTGCGCAGGAG 300
DB 278 CTGATGTCATGTCCTAGCAGGCTGATCCAGAGGCTGCGCAGAGGCTGCGCAGGAG 337
OY 301 GGCAGGCTGCTAGAGAGATGGCTCCAGAGAGGCGCCCAAGATGTCGCAAGATTTGG 360
DB 338 GGCAGGCTGCTAGAGAGATGGCTCCAGAGAGGCGCCCAAGATGTCGCAAGATTTGG 397
OY 361 TTCTGAGAGAGCCCGAGAGAGAAATTCATGACAGTGTCTGGGCTGCCCAAGAGAGTCG 420
DB 398 TTCTGAGAGAGCCCGAGAGAGAAATTCATGACAGTGTCTGGGCTGCCCAAGAGAGTCG 456
OY 421 CCCGTGATCATTTTCAGAGGCAATGTGAAGAAACACAGACCAAGGACACAGAG 476
DB 457 CCNCTGATCTTCTTCAAGGGC-ATGTGAAGAAACACAGACCAAGGACACAGAG 511

```

## RESULT 2

```

US-60-480-590-3106
; Sequence 3106, Application US/60480590
; GENERAL INFORMATION:
; APPLICANT: Monsanto
; APPLICANT: Monsanto
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Soybean polymorphisms and Methods of Genotyping
; FILE REFERENCE: 38-15 (53382)
; CURRENT APPLICATION NUMBER: US/60/480,590
; CURRENT FILING DATE: 2003-06-20
; NUMBER OF SEQ ID NOS: 6578
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3106
; LENGTH: 791
; TYPE: DNA
; ORGANISM: Glycine max
US-60-480-590-3106

```

```

Query Match 4.48; Score 39.6; DB 7; Length 791;
Best Local Similarity 58.58; Pred. No. 0.047;
Matches 69; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
OY 439 GGCATATGAGAAACAAAGACCAAGCAGCAGAGCAAGCAAGCATTCACAG 498
DB 62 GGCATATGAGAAACAAAGATTAAGCAATGAAACAAATGGAACCAAGCAGCATCTCTAT 121
OY 499 GCGTCCAGCAATTTCTCAACAATGTCAGCTAAGAGATTTGCTCTGCTGCTGAGG 556
DB 122 GCGTCCAGCAATTAACCTATCAATGCTGCTGAGCAGCTTTCGCCCTTGTATTATAG 179

```

## RESULT 3

```

US-60-487-610-19426
; Sequence 19426, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: CARGILL, Michele
; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,

```

```

; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19426
; LENGTH: 170991
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-487-610-19426

```

```

Query Match 4.48; Score 39; DB 7; Length 170991;
Best Local Similarity 58.08; Pred. No. 1.1;
Matches 69; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

```

```

OY 421 CCCGTGATCATTTTCAGAGGCAATGTGAAGAAACAGACCAAGGACACAGAG 480
DB 146742 CCCGTGATCATTTTCAGAGGCAATGTGAAGAAACAGACCAAGGACACAGAG 146801
OY 481 CCAACAGAGCATTTCCAGAGGCTGCGCAGCATTTCTCAAGATGTCAGTAAAGCTT 539
DB 146802 CATACAGCTGATTTCCAAAGCCTGACAGAGATAGCCCTTAACAGAAACATACAGATTTT 146860

```

## RESULT 4

```

US-60-495-114-16664
; Sequence 16664, Application US/60495114
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN PROTEASE PROTEINS, METHODS OF DETECTION AND
; FILE REFERENCE: CL001480
; CURRENT APPLICATION NUMBER: US/60/495,114
; CURRENT FILING DATE: 2003-08-15
; NUMBER OF SEQ ID NOS: 91238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16664
; LENGTH: 71246
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (1)...(71246)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables
US-60-495-114-16664

```

```

Query Match 4.38; Score 38.2; DB 7; Length 71246;
Best Local Similarity 50.68; Pred. No. 1.2;
Matches 117; Conservative 0; Mismatches 113; Indels 1; Gaps 1;

```

```

OY 540 TGCTTGCTGCTTTGTAGAGGCTGAGGCGCCACTCTTCCAAATTAACATTTTCAGCCAG 599
DB 35241 TGCTTGCTGCTTTGTAGAGGCTGAGGCGCCACTCTTCCAAATTAACATTTTCAGCCAG 35300
OY 600 AAGACAGTAGACA-CACCTACAGACACTTTCTTCCACCTACTCTCCCACTGTAC 658
DB 35301 AAGACAGTAGACA-CACCTACAGACACTTTCTTCCACCTACTCTCCCACTGTAC 35360
OY 659 CACCCCTTAATCATTTCCAGAGGCTGTCGAAAGAGATTTTTCAGATCATTTTGTGT 718
DB 35361 CACCCCTTAATCATTTCCAGAGGCTGTCGAAAGAGATTTTTCAGATCATTTTGTGT 718
OY 719 TGCTTGCTGCTTTGTAGAGGCTGAGGCGCCACTCTTCCAAATTAACATTTTCAGCCAG 769
DB 35421 TGCTTGCTGCTTTGTAGAGGCTGAGGCGCCACTCTTCCAAATTAACATTTTCAGCCAG 35471

```

## RESULT 5

```

US-60-480-590-2427/c
; Sequence 2427, Application US/60480590
; GENERAL INFORMATION:

```

```

; APPLICANT: Monsanto
; APPLICANT: Monsanto
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Soybean Polymorphisms and Methods of Genotyping
; FILE REFERENCE: 38-15 (53382)
; CURRENT APPLICATION NUMBER: US/60/480,550
; CURRENT FILING DATE: 2003-06-20
; NUMBER OF SEQ ID NOS: 6578
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2427
; LENGTH: 961
; TYPE: DNA
; ORGANISM: Glycine max
US-60-480-590-2427

```

Query Match Best Local Similarity 57.6%; Score 38; DB 7; Length 961;

Matches 68; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

```

QY 439 GGCATGTGAGAAAAAGACACCAAGCCACAGAAAGCCAAACAGCATTCAGCA 498
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 901 GCCTTATTCAGAAATTTGAGGCCAAATTTGAACAAATGGAACCAAGATTTCTAT 842
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 499 GCCTGCCACCAATTTCTCAACAATGTCAGCTTAGAAGCTTTGCTGCTTTGTAGG 556
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 841 GGCCTGGCAGAAATTAATTAATGATGCTGTGACAGCTTGCCTGTTTATATG 784
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

## RESULT 6

US-60-500-337-19019/c

```

; Sequence 19019, Application US/60500337
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN KINASE PROTEINS, METHODS OF DETECTION AND
; FILE REFERENCE: CL001483
; CURRENT APPLICATION NUMBER: US/60/500,337
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 123188
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19019
; LENGTH: 305565
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(305565)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-60-500-337-19019

```

Query Match Best Local Similarity 45.3%; Score 37.2; DB 7; Length 305565;

Matches 126; Conservative 2; Mismatches 150; Indels 0; Gaps 0;

```

QY 45 TCGCCCTCAAAATGGAGCGCTGGCGGACTAAGACATAGACCACGAGCTGATATCC 104
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 31803 TCACCAAGATGTGACCAAGCTGGCACTCACCGGGCGCAACCAAGACCAATTAAGAT 31744
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 105 TGACCTGAGTCATCCCGCAGGATCAGAGCCTCCACAGGAACTTCATTTATTTCTT 164
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 31743 GGGAGATTAATTAACCCAGCTGTGATCAAGAAAAACAGGAGAAATTTAAATTCGACCTT 31684
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 165 CAAGCACTTACAGCTGCACCGACGATGCGATGAAGTCTTATCTCCCTCCCT 224
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 31683 CACCCAGCTCACAGCTGTCTCAGCTTTCTTAAAGAAATAGCTCTCCACCTTCCACCT 31624
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 225 GTTGTGCCACTAATGCTGATGTCAGATGCTCTACAGGCTGAATTCAGAGGCTGCCAG 284
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 31623 GTTTCAGATTTAATTAAGTATGTTGTCACATTTCTTAACATGAGAGAACTTTCTTA 31564
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 285 AGGCCACAGGAGCCAGGCTTCTAGAGATGCC 322
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

DB 31563 ACCMACATGCRCTTGMACTACCAAGCAGAGATGAC 31526

## RESULT 7

US-60-500-337-19091

```

; Sequence 19091, Application US/60500337
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN KINASE PROTEINS, METHODS OF DETECTION AND
; FILE REFERENCE: CL001483
; CURRENT APPLICATION NUMBER: US/60/500,337
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 123188
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19091
; LENGTH: 443524
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(443524)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables
US-60-500-337-19091

```

Query Match Best Local Similarity 49.2%; Score 36.6; DB 7; Length 443524;

Matches 96; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

```

QY 613 CACCTACAGACACTCTTTCTCCACCTCACTCTCCACGTATACCAACCCCTAAATGA 672
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 131435 CACCTTCCCAAGTGTCTCCCTCCTCTGTTCTCTCTCTCCACCCCTACCTCT 131494
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 673 TTCCAGTGTCTCAAAAAGATGTTTCAAGATCATTTGTTGTTGCTCTCTAGTG 732
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 131495 TTCCCTTTTCTTTCTCTCCCATTTTCATGCTTTCTTTCTTCCCTGCACCCCT 131554
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 733 TCTTCTTCTGTCAGTCTTAGCTGTGCCCCCTTACCAGGCTTAGGCTTAATTA 792
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 131555 TCTTCTTCTTCTTTTCTCTCTCCACCTCTCTCCACCTCTGACAGCTGACAGGCTCTG 131614
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 793 CCTGAAGATTCAG 807
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 131615 TCTGTGGGTTTCAG 131629
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

## RESULT 8

PCT-US03-26220-118

```

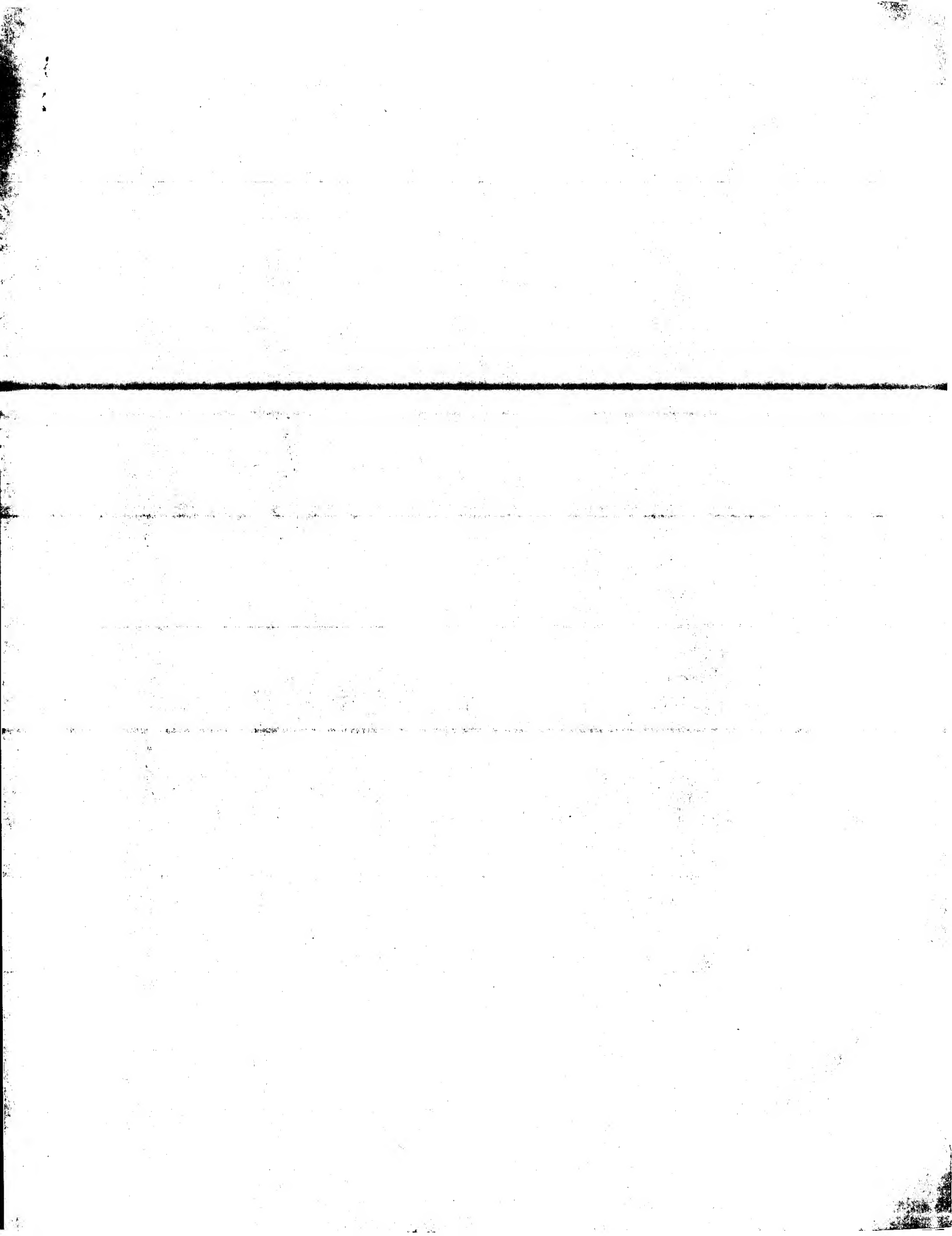
; Sequence 118, Application PC/TUS0326220
; GENERAL INFORMATION:
; APPLICANT: Regulome Corporation
; APPLICANT: Stamatoyanopoulos, John A.
; APPLICANT: McArthur, Michael
; APPLICANT: Sabo, Peter J.
; TITLE OF INVENTION: FUNCTIONAL SITES
; FILE REFERENCE: 11207-012-228
; CURRENT APPLICATION NUMBER: PCT/US03/26220
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: 60/404,121
; NUMBER OF SEQ ID NOS: 37172
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 118
; LENGTH: 117
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Table Reference ID CID: 171095
PCT-US03-26220-118

```

Query Match Best Local Similarity 4.1%; Score 36.4; DB 1; Length 117;







GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2003, 19:48:32 ; Search time 254.83 Seconds

(without alignments)  
9113.362 Million cell updates/sec

Title: US-09-700-770-5

Perfect score: 895  
1 ctaactcgtacgtacagc.....ataataattttaaatgctc 895

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1731049 seqs, 1297405648 residues

Total number of hits satisfying chosen parameters: 3462098

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/2/pubpna/FCI\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/PCURS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
16: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
17: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	895	100.0	895	11	US-09-788-990-2 Sequence 2, Appl1
2	895	100.0	1171	11	US-09-788-990-6 Sequence 6, Appl1
3	895	100.0	1171	14	US-10-237-435-4 Sequence 4, Appl1
4	852	95.2	870	9	US-09-989-722-164 Sequence 164, App
5	852	95.2	870	9	US-09-989-723-164 Sequence 164, App
6	852	95.2	870	9	US-09-989-727-164 Sequence 164, App
7	852	95.2	870	9	US-09-989-727-164 Sequence 164, App
8	852	95.2	870	10	US-09-989-731-164 Sequence 164, App
9	852	95.2	870	10	US-09-989-732-164 Sequence 164, App
10	852	95.2	870	10	US-09-991-073-164 Sequence 164, App
11	852	95.2	870	10	US-09-990-442-164 Sequence 164, App
12	852	95.2	870	10	US-09-991-163-164 Sequence 164, App
13	852	95.2	870	10	US-09-993-604-164 Sequence 164, App
14	852	95.2	870	10	US-09-990-456-164 Sequence 164, App
15	852	95.2	870	10	US-09-989-721-164 Sequence 164, App
16	852	95.2	870	10	US-09-992-598-164 Sequence 164, App

17	852	95.2	870	10	US-09-989-293A-164	Sequence 164, App
18	852	95.2	870	10	US-09-989-735-164	Sequence 164, App
19	852	95.2	870	10	US-09-990-444-164	Sequence 164, App
20	852	95.2	870	10	US-09-991-181-164	Sequence 164, App
21	852	95.2	870	10	US-09-989-730-164	Sequence 164, App
22	852	95.2	870	10	US-09-990-436-164	Sequence 164, App
23	852	95.2	870	10	US-09-993-687-164	Sequence 164, App
24	852	95.2	870	11	US-09-989-734-164	Sequence 164, App
25	852	95.2	870	11	US-09-997-653-164	Sequence 164, App
26	852	95.2	870	11	US-09-993-667-164	Sequence 164, App
27	852	95.2	870	11	US-09-997-428-164	Sequence 164, App
28	852	95.2	870	11	US-09-997-666-164	Sequence 164, App
29	852	95.2	870	11	US-09-990-438-164	Sequence 164, App
30	852	95.2	870	11	US-09-990-562-164	Sequence 164, App
31	852	95.2	870	11	US-09-990-711-164	Sequence 164, App
32	852	95.2	870	11	US-09-989-726-164	Sequence 164, App
33	852	95.2	870	11	US-09-998-156-164	Sequence 164, App
34	852	95.2	870	11	US-09-990-437-164	Sequence 164, App
35	852	95.2	870	11	US-09-991-157-164	Sequence 164, App
36	852	95.2	870	11	US-09-997-514-164	Sequence 164, App
37	852	95.2	870	11	US-09-997-573-164	Sequence 164, App
38	852	95.2	870	11	US-09-991-172-164	Sequence 164, App
39	852	95.2	870	11	US-09-990-726-164	Sequence 164, App
40	852	95.2	870	11	US-09-997-559-164	Sequence 164, App
41	852	95.2	870	11	US-09-997-601-164	Sequence 164, App
42	852	95.2	870	11	US-09-990-443-164	Sequence 164, App
43	852	95.2	870	11	US-09-991-854-164	Sequence 164, App
44	852	95.2	870	11	US-09-997-628-164	Sequence 164, App
45	852	95.2	870	11	US-09-997-683-164	Sequence 164, App

## ALIGNMENTS

RESULT 1  
US-09-788-990-2  
Sequence 2, Application US/09788990  
General Information: US20030049617A1  
Applicant: Chen, Sei Yu  
Applicant: Sun, Yongming  
Applicant: Macina, Roberto  
Title of Invention: Method of Diagnosing, Monitoring, Staging, Imaging and  
Title of Invention: Treating Lung Cancer  
File Reference: DEX-0140  
Current Application Number: US/09/788,990  
Current Filing Date: 2001-02-20  
Prior Application Number: 60/183,188  
Prior Filing Date: 2000-02-17  
Number of Seq ID NOS: 11  
Software: Patent In Ver. 2.1  
Seq ID No 2  
Length: 895  
Type: DNA  
Organism: Homo sapiens  
US-09-788-990-2

Query Match 100.0%; Score 895; DB 11; Length 895;  
Best Local Similarity 100.0%; Pred. No. 2e-285;  
Matches 895; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTAATCTGTAGTAAACAGACAGAGCTTCACTTCTGCTGCTCAATGGGA 60  
DB 1 CTAATCTGTAGTAAACAGACAGAGCTTCACTTCTGCTGCTCAATGGGA 60  
QY 61 ACCTGCGCTGGAGCTAAAGCATAGACACAGAGCTGAGTATCTGACTGATCC 120  
DB 61 ACCTGCGCTGGAGCTAAAGCATAGACACAGAGCTGAGTATCTGACTGATCC 120  
QY 121 CAGGATTCAGGAGCTCCAGACAGGAACTTCATATTTCTTCAAGCACTTACAGT 180  
DB 121 CAGGATTCAGGAGCTCCAGACAGGAACTTCATATTTCTTCAAGCACTTACAGT 180



[illegible]

	Best Local Similarity	100.0%	Pred. No. 2,36-285	Matches 895	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	CTAATCTGTTACGTAACGACGAACAGCGTCACCTCACCCTGTTCTCGCCCTCAATGGGA	60					
Db	22	CTAATCTGTTAGTAACAGCAAGACAGAGGTCACCTCACCTGTTCTCGCCCTCAATGGGA	81					
QY	61	ACGCTGGCCTGGGACCTAAAGCATACACCAACGAGGTGAGTATCCGACCTGACATCACC	120					
Db	82	ACGCTGGCCTGGGACCTAAAGCATACACCAACGAGGTGAGTATCCGACCTGACATCACC	141					
QY	121	CAGGATCAGAGAGCCTCCAGCAGGAGAACCTTCATATATTTCTTCAGCACTTACAGCT	180					
Db	142	CAGGATCAGAGAGCCTCCAGCAGGAGAACCTTCATATATTTCTTCAGCACTTACAGCT	201					
QY	181	GCACGCAAGTGGCATGAAGTCTATATCTTCTTCCCTCCCTGTTGCTGCCACTAATG	240					
Db	202	GCACGCAAGTGGCATGAAGTCTATATCTTCTTCCCTCCCTGTTGCTGCCACTAATG	261					
QY	241	CTGATGTCATATGTTCTTACGAGCCTGTAATCAGAGGGGTGGCAGAGGCAACAGGACCGA	300					
Db	262	CTGATGTCATATGTTCTTACGAGCCTGTAATCAGAGGGGTGGCAGAGGCAACAGGACCGA	321					
QY	301	GGCCAGGCTTTAGAGATGCGCTCCAGAGAGGGGCCAAGATGTGATGTCMAAGATTGG	360					
Db	322	GGCCAGGCTTTAGAGATGCGCTCCAGAGAGGGGCCAAGATGTGATGTCMAAGATTGG	381					
QY	361	TTCCGACAGGCCCCGAGAGAAATTCATATGACATGTCCTGGGCTGCCAAGAGACATGC	420					
Db	382	TTCCGACAGGCCCCGAGAGAAATTCATATGACATGTCCTGGGCTGCCAAGAGACATGC	441					
QY	421	CCCTGTGATCATTTTCAAGGGCAATGTGTAAGAAACAAAGACACCAAGAGCAACAGAAAG	480					
Db	442	CCCTGTGATCATTTTCAAGGGCAATGTGTAAGAAACAAAGACACCAAGAGCAACAGAAAG	501					
QY	481	CCAAACAAAGCATTTCCAGAGCCTGCCAGCAATTTTCTCAACAAATGTCACTAAGAAAGTTT	540					
Db	502	CCAAACAAAGCATTTCCAGAGCCTGCCAGCAATTTTCTCAACAAATGTCACTAAGAAAGTTT	561					
QY	541	GCTGTGCTTGTGTAGAGACTGTGAGAGCCGCCACTTTCATTAATTAACATTCGCAGAGA	600					
Db	562	GCTGTGCTTGTGTAGAGACTGTGAGAGCCGCCACTTTCATTAATTAACATTCGCAGAGA	621					
QY	601	AGACAGTGAAGCACACCTACAGACACTTCTTCTGCCACCTCACTCTCCACATGTACCC	660					
Db	622	AGACAGTGAAGCACACCTACAGACACTTCTTCTGCCACCTCACTCTCCACATGTACCC	681					
QY	661	ACCCCTTAATCATTCAGTGTCTCCAAAAGAGCATTTTTCAGAGATATTTTGTGTG	720					
Db	682	ACCCCTTAATCATTCAGTGTCTCCAAAAGAGCATTTTTCAGAGATATTTTGTGTG	741					
QY	721	CTCTCTAGTGTCTTCTCTCTGTCAGTCTTACGCTGTGACCTGCCCTTACCCAGAGCT	780					
Db	742	CTCTCTAGTGTCTTCTCTCTGTCAGTCTTACGCTGTGACCTGCCCTTACCCAGAGCT	801					
QY	781	TAGGCTTAATTTACCTGAAAGATTCCAGAGAACTGTAGCTTCTAGCTAGTGCATTTAAC	840					
Db	802	TAGGCTTAATTTACCTGAAAGATTCCAGAGAACTGTAGCTTCTAGCTAGTGCATTTAAC	861					
QY	841	CTTAAATGCAATCAGAGAAATAGCAAAACAAGTCAATTAATTTTAAATGTC	895					
Db	862	CTTAAATGCAATCAGAGAAATAGCAAAACAAGTCAATTAATTTTAAATGTC	916					

```

; FILE REFERENCE: PB-0019 US
; CURRENT APPLICATION NUMBER: US/10/237,435
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/317,822
; PRIOR FILING DATE: 09-07-2001
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 1171
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No. US20030124580A1 221807.2
US-10-237-435-4

```

```

Query Match      100.0%  Score 895:  DB 14:  Length 1171:
Best Local Similarity 100.0%:  Pred. No. 2.3e-285;
Matches 895:  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

OY 1 CTAATCTGTAGTAAACAGACAGACAGGCTACCTACCTGTTCTGCGCCCTCAATGGGA 60
DB 22 CTAATCTGTAGTAAACAGACAGACAGGCTACCTACCTGTTCTGCGCCCTCAATGGGA 81
OY 61 ACGCTGGCTGGGACTAAAGCATAGACACACAGGCTGATCTGACCTGATGATCC 120
DB 82 ACGCTGGCTGGGACTAAAGCATAGACACACAGGCTGATCTGACCTGATGATCC 141
OY 121 CAGGATCAGAGGCTCCAGGAGGAGGAGCTTCAATATTTTCAAGCAATTTACGT 180
DB 142 CAGGATCAGAGGCTCCAGGAGGAGGAGCTTCAATATTTTCAAGCAATTTACGT 201
OY 181 GCACGACAGTGGCGATGAAGTTCTAATCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 202 GCACGACAGTGGCGATGAAGTTCTAATCTCTCTCTCTCTCTCTCTCTCTCTCT 261
OY 241 CTGATGTCCATGTCTCTAGCAGCCTGATCCAGGGGTCGCCAGAGCCACAGGACGA 300
DB 262 CTGATGTCCATGTCTCTAGCAGCCTGATCCAGGGGTCGCCAGAGCCACAGGACGA 321
OY 301 GGCCAGGCTTCTAGAGATGGCTCCAGAGAGGCGCCAGAAATGAGTGAAGATTTGG 360
DB 322 GGCCAGGCTTCTAGAGATGGCTCCAGAGAGGCGCCAGAAATGAGTGAAGATTTGG 381
OY 361 TTCTGAGAGGCGCCAGAGAAATTTATGACAGTGTCTGGGCTCCCAAGAGCAGTGC 420
DB 382 TTCTGAGAGGCGCCAGAGAAATTTATGACAGTGTCTGGGCTCCCAAGAGCAGTGC 441
OY 421 CCCTGTGATCATTTCAAGGGCAATGTGAAGAAACAGACACCAAGGACCCAGAAAG 480
DB 442 CCCTGTGATCATTTCAAGGGCAATGTGAAGAAACAGACACCAAGGACCCAGAAAG 501
OY 481 CCAACAGACATTCAGAGGCTCCAGAGATTTCTCAACATATGAGTGAAGATTTG 540
DB 502 CCAACAGACATTCAGAGGCTCCAGAGATTTCTCAACATATGAGTGAAGATTTG 561
OY 541 GCTGTGCTTTGTAGAGCTCTGAGCGCCACTCTTCCAAATTTAACTTTGAGCCAGA 600
DB 562 GCTGTGCTTTGTAGAGCTCTGAGCGCCACTCTTCCAAATTTAACTTTGAGCCAGA 621
OY 601 AGACAGTAGACACCTACACAGACACTCTTCTTCCCACTCACTCTCCACTGATACC 660
DB 622 AGACAGTAGACACCTACACAGACACTCTTCTTCCCACTCACTCTCCACTGATACC 681
OY 661 ACCCTAATCATTCAGTGGCTCCAAAGAGATTTTTCAGATATTTGTTGTTG 720
DB 682 ACCCTAATCATTCAGTGGCTCCAAAGAGATTTTTCAGATATTTGTTGTTG 741
OY 721 CTCTCTAGTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
DB 742 CTCTCTAGTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 801
OY 781 TAGGCTTAATTAACCTGAAAGATTCAGAGAACTGAGTCTCTAGCTAGTGTCAATTAA 840

```

```

DB 802 TAGGCTTAATTAACCTGAAAGATTCAGAGAACTGAGTCTCTAGCTAGTGTCAATTAA 861
OY 841 CTTAATGCAATCAGAAAGTGAAGAAAGTCAATTAATTTTAAATGTC 895
DB 862 CTTAATGCAATCAGAAAGTGAAGAAAGTCAATTAATTTTAAATGTC 916

RESULT 4
US-09-989-722-164
; Sequence 164, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kjaevla, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P163
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025

```

;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088026  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088028  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088029  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088030  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088033  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088326  
;; PRIOR FILING DATE: 1998-06-04  
;; PRIOR APPLICATION NUMBER: 60/088167  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088202  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088212  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088217  
;; PRIOR FILING DATE: 1998-06-05  
;; PRIOR APPLICATION NUMBER: 60/088655  
;; PRIOR FILING DATE: 1998-06-09  
;; PRIOR APPLICATION NUMBER: 60/088734  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088738  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088742  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088810  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088824  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088826  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088858  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/088861  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/088876  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/089105  
;; PRIOR FILING DATE: 1998-06-12  
;; PRIOR APPLICATION NUMBER: 60/089440  
;; PRIOR FILING DATE: 1998-06-16  
;; PRIOR APPLICATION NUMBER: 60/089512  
;; PRIOR FILING DATE: 1998-06-16  
;; PRIOR APPLICATION NUMBER: 60/089514  
;; PRIOR FILING DATE: 1998-06-16  
;; PRIOR APPLICATION NUMBER: 60/089532  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089538  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089598  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089599  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089600  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089653  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089801  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/089907  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/089908  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/089947  
;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/089948  
;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/089952  
;; PRIOR FILING DATE: 1998-06-19

;; PRIOR APPLICATION NUMBER: 60/090246  
;; PRIOR FILING DATE: 1998-06-22  
;; PRIOR APPLICATION NUMBER: 60/090252  
;; PRIOR FILING DATE: 1998-06-22  
;; PRIOR APPLICATION NUMBER: 60/090254  
;; PRIOR FILING DATE: 1998-06-22  
;; PRIOR APPLICATION NUMBER: 60/090349  
;; PRIOR FILING DATE: 1998-06-23  
;; PRIOR APPLICATION NUMBER: 60/090355  
;; PRIOR FILING DATE: 1998-06-23  
;; PRIOR APPLICATION NUMBER: 60/090429  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090431  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090435  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090444  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090445  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090472  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090535  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090540  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090542  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090557  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090676  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090678  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090690  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090694  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090695  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090696  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090862  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/090863  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 95.2%; Score 852; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 3,4e-271;  
Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 44 CTGCCTCAATGGAAGCCTGGGACTTAAGCATAGACCAAGCTGAGTATC 103  
|||||  
Db 1 CTGCCTCAATGGAAGCCTGGGACTTAAGCATAGACCAAGCTGAGTATC 60



;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088738  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088742  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088810  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088824  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088826  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088858  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/088861  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/088876  
;; PRIOR FILING DATE: 1998-06-11  
;; PRIOR APPLICATION NUMBER: 60/089105  
;; PRIOR FILING DATE: 1998-06-12  
;; PRIOR APPLICATION NUMBER: 60/089440  
;; PRIOR FILING DATE: 1998-06-16  
;; PRIOR APPLICATION NUMBER: 60/089512  
;; PRIOR FILING DATE: 1998-06-16  
;; PRIOR APPLICATION NUMBER: 60/089514  
;; PRIOR FILING DATE: 1998-06-16  
;; PRIOR APPLICATION NUMBER: 60/089532  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089538  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089598  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089599  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089600  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089653  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089801  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/089907  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/089908  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/089947  
;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/089948  
;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/089952  
;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/090246  
;; PRIOR FILING DATE: 1998-06-22  
;; PRIOR APPLICATION NUMBER: 60/090252  
;; PRIOR FILING DATE: 1998-06-22  
;; PRIOR APPLICATION NUMBER: 60/090254  
;; PRIOR FILING DATE: 1998-06-22  
;; PRIOR APPLICATION NUMBER: 60/090349  
;; PRIOR FILING DATE: 1998-06-23  
;; PRIOR APPLICATION NUMBER: 60/090355  
;; PRIOR FILING DATE: 1998-06-23  
;; PRIOR APPLICATION NUMBER: 60/090429  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090431  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090435  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090444  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090445  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090472  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090535  
;; PRIOR FILING DATE: 1998-06-24

;; PRIOR APPLICATION NUMBER: 60/090540  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090542  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090557  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090676  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090678  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090690  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090694  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090695  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090696  
;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090862  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/090863  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 95.28; Score 852; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 3.4e-771;  
Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 CTGCGCTCAAAATGGGAACGCTGGCGGACTAAGCATAGACACAGGCTAGATC 103  
DB 1 CTGCGCTCAAAATGGGAACGCTGGCGGACTAAGCATAGACACAGGCTAGATC 60  
QY 104 CTGACCTAGTCAATCCCGAGGATCAGAGGCTCCAGAGGAACCTTCCATTATTC 163  
DB 61 CTGACCTAGTCAATCCCGAGGATCAGAGGCTCCAGAGGAACCTTCCATTATTC 120  
QY 164 TCAAGCACTTACAGCTGCACCGACGAGTGGATGAAGAATTCTATCTTCCCTCC 223  
DB 121 TCAAGCACTTACAGCTGCACCGACGAGTGGATGAAGAATTCTATCTTCCCTCC 180  
QY 224 TGTGCTGCACATATGCTATGTCATGCTTACACGCTTAATCCAGGGTCCCA 283  
DB 181 TGTGCTGCACATATGCTATGTCATGCTTACACGCTTAATCCAGGGTCCCA 240  
QY 284 GAGGCCAGAGGACCGAGGCGAGGCTTCTAGAGATGGCTCCAGAGGCGCCAGAT 343  
DB 241 GAGGCCAGAGGACCGAGGCGAGGCTTCTAGAGATGGCTCCAGAGGCGCCAGAT 300  
QY 344 GTGAGTCAAAAGATGTTCTTGAAGCCCCGAGAAATAATTCATGACAGTGTGGC 403  
DB 301 GTGAGTCAAAAGATGTTCTTGAAGCCCCGAGAAATAATTCATGACAGTGTGGC 360  
QY 404 TGGCAAGAGCAGTGGCCCTGATCATTTCAAGGCAATGTCAGAAAAACAAGACC 463  
DB 361 TGGCAAGAGCAGTGGCCCTGATCATTTCAAGGCAATGTCAGAAAAACAAGACC 420

QY	464	AAAGGACACAGAAAGCCAAACAGACATTCAGAGAGCCGCGAGCAATTCGCAACAAAT	523
Db	421	AAAGGACACAGAAAGCCAAACAGACATTCAGAGAGCCGCGAGCAATTCGCAACAAAT	480
QY	524	GTCAGCTAAGAAGCTTGTGCTCTGCTTGTAGAGCTGTGAGCGGCCACTCTTCCAAATTA	583
Db	481	GTCAGCTAAGAAGCTTGTGCTCTGCTTGTAGAGCTGTGAGCGGCCACTCTTCCAAATTA	540
QY	584	AACATTCACACCAAGAAAGACAGTAGACACACCTACACAGACACTCTTCTTCTCCACCTC	643
Db	541	AACATTCACACCAAGAAAGACAGTAGACACACCTACACAGACACTCTTCTTCTCCACCTC	600
QY	644	ACTCTCCACAGTAGACCCACCCCTTAATCATTCGCAGTGCCTCTCAAAAAGCATGTTTTCAA	703
Db	601	ACTCTCCACAGTAGACCCACCCCTTAATCATTCAGTGCCTCTCAAAAAGCATGTTTTCAA	660
QY	704	GATCATTTTGTGTTGTGCTCTCTCTAGTGTCTTCTTCTCTCGTAGCTTTAGGCTGTGCC	763
Db	661	GATCATTTTGTGTTGTGCTCTCTCTAGTGTCTTCTTCTCTCGTAGCTTTAGGCTGTGCC	720
QY	764	CTCCCCCTAACCCAGGCTTAGGCTTAATTAACCGAAAGATTCAGAGAAACTGTAGCTGCGCT	823
Db	721	CTCCCCCTAACCCAGGCTTAGGCTTAATTAACCGAAAGATTCAGAGAAACTGTAGCTGCGCT	780
QY	824	AGTAGTGTCAATTTAACCTTAATGCAATCAGAGAAAGTAGCAAAACAGAAATCAATTAATA	883
Db	781	AGTAGTGTCAATTTAACCTTAATGCAATCAGAGAAAGTAGCAAAACAGAAATCAATTAATA	840
QY	884	TTTTTAATGTC 895	
Db	841	TTTTTAATGTC 852	

RESULT 6  
 US-09-989-279-164  
 Sequence 164, Application US/09989279  
 Patent No. US20020072496A1  
 GENERAL INFORMATION:  
 APPLICANT: Asnkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gertlisen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kijavlin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paonli, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730P1C56  
 CURRENT APPLICATION NUMBER: US/09/989,279  
 PRIOR FILING DATE: 2001-11-19  
 PRIOR APPLICATION NUMBER: 60/049787  
 PRIOR FILING DATE: 1997-06-16  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/065186  
 PRIOR FILING DATE: 1997-11-12

1	PRIOR APPLICATION NUMBER: 60/065311
2	PRIOR FILING DATE: 1997-11-13
3	PRIOR APPLICATION NUMBER: 60/066770
4	PRIOR FILING DATE: 1997-11-24
5	PRIOR APPLICATION NUMBER: 60/075945
6	PRIOR FILING DATE: 1998-02-25
7	PRIOR APPLICATION NUMBER: 60/078910
8	PRIOR FILING DATE: 1998-03-20
9	PRIOR APPLICATION NUMBER: 60/083322
10	PRIOR FILING DATE: 1998-04-28
11	PRIOR APPLICATION NUMBER: 60/084600
12	PRIOR FILING DATE: 1998-05-07
13	PRIOR APPLICATION NUMBER: 60/087106
14	PRIOR FILING DATE: 1998-05-28
15	PRIOR APPLICATION NUMBER: 60/087607
16	PRIOR FILING DATE: 1998-06-02
17	PRIOR APPLICATION NUMBER: 60/087609
18	PRIOR FILING DATE: 1998-06-02
19	PRIOR APPLICATION NUMBER: 60/087759
20	PRIOR FILING DATE: 1998-06-02
21	PRIOR APPLICATION NUMBER: 60/087827
22	PRIOR FILING DATE: 1998-06-03
23	PRIOR APPLICATION NUMBER: 60/088021
24	PRIOR FILING DATE: 1998-06-04
25	PRIOR APPLICATION NUMBER: 60/088025
26	PRIOR FILING DATE: 1998-06-04
27	PRIOR APPLICATION NUMBER: 60/088026
28	PRIOR FILING DATE: 1998-06-04
29	PRIOR APPLICATION NUMBER: 60/088028
30	PRIOR FILING DATE: 1998-06-04
31	PRIOR APPLICATION NUMBER: 60/088029
32	PRIOR FILING DATE: 1998-06-04
33	PRIOR APPLICATION NUMBER: 60/088030
34	PRIOR FILING DATE: 1998-06-04
35	PRIOR APPLICATION NUMBER: 60/088033
36	PRIOR FILING DATE: 1998-06-04
37	PRIOR APPLICATION NUMBER: 60/088326
38	PRIOR FILING DATE: 1998-06-04
39	PRIOR APPLICATION NUMBER: 60/088177
40	PRIOR FILING DATE: 1998-06-05
41	PRIOR APPLICATION NUMBER: 60/088202
42	PRIOR FILING DATE: 1998-06-05
43	PRIOR APPLICATION NUMBER: 60/088212
44	PRIOR FILING DATE: 1998-06-05
45	PRIOR APPLICATION NUMBER: 60/088217
46	PRIOR FILING DATE: 1998-06-05
47	PRIOR APPLICATION NUMBER: 60/088555
48	PRIOR FILING DATE: 1998-06-09
49	PRIOR APPLICATION NUMBER: 60/088734
50	PRIOR FILING DATE: 1998-06-10
51	PRIOR APPLICATION NUMBER: 60/088738
52	PRIOR FILING DATE: 1998-06-10
53	PRIOR APPLICATION NUMBER: 60/088742
54	PRIOR FILING DATE: 1998-06-10
55	PRIOR APPLICATION NUMBER: 60/088810
56	PRIOR FILING DATE: 1998-06-10
57	PRIOR APPLICATION NUMBER: 60/088824
58	PRIOR FILING DATE: 1998-06-10
59	PRIOR APPLICATION NUMBER: 60/088826
60	PRIOR FILING DATE: 1998-06-10
61	PRIOR APPLICATION NUMBER: 60/088858
62	PRIOR FILING DATE: 1998-06-11
63	PRIOR APPLICATION NUMBER: 60/088861
64	PRIOR FILING DATE: 1998-06-11
65	PRIOR APPLICATION NUMBER: 60/088876
66	PRIOR FILING DATE: 1998-06-11
67	PRIOR APPLICATION NUMBER: 60/089105
68	PRIOR FILING DATE: 1998-06-12
69	PRIOR APPLICATION NUMBER: 60/089440
70	PRIOR FILING DATE: 1998-06-16
71	PRIOR APPLICATION NUMBER: 60/089512
72	PRIOR FILING DATE: 1998-06-16
73	PRIOR APPLICATION NUMBER: 60/089514

PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089598  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089599  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089600  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089907  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089908  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089947  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089948  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089952  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090246  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090252  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090254  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090349  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090355  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090429  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090431  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090435  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090444  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090445  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090472  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090535  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090540  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090542  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090676  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090678  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090690  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090694  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090695  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090696  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090862  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01

PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 95.2%; Score 852; DB 9; Length 870;  
Best Local Similarity 100.0%; Pred. No. 3.4e-271;  
Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

44 CTGCCCCCAATGAGAGCGCTGGCCCTGGAGCTAAGCATAGACACAGGCTGAGTATC 103  
1 CTGCCCCCAATGAGAGCGCTGGCCCTGGAGCTAAGCATAGACACAGGCTGAGTATC 60  
104 CTGACCTGAGTCAATCCCGAGGATCAGAGGCTCCAGAGGAACCTTCATATATTC 163  
61 CTGACCTGAGTCAATCCCGAGGATCAGAGGCTCCAGAGGAACCTTCATATATTC 120  
164 TCAAGCACTTACAGCTGACCGACGACGATGCAATGAAGTTCAATCTTCCCTCC 223  
121 TCAAGCACTTACAGCTGACCGACGACGATGCAATGAAGTTCAATCTTCCCTCC 180  
224 TGTTCGTCACATTAATGCTATATGCTGCTCTAGACCTGATCCAGGGTGCCCA 283  
181 TGTTCGTCACATTAATGCTATATGCTGCTCTAGACCTGATCCAGGGTGCCCA 240  
284 GAGGCCACAGAGCAGGAGCGGAGGCTCTAGAGATGGCTCCAGGAAGGGGCAAGAT 343  
241 GAGGCCACAGAGCAGGAGCGGAGGCTCTAGAGATGGCTCCAGGAAGGGGCAAGAT 300  
344 GTAGGTGCAAAATGTTGCTCTAGAGCCCGAGGAATTCATGACAGTGTGGGC 403  
301 GTAGGTGCAAAATGTTGCTCTAGAGCCCGAGGAATTCATGACAGTGTGGGC 360  
404 TGCCAAAGAGAGCGTGGCCCTGATCATTTCAAGGCCAATGGAAGAAACAGACAC 463  
361 TGCCAAAGAGAGCGTGGCCCTGATCATTTCAAGGCCAATGGAAGAAACAGACAC 420  
464 AAAGCAGCAGAGAAAGCCAAACAGCATTCAGAGCTGCCAGCAATTTCTCAACAT 523  
421 AAAGCAGCAGAGAAAGCCAAACAGCATTCAGAGCTGCCAGCAATTTCTCAACAT 480  
524 GTAGGTGAGAGCTTGTCTCTGCTGCTGTTGAGAGCTGTAGAGGCCCACTTCAATTA 583  
481 GTAGGTGAGAGCTTGTCTCTGCTGCTGTTGAGAGCTGTAGAGGCCCACTTCAATTA 540  
584 AACATTCAGAGCAG 643  
541 AACATTCAGAGCAG 600  
644 ACTCTCCACTGATACCCACCCCTAATCATTCAGAGTGTCTCAAAAAGAGAGTTTCA 703  
601 ACTCTCCACTGATACCCACCCCTAATCATTCAGAGTGTCTCAAAAAGAGAGTTTCA 660  
704 GATCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 763  
661 GATCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 720  
764 CTCCTTACCCAGGCTTAGGCTTATATACGTGAAGATTCAGAGAACTGAGCTTCT 823  
721 CTCCTTACCCAGGCTTAGGCTTATATACGTGAAGATTCAGAGAACTGAGCTTCT 780



QY 824 AGCTGCTGCTATTACCTTAATGCATCAGGAAAGTAGCAACAGATCATTAATA 883  
DB 781 AGCTGCTGCTATTACCTTAATGCATCAGGAAAGTAGCAACAGATCATTAATA 840  
QY 884 TTTTAAATGTC 895  
DB 841 TTTTAAATGTC 852

RESULT 7  
US-09-989-727-164  
Sequence 164: Application US/09989727  
Patent No. US20020072497A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertelsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, V. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC65  
CURRENT APPLICATION NUMBER: US/09/989,727  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087609  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087827  
PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088025  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088026  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088028  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088030  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088033  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088326  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088167  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088202  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088212  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088217  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088655  
PRIOR FILING DATE: 1998-06-09  
PRIOR APPLICATION NUMBER: 60/088734  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088738  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088742  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088810  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088826  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088876  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089440  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089512  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089598  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089599  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089600  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089907  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089908  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089947  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089948  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089952

PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090246  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090252  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090254  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090349  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090355  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090429  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090431  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090435  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090444  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090445  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090472  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090535  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090540  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090542  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090676  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090678  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090690  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090694  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090695  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090696  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090862  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 95.2%; Score 852; DB 9; Length 870;

Best Local Similarity 100.0%; Pred. No. 3.4e-271; Indels 0; Gaps 0;

Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

44 CTCGCCCTCAATGGGAACGCTGGGCTGGAATAAGCATAGACACAGGCTGATATC 103  
|||||  
1 CTCGCCCTCAATGGGAACGCTGGGCTGGAATAAGCATAGACACAGGCTGATATC 60

104 CTGACCTGATGATCCCAAGGATGAGAGCCTCCAGCAGGGAACCTTCATATATTC 163  
|||||  
61 CTGACCTGATGATCCCAAGGATGAGAGCCTCCAGCAGGGAACCTTCATATATTC 120  
164 TCAGCAACTTACAGCTGACACGACAGCTTGCATGAAATTTCTATCTTCCCTCC 223  
121 TCAGCAACTTACAGCTGACACGACAGCTTGCATGAAATTTCTATCTTCCCTCC 180  
224 TGTTCGTCACATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 283  
181 TGTTCGTCACATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
284 GAGGCCACAGGAGCCAGGACGCTTGAAGATGCTCCAGAGGCGGCAAGAT 343  
241 GAGGCCACAGGAGCCAGGACGCTTGAAGATGCTCCAGAGGCGGCAAGAT 300  
344 GTGAGTGCAGAAATTTGTTCTCTAGAGCCCGGAGAAATTCATGACATGCTGG 403  
301 GTGAGTGCAGAAATTTGTTCTCTAGAGCCCGGAGAAATTCATGACATGCTGG 360  
404 TGCCAAAGAGAGAGTGCCTGATGATGATGATGATGATGATGATGATGATGATG 463  
361 TGCCAAAGAGAGAGTGCCTGATGATGATGATGATGATGATGATGATGATGATG 420  
464 AAAGCAGCAG 523  
421 AAAGCAGCAG 480  
524 GTGAGTGCAGAAATTTGTTCTCTAGAGCCCGGAGAAATTCATGACATGCTGG 583  
481 GTGAGTGCAGAAATTTGTTCTCTAGAGCCCGGAGAAATTCATGACATGCTGG 540  
584 AACATTCAGCAG 643  
541 AACATTCAGCAG 600  
644 ACCTCCAGTACAG 703  
601 ACCTCCAGTACAG 660  
704 GATCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 763  
661 GATCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 720  
764 CTCGCCCTTACCAAGGCTTAAATTAATTAATTAATTAATTAATTAATTAATTA 823  
721 CTCGCCCTTACCAAGGCTTAAATTAATTAATTAATTAATTAATTAATTAATTA 780  
824 AGCTAGTGCATTTAACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 883  
781 AGCTAGTGCATTTAACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 840  
884 TTTTAAATGTC 895  
841 TTTTAAATGTC 852

## RESULT 8

US-09-989-731-164

; Sequence 164, Application US/09989731

; Patent No. US20020103125A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gertsen, Mary E.

; APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Guiney, Austin L.  
 APPLICANT: Kijavlin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730P1C70  
 CURRENT APPLICATION NUMBER: US/09/989,731  
 CURRENT FILING DATE: 2001-11-20  
 PRIOR APPLICATION NUMBER: 60/049787  
 PRIOR FILING DATE: 1997-06-16  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/065186  
 PRIOR FILING DATE: 1997-11-12  
 PRIOR APPLICATION NUMBER: 60/065311  
 PRIOR FILING DATE: 1997-11-13  
 PRIOR APPLICATION NUMBER: 60/066770  
 PRIOR FILING DATE: 1997-11-24  
 PRIOR APPLICATION NUMBER: 60/075945  
 PRIOR FILING DATE: 1998-02-25  
 PRIOR APPLICATION NUMBER: 60/078910  
 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: 60/083322  
 PRIOR FILING DATE: 1998-04-28  
 PRIOR APPLICATION NUMBER: 60/084600  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/087106  
 PRIOR FILING DATE: 1998-05-28  
 PRIOR APPLICATION NUMBER: 60/087607  
 PRIOR FILING DATE: 1998-06-02  
 PRIOR APPLICATION NUMBER: 60/087609  
 PRIOR FILING DATE: 1998-06-02  
 PRIOR APPLICATION NUMBER: 60/087759  
 PRIOR FILING DATE: 1998-06-02  
 PRIOR APPLICATION NUMBER: 60/087827  
 PRIOR FILING DATE: 1998-06-03  
 PRIOR APPLICATION NUMBER: 60/088021  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088025  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088026  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088028  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088029  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088030  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088033  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088326  
 PRIOR FILING DATE: 1998-06-04  
 PRIOR APPLICATION NUMBER: 60/088167  
 PRIOR FILING DATE: 1998-06-05  
 PRIOR APPLICATION NUMBER: 60/088202  
 PRIOR FILING DATE: 1998-06-05  
 PRIOR APPLICATION NUMBER: 60/088212  
 PRIOR FILING DATE: 1998-06-05  
 PRIOR APPLICATION NUMBER: 60/088217  
 PRIOR FILING DATE: 1998-06-05  
 PRIOR APPLICATION NUMBER: 60/088655  
 PRIOR FILING DATE: 1998-06-09

PRIOR APPLICATION NUMBER: 60/088734  
 PRIOR FILING DATE: 1998-06-10  
 PRIOR APPLICATION NUMBER: 60/088738  
 PRIOR FILING DATE: 1998-06-10  
 PRIOR APPLICATION NUMBER: 60/088742  
 PRIOR FILING DATE: 1998-06-10  
 PRIOR APPLICATION NUMBER: 60/088810  
 PRIOR FILING DATE: 1998-06-10  
 PRIOR APPLICATION NUMBER: 60/088824  
 PRIOR FILING DATE: 1998-06-10  
 PRIOR APPLICATION NUMBER: 60/088826  
 PRIOR FILING DATE: 1998-06-10  
 PRIOR APPLICATION NUMBER: 60/088858  
 PRIOR FILING DATE: 1998-06-11  
 PRIOR APPLICATION NUMBER: 60/088861  
 PRIOR FILING DATE: 1998-06-11  
 PRIOR APPLICATION NUMBER: 60/088876  
 PRIOR FILING DATE: 1998-06-11  
 PRIOR APPLICATION NUMBER: 60/089105  
 PRIOR FILING DATE: 1998-06-12  
 PRIOR APPLICATION NUMBER: 60/089440  
 PRIOR FILING DATE: 1998-06-16  
 PRIOR APPLICATION NUMBER: 60/089512  
 PRIOR FILING DATE: 1998-06-16  
 PRIOR APPLICATION NUMBER: 60/089514  
 PRIOR FILING DATE: 1998-06-16  
 PRIOR APPLICATION NUMBER: 60/089532  
 PRIOR FILING DATE: 1998-06-17  
 PRIOR APPLICATION NUMBER: 60/089538  
 PRIOR FILING DATE: 1998-06-17  
 PRIOR APPLICATION NUMBER: 60/089598  
 PRIOR FILING DATE: 1998-06-17  
 PRIOR APPLICATION NUMBER: 60/089599  
 PRIOR FILING DATE: 1998-06-17  
 PRIOR APPLICATION NUMBER: 60/089600  
 PRIOR FILING DATE: 1998-06-17  
 PRIOR APPLICATION NUMBER: 60/089653  
 PRIOR FILING DATE: 1998-06-17  
 PRIOR APPLICATION NUMBER: 60/089801  
 PRIOR FILING DATE: 1998-06-18  
 PRIOR APPLICATION NUMBER: 60/089907  
 PRIOR FILING DATE: 1998-06-18  
 PRIOR APPLICATION NUMBER: 60/089908  
 PRIOR FILING DATE: 1998-06-18  
 PRIOR APPLICATION NUMBER: 60/089947  
 PRIOR FILING DATE: 1998-06-19  
 PRIOR APPLICATION NUMBER: 60/089948  
 PRIOR FILING DATE: 1998-06-19  
 PRIOR APPLICATION NUMBER: 60/089952  
 PRIOR FILING DATE: 1998-06-19  
 PRIOR APPLICATION NUMBER: 60/090246  
 PRIOR FILING DATE: 1998-06-22  
 PRIOR APPLICATION NUMBER: 60/090252  
 PRIOR FILING DATE: 1998-06-22  
 PRIOR APPLICATION NUMBER: 60/090254  
 PRIOR FILING DATE: 1998-06-22  
 PRIOR APPLICATION NUMBER: 60/090349  
 PRIOR FILING DATE: 1998-06-23  
 PRIOR APPLICATION NUMBER: 60/090355  
 PRIOR FILING DATE: 1998-06-23  
 PRIOR APPLICATION NUMBER: 60/090429  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090431  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090435  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090444  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090445  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090472  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090535



1	PRIOR FILING DATE: 1997-11-12
2	PRIOR APPLICATION NUMBER: 60/065311
3	PRIOR FILING DATE: 1997-11-13
4	PRIOR APPLICATION NUMBER: 60/066770
5	PRIOR FILING DATE: 1997-11-24
6	PRIOR APPLICATION NUMBER: 60/075545
7	PRIOR FILING DATE: 1998-02-25
8	PRIOR APPLICATION NUMBER: 60/078910
9	PRIOR FILING DATE: 1998-03-20
10	PRIOR APPLICATION NUMBER: 60/083322
11	PRIOR FILING DATE: 1998-04-28
12	PRIOR APPLICATION NUMBER: 60/084600
13	PRIOR FILING DATE: 1998-05-07
14	PRIOR APPLICATION NUMBER: 60/087106
15	PRIOR FILING DATE: 1998-05-28
16	PRIOR APPLICATION NUMBER: 60/087607
17	PRIOR FILING DATE: 1998-06-02
18	PRIOR APPLICATION NUMBER: 60/087609
19	PRIOR FILING DATE: 1998-06-02
20	PRIOR APPLICATION NUMBER: 60/087759
21	PRIOR FILING DATE: 1998-06-02
22	PRIOR APPLICATION NUMBER: 60/087827
23	PRIOR FILING DATE: 1998-06-03
24	PRIOR APPLICATION NUMBER: 60/088021
25	PRIOR FILING DATE: 1998-06-04
26	PRIOR APPLICATION NUMBER: 60/088025
27	PRIOR FILING DATE: 1998-06-04
28	PRIOR APPLICATION NUMBER: 60/088026
29	PRIOR FILING DATE: 1998-06-04
30	PRIOR APPLICATION NUMBER: 60/088028
31	PRIOR FILING DATE: 1998-06-04
32	PRIOR APPLICATION NUMBER: 60/088029
33	PRIOR FILING DATE: 1998-06-04
34	PRIOR APPLICATION NUMBER: 60/088030
35	PRIOR FILING DATE: 1998-06-04
36	PRIOR APPLICATION NUMBER: 60/088033
37	PRIOR FILING DATE: 1998-06-04
38	PRIOR APPLICATION NUMBER: 60/088326
39	PRIOR FILING DATE: 1998-06-04
40	PRIOR APPLICATION NUMBER: 60/088167
41	PRIOR FILING DATE: 1998-06-05
42	PRIOR APPLICATION NUMBER: 60/088202
43	PRIOR FILING DATE: 1998-06-05
44	PRIOR APPLICATION NUMBER: 60/088212
45	PRIOR FILING DATE: 1998-06-05
46	PRIOR APPLICATION NUMBER: 60/088217
47	PRIOR FILING DATE: 1998-06-05
48	PRIOR APPLICATION NUMBER: 60/088655
49	PRIOR FILING DATE: 1998-06-09
50	PRIOR APPLICATION NUMBER: 60/088734
51	PRIOR FILING DATE: 1998-06-10
52	PRIOR APPLICATION NUMBER: 60/088738
53	PRIOR FILING DATE: 1998-06-10
54	PRIOR APPLICATION NUMBER: 60/088742
55	PRIOR FILING DATE: 1998-06-10
56	PRIOR APPLICATION NUMBER: 60/088810
57	PRIOR FILING DATE: 1998-06-10
58	PRIOR APPLICATION NUMBER: 60/088824
59	PRIOR FILING DATE: 1998-06-10
60	PRIOR APPLICATION NUMBER: 60/088826
61	PRIOR FILING DATE: 1998-06-10
62	PRIOR APPLICATION NUMBER: 60/088858
63	PRIOR FILING DATE: 1998-06-11
64	PRIOR APPLICATION NUMBER: 60/088861
65	PRIOR FILING DATE: 1998-06-11
66	PRIOR APPLICATION NUMBER: 60/088876
67	PRIOR FILING DATE: 1998-06-11
68	PRIOR APPLICATION NUMBER: 60/089105
69	PRIOR FILING DATE: 1998-06-12
70	PRIOR APPLICATION NUMBER: 60/089440
71	PRIOR FILING DATE: 1998-06-16
72	PRIOR APPLICATION NUMBER: 60/089512
73	PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090697
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090698
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360

```

; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      95.2%; Score 852; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 3,4e-271;
Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      44      CTCGCCCTCAAAATGGGAAGCTGGCTGGGACTAAAGCATATGACACACAGGCTGAGTATC 103
Db      1      CTCGCCCTCAAAATGGGAAGCTGGCTGGGACTAAAGCATATGACACACAGGCTGAGTATC 60

QY      104     CTGACTGAGTCAATCCCGAGGATCAGAGACCTCCAGCAGGAACTTCCATTATATCT 163
Db      61      CTGACTGAGTCAATCCCGAGGATCAGAGACCTCCAGCAGGAACTTCCATTATATCT 120

QY      164     TCAAGCACTTACAGCTGCAACCGACACTTCGATGGAAGTTCTATCTCTTCCCTCC 223
Db      121     TCAAGCACTTACAGCTGCAACCGACACTTCGATGGAAGTTCTATCTCTTCCCTCC 180

QY      224     TGTGTGCTCCACTATGCTATGTCATGCTCTCTACAGCCTGATCAGAGGGTCCGCA 283
Db      181     TGTGTGCTCCACTATGCTATGTCATGCTCTCTACAGCCTGATCAGAGGGTCCGCA 240

QY      284     GAGGCCACAGGAGCCGAGCCAGGCTTCTAGAGAGTGGCTCCAGAAAGGCGCCAGANT 343
Db      241     GAGGCCACAGGAGCCGAGCCAGGCTTCTAGAGAGTGGCTCCAGAAAGGCGCCAGANT 300

QY      344     GTGAGTCAAAAGATGGTCTCTGAGAGCCCGCAAAATTCATACAGTGTCTGGCC 403
Db      301     GTGAGTCAAAAGATGGTCTCTGAGAGCCCGCAAAATTCATACAGTGTCTGGCC 360

QY      404     TGCCAAAGAGAGAGTGGCCCTGTGATCATTTCAAGGCAATGTGAAAGAAACAAGACAC 463
Db      361     TGCCAAAGAGAGAGTGGCCCTGTGATCATTTCAAGGCAATGTGAAAGAAACAAGACAC 420

QY      464     AAGAGCCACAGAAAGCCAAACAGATTCACAGAGCCTGCCAGCAATTTCTCAACAT 523
Db      421     AAGAGCCACAGAAAGCCAAACAGATTCACAGAGCCTGCCAGCAATTTCTCAACAT 480

QY      524     GTGAGTCAAAAGATGGTCTCTGAGAGCCCGCAAAATTCATACAGTGTCTGGCC 583
Db      481     GTGAGTCAAAAGATGGTCTCTGAGAGCCCGCAAAATTCATACAGTGTCTGGCC 540

QY      584     AACATTCTCAGCAAGAGACAGTGAACACACTTACAGACACTTCTTCTCCACCTC 643
Db      541     AACATTCTCAGCAAGAGACAGTGAACACACTTACAGACACTTCTTCTCCACCTC 600

QY      644     ACTCTCCACTGTAACCCACCCCTAAATCATTCAGTGTCTCTCAAAAAGCATGTTTTCAA 703
Db      601     ACTCTCCACTGTAACCCACCCCTAAATCATTCAGTGTCTCTCAAAAAGCATGTTTTCAA 660

QY      704     GATCATTTTGTGTGCTCTCTCTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 763
Db      661     GATCATTTTGTGTGCTCTCTCTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720

QY      764     CTCCTTACAGAGCTTAAAGTAAATTAATTCAGTAAAGATTCAGAGAACTGAGCTTCGT 823
Db      721     CTCCTTACAGAGCTTAAAGTAAATTAATTCAGTAAAGATTCAGAGAACTGAGCTTCGT 780
```

```

QY      824     AGCTAGTGTCAATTTAACTTAATGCAATCAGAAAGTAGCAAGCAAGTCAATTAATA 883
Db      781     AGCTAGTGTCAATTTAACTTAATGCAATCAGAAAGTAGCAAGCAAGTCAATTAATA 840

QY      884     TTTTAAATGTC 895
Db      841     TTTTAAATGTC 852

RESULT 10
US-09-991-073-164
; Sequence 164, Application US/09991073
; Patent No. US20020127576A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottfredson, Mary E.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavich, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemlin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C15
; CURRENT APPLICATION NUMBER: US/09/991,073
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
```

```

1 PRIOR APPLICATION NUMBER: 60/089952
2 PRIOR FILING DATE: 1998-06-19
3 PRIOR APPLICATION NUMBER: 60/090246
4 PRIOR FILING DATE: 1998-06-22
5 PRIOR APPLICATION NUMBER: 60/090252
6 PRIOR FILING DATE: 1998-06-22
7 PRIOR APPLICATION NUMBER: 60/090254
8 PRIOR FILING DATE: 1998-06-22
9 PRIOR APPLICATION NUMBER: 60/090349
10 PRIOR FILING DATE: 1998-06-23
11 PRIOR APPLICATION NUMBER: 60/090355
12 PRIOR FILING DATE: 1998-06-23
13 PRIOR APPLICATION NUMBER: 60/090429
14 PRIOR FILING DATE: 1998-06-24
15 PRIOR APPLICATION NUMBER: 60/090431
16 PRIOR FILING DATE: 1998-06-24
17 PRIOR APPLICATION NUMBER: 60/090435
18 PRIOR FILING DATE: 1998-06-24
19 PRIOR APPLICATION NUMBER: 60/090444
20 PRIOR FILING DATE: 1998-06-24
21 PRIOR APPLICATION NUMBER: 60/090445
22 PRIOR FILING DATE: 1998-06-24
23 PRIOR APPLICATION NUMBER: 60/090472
24 PRIOR FILING DATE: 1998-06-24
25 PRIOR APPLICATION NUMBER: 60/090535
26 PRIOR FILING DATE: 1998-06-24
27 PRIOR APPLICATION NUMBER: 60/090540
28 PRIOR FILING DATE: 1998-06-24
29 PRIOR APPLICATION NUMBER: 60/090542
30 PRIOR FILING DATE: 1998-06-24
31 PRIOR APPLICATION NUMBER: 60/090557
32 PRIOR FILING DATE: 1998-06-24
33 PRIOR APPLICATION NUMBER: 60/090676
34 PRIOR FILING DATE: 1998-06-25
35 PRIOR APPLICATION NUMBER: 60/090678
36 PRIOR FILING DATE: 1998-06-25
37 PRIOR APPLICATION NUMBER: 60/090690
38 PRIOR FILING DATE: 1998-06-25
39 PRIOR APPLICATION NUMBER: 60/090694
40 PRIOR FILING DATE: 1998-06-25
41 PRIOR APPLICATION NUMBER: 60/090695
42 PRIOR FILING DATE: 1998-06-25
43 PRIOR APPLICATION NUMBER: 60/090696
44 PRIOR FILING DATE: 1998-06-25
45 PRIOR APPLICATION NUMBER: 60/090862
46 PRIOR FILING DATE: 1998-06-26
47 PRIOR APPLICATION NUMBER: 60/090863
48 PRIOR FILING DATE: 1998-06-26
49 PRIOR APPLICATION NUMBER: 60/091360
50 PRIOR FILING DATE: 1998-07-01
51 PRIOR APPLICATION NUMBER: 60/091478
52 PRIOR FILING DATE: 1998-07-02
53 PRIOR APPLICATION NUMBER: 60/091544
54 PRIOR FILING DATE: 1998-07-01
55 PRIOR APPLICATION NUMBER: 60/091519
56 PRIOR FILING DATE: 1998-07-02
57 PRIOR APPLICATION NUMBER: 60/091526
58 PRIOR FILING DATE: 1998-07-02
59 PRIOR APPLICATION NUMBER: 60/091633
60 PRIOR FILING DATE: 1998-07-02
61 PRIOR APPLICATION NUMBER: 60/091978
62 PRIOR FILING DATE: 1998-07-07
63 PRIOR APPLICATION NUMBER: 60/091982
64 PRIOR FILING DATE: 1998-07-07
65 PRIOR APPLICATION NUMBER: 60/092182
66 PRIOR FILING DATE: 1998-07-09
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
7
```



Db 1 CTCGCCCTCAATGGGAACGCTGGCTGGAGCTAAGACATAGACCACAGGCTGAGATC 60  
 QY 104 CTGACCTGACGATCCCAAGGATCAGAGCTCCAGAGGAGACCTTCAATATATCT 163  
 Db 61 CTGACCTGACGATCCCAAGGATCAGAGCTCCAGAGGAGACCTTCAATATATCT 120  
 QY 164 TCAAGCACTTACAGCTCAGCAGAGCTGAGATGAAAGTCTAATCTCTCTCCCTCC 223  
 Db 121 TCAAGCACTTACAGCTCAGCAGAGCTGAGATGAAAGTCTAATCTCTCTCCCTCC 180  
 QY 224 TGTGCTGCTCCTAATGCTGATGTCATGAGTCTCTAGAGCTTCAATCCAGGGGTCCGA 283  
 Db 181 TGTGCTGCTCCTAATGCTGATGTCATGAGTCTCTAGAGCTTCAATCCAGGGGTCCGA 240  
 QY 284 GAGGCTCAGAGGAGCAGAGGCTTCTAGAGATGCTCAGAGAGGCGCCCAAGAT 343  
 Db 241 GAGGCTCAGAGGAGCAGAGGCTTCTAGAGATGCTCAGAGAGGCGCCCAAGAT 300  
 QY 344 GTGAGTGCAGAAATGTTGTTCTGAGAGCCCGAGAGAAATTCATGACAGTGTCTGGGC 403  
 Db 301 GTGAGTGCAGAAATGTTGTTCTGAGAGCCCGAGAGAAATTCATGACAGTGTCTGGGC 360  
 QY 404 TGCCAAAGACAGTGGCTGTGATCTATTCAGAGGCAATGTGAAGAAACAAACACACC 463  
 Db 361 TGCCAAAGACAGTGGCTGTGATCTATTCAGAGGCAATGTGAAGAAACAAACACACC 420  
 QY 464 AAAGCAGCAG 523  
 Db 421 AAAGCAGCAG 480  
 QY 524 GTGAGTGCAGAAATGTTGTTCTGAGAGCCCGAGAGAAATTCATGACAGTGTCTGGGC 583  
 Db 481 GTGAGTGCAGAAATGTTGTTCTGAGAGCCCGAGAGAAATTCATGACAGTGTCTGGGC 540  
 QY 584 AACATTCAGAGCAG 643  
 Db 541 AACATTCAGAGCAG 600  
 QY 644 ACTCTCCACAGTGTACCCACCCCTAATATTCAGTGTCTCTCAAAAGAGATGTTTCA 703  
 Db 601 ACTCTCCACAGTGTACCCACCCCTAATATTCAGTGTCTCTCAAAAGAGATGTTTCA 660  
 QY 704 GATCATTTTGTGTTGCTCTCTCTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 763  
 Db 661 GATCATTTTGTGTTGCTCTCTCTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720  
 QY 764 CTCGCCCTTACCCAGGCTTACGCTTAAATTCAGTGTCTCTCTCTCTCTCTCTCTCT 823  
 Db 721 CTCGCCCTTACCCAGGCTTACGCTTAAATTCAGTGTCTCTCTCTCTCTCTCTCTCT 780  
 QY 824 ACCTAGTGTCAATTAACCTTAATTCAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 883  
 Db 781 ACCTAGTGTCAATTAACCTTAATTCAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 840  
 QY 884 TTTTAAATGTC 895  
 Db 841 TTTTAAATGTC 852

RESULT 11  
 US-09-990-442-164  
 ; Sequence 164, Application US/09990442  
 ; Patent No. US20020132252A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnovers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gertlisen, Mary E.

; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Kijavins, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tamas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: P2730P1C8  
 ; CURRENT APPLICATION NUMBER: US/09/990,442  
 ; PRIOR FILING DATE: 2001-11-14  
 ; PRIOR APPLICATION NUMBER: 60/049787  
 ; PRIOR FILING DATE: 1997-06-16  
 ; PRIOR APPLICATION NUMBER: 60/062250  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/065186  
 ; PRIOR FILING DATE: 1997-11-12  
 ; PRIOR APPLICATION NUMBER: 60/065311  
 ; PRIOR FILING DATE: 1997-11-13  
 ; PRIOR APPLICATION NUMBER: 60/066770  
 ; PRIOR FILING DATE: 1997-11-24  
 ; PRIOR APPLICATION NUMBER: 60/075945  
 ; PRIOR FILING DATE: 1998-02-25  
 ; PRIOR APPLICATION NUMBER: 60/078910  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/083322  
 ; PRIOR FILING DATE: 1998-04-28  
 ; PRIOR APPLICATION NUMBER: 60/084600  
 ; PRIOR FILING DATE: 1998-05-07  
 ; PRIOR APPLICATION NUMBER: 60/087106  
 ; PRIOR FILING DATE: 1998-05-28  
 ; PRIOR APPLICATION NUMBER: 60/087607  
 ; PRIOR FILING DATE: 1998-06-02  
 ; PRIOR APPLICATION NUMBER: 60/087609  
 ; PRIOR FILING DATE: 1998-06-02  
 ; PRIOR APPLICATION NUMBER: 60/087759  
 ; PRIOR FILING DATE: 1998-06-02  
 ; PRIOR APPLICATION NUMBER: 60/087827  
 ; PRIOR FILING DATE: 1998-06-03  
 ; PRIOR APPLICATION NUMBER: 60/088021  
 ; PRIOR FILING DATE: 1998-06-04  
 ; PRIOR APPLICATION NUMBER: 60/088025  
 ; PRIOR FILING DATE: 1998-06-04  
 ; PRIOR APPLICATION NUMBER: 60/088026  
 ; PRIOR FILING DATE: 1998-06-04  
 ; PRIOR APPLICATION NUMBER: 60/088028  
 ; PRIOR FILING DATE: 1998-06-04  
 ; PRIOR APPLICATION NUMBER: 60/088029  
 ; PRIOR FILING DATE: 1998-06-04  
 ; PRIOR APPLICATION NUMBER: 60/088030  
 ; PRIOR FILING DATE: 1998-06-04  
 ; PRIOR APPLICATION NUMBER: 60/088033  
 ; PRIOR FILING DATE: 1998-06-04  
 ; PRIOR APPLICATION NUMBER: 60/088326  
 ; PRIOR FILING DATE: 1998-06-04  
 ; PRIOR APPLICATION NUMBER: 60/088167  
 ; PRIOR FILING DATE: 1998-06-05  
 ; PRIOR APPLICATION NUMBER: 60/088202  
 ; PRIOR FILING DATE: 1998-06-05  
 ; PRIOR APPLICATION NUMBER: 60/088212  
 ; PRIOR FILING DATE: 1998-06-05  
 ; PRIOR APPLICATION NUMBER: 60/088217  
 ; PRIOR FILING DATE: 1998-06-05  
 ; PRIOR APPLICATION NUMBER: 60/088655

PRIOR FILING DATE: 1998-06-09  
PRIOR APPLICATION NUMBER: 60/088734  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088738  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088742  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088810  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088826  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088876  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089440  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089512  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089598  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089599  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089600  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089907  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089908  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089947  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089948  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089952  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090246  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090252  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090254  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090349  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090355  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090429  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090431  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090435  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090444  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090445  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090472  
PRIOR FILING DATE: 1998-06-24

PRIOR APPLICATION NUMBER: 60/090535  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090540  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090542  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090676  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090678  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090690  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090694  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090695  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090696  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090862  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 95.2%; Score 852; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 3.4e-271;  
Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 CTCGCCCTCAAAATGGAAAGCTGGCGCTGAGACTAAAGCATAGACCCAGGCTGAGTATC 103  
|||||  
DB 1 CTCGCCCTCAAAATGGAAAGCTGGCGCTGAGACTAAAGCATAGACCCAGGCTGAGTATC 60  
|||||

QY 104 CTGACCTGAGTCATCCCGAGGATCAGAGCTCCAGCAGGACCTTCATTATATCT 163  
|||||  
DB 61 CTGACCTGAGTCATCCCGAGGATCAGAGCTCCAGCAGGACCTTCATTATATCT 120  
|||||

QY 164 TCAAGCAACTTACAGCTGACCGACAGTGGCATGAAAGTTCTATCTCTCCCTCC 223  
|||||  
DB 121 TCAAGCAACTTACAGCTGACCGACAGTGGCATGAAAGTTCTATCTCTCCCTCC 180  
|||||

QY 224 TGTTCGTGCCACTAATGCTGATGTCATGCTCTTACAGCGCTGAATCCAGGGTCCCA 283  
|||||  
DB 181 TGTTCGTGCCACTAATGCTGATGTCATGCTCTTACAGCGCTGAATCCAGGGTCCCA 240  
|||||

QY 284 GAGGCCACAGGAGGAGGCGGCGGCTTCAGAGATGGCTCCAGAGGGGCGCAAGAT 343  
|||||  
DB 241 GAGGCCACAGGAGGAGGCGGCGGCTTCAGAGATGGCTCCAGAGGGGCGCAAGAT 300  
|||||

QY 344 GTGAGTCAAAAGATGTTCTCTGAGAGCCCGAAGAAATTCATGACATGTCGTGGGC 403  
|||||  
DB 301 GTGAGTCAAAAGATGTTCTCTGAGAGCCCGAAGAAATTCATGACATGTCGTGGGC 360  
|||||

QY 404 TGCCAAAGACAGCTGCCCTGTGATCATTTCAAGGCGCATGTGAAGAAAACAAGACAC 463  
|||||



PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089598  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089599  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089600  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089907  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089908  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089947  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089948  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089952  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090246  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090252  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090254  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090349  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090355  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090429  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090431  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090435  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090444  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090445  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090472  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090535  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090540  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090542  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090676  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090678  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090690  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090694  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090695  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090696  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090862  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26

PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 95.2%; Score 852; DB 10; Length 870;  
Best Local Similarity 100.0%; Pred. No. 3.4e-271;  
Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 CTCGCCCTCAATGGGAACGCTGGGACTAAGCATACACAGCGTGAATC 103  
DB 1 CTCGCCCTCAATGGGAACGCTGGGACTAAGCATACACAGCGTGAATC 60  
QY 104 CTGACCTGATCATCCCGAGGATCAGAGCCTCCAGCAGGAGCCTTCATATATCT 163  
DB 61 CTGACCTGATCATCCCGAGGATCAGAGCCTCCAGCAGGAGCCTTCATATATCT 120  
QY 164 TCACGAACCTTACAGCTGACCGACAGTTCGATGAAGTTCTTAATCTCTCCCTCC 223  
DB 121 TCACGAACCTTACAGCTGACCGACAGTTCGATGAAGTTCTTAATCTCTCCCTCC 180  
QY 224 TTTTGTGCTCACTAATGCTGATGTCATGTCCTTACAGCCTGAATCCAGGGTCCCA 283  
DB 181 TTTTGTGCTCACTAATGCTGATGTCATGTCCTTACAGCCTGAATCCAGGGTCCCA 240  
QY 284 GAGGCCACGAGGACGAGGACGAGGCTTCAGAGAGATGGCTCCAGGAAGGCGCCAAAGAT 343  
DB 241 GAGGCCACGAGGACGAGGACGAGGCTTCAGAGAGATGGCTCCAGGAAGGCGCCAAAGAT 300  
QY 344 GTGATGCAAGATGTTCTCTGAGAGCCCGAGAGAAATTCATGACAGTGTGGGC 403  
DB 301 GTGATGCAAGATGTTCTCTGAGAGCCCGAGAGAAATTCATGACAGTGTGGGC 360  
QY 404 TGCCAAAGAGCAGTGCCCTGTGTATCATTTCAAGGGCAATGTAAGAAACAGACACC 463  
DB 361 TGCCAAAGAGCAGTGCCCTGTGTATCATTTCAAGGGCAATGTAAGAAACAGACACC 420  
QY 464 AAAGCACACAGAAAGCAAGCAAGCAATTCACAGGCTCCAGCAATTTCCAAAGAT 523  
DB 421 AAAGCACACAGAAAGCAAGCAAGCAATTCACAGGCTCCAGCAATTTCCAAAGAT 480  
QY 524 GTACACTAAGAGCTTTGCTGTGCTTTGTAGAGCTGTGAGCGCCACTCTTCCAAATTA 583  
DB 481 GTACACTAAGAGCTTTGCTGTGCTTTGTAGAGCTGTGAGCGCCACTCTTCCAAATTA 540  
QY 584 AACATTCTAGCAGAAAGAGACAGTAGACACCTTACAGACACTCTTCTTCCACCTC 643  
DB 541 AACATTCTAGCAGAAAGAGACAGTAGACACCTTACAGACACTCTTCTTCCACCTC 600  
QY 644 ACTCTCCACGTACACACCCCTTAATCATTCACAGGCTCCAAAGAGATTTTTCAA 703  
DB 601 ACTCTCCACGTACACACCCCTTAATCATTCACAGGCTCCAAAGAGATTTTTCAA 660  
QY 704 GATCATTTTGTGTTGTGCTCTCTAGTGTCTTCTCTCTCAGTCTTACCTGTGACC 763  
DB 661 GATCATTTTGTGTTGTGCTCTCTAGTGTCTTCTCTCTCAGTCTTACCTGTGACC 720  
QY 764 CTCGCCCTTACCGAGGCTTATGCTTAATTAAGTGAAGATTCAGGAAGACTAGCTTCT 823  
DB 764 CTCGCCCTTACCGAGGCTTATGCTTATTAAGTGAAGATTCAGGAAGACTAGCTTCT

Db 721 CCCCCCTTACCCAGGCTTACGCTTAATTACCTGAAAGATTCCAGGAACGTAGCTTCT 780  
 Oy 824 AGCTAGTGTCTTTAACTTAATGCATCAGGAAGTAGCAAAAGCTCATATAATA 883  
 Db 781 AGCTAGTGTCTTTAACTTAATGCATCAGGAAGTAGCAAAAGCTCATATAATA 840  
 Oy 884 TTTTAAAGTC 895  
 Db 841 TTTTAAATGTC 852

RESULT 13  
 US-09-993-604-164  
 ; Sequence 164, Application US/09993604  
 ; Patent No. US20020137075A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Kijavlin, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: P2730P1C25  
 ; CURRENT APPLICATION NUMBER: US/09/993,604  
 ; CURRENT FILING DATE: 2001-11-14  
 ; PRIOR APPLICATION NUMBER: 60/049787  
 ; PRIOR FILING DATE: 1997-06-16  
 ; PRIOR APPLICATION NUMBER: 60/062250  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/065186  
 ; PRIOR FILING DATE: 1997-11-12  
 ; PRIOR APPLICATION NUMBER: 60/065311  
 ; PRIOR FILING DATE: 1997-11-13  
 ; PRIOR APPLICATION NUMBER: 60/066770  
 ; PRIOR FILING DATE: 1997-11-24  
 ; PRIOR APPLICATION NUMBER: 60/075945  
 ; PRIOR FILING DATE: 1998-02-25  
 ; PRIOR APPLICATION NUMBER: 60/078910  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/083322  
 ; PRIOR FILING DATE: 1998-04-28  
 ; PRIOR APPLICATION NUMBER: 60/084600  
 ; PRIOR FILING DATE: 1998-05-07  
 ; PRIOR APPLICATION NUMBER: 60/087106  
 ; PRIOR FILING DATE: 1998-05-28  
 ; PRIOR APPLICATION NUMBER: 60/087607  
 ; PRIOR FILING DATE: 1998-06-02  
 ; PRIOR APPLICATION NUMBER: 60/087609  
 ; PRIOR FILING DATE: 1998-06-02  
 ; PRIOR APPLICATION NUMBER: 60/087759  
 ; PRIOR FILING DATE: 1998-06-02  
 ; PRIOR APPLICATION NUMBER: 60/087827  
 ; PRIOR FILING DATE: 1998-06-03

;; PRIOR APPLICATION NUMBER: 60/088021  
 ;; PRIOR FILING DATE: 1998-06-04  
 ;; PRIOR APPLICATION NUMBER: 60/088025  
 ;; PRIOR FILING DATE: 1998-06-04  
 ;; PRIOR APPLICATION NUMBER: 60/088026  
 ;; PRIOR FILING DATE: 1998-06-04  
 ;; PRIOR APPLICATION NUMBER: 60/088028  
 ;; PRIOR FILING DATE: 1998-06-04  
 ;; PRIOR APPLICATION NUMBER: 60/088029  
 ;; PRIOR FILING DATE: 1998-06-04  
 ;; PRIOR APPLICATION NUMBER: 60/088030  
 ;; PRIOR FILING DATE: 1998-06-04  
 ;; PRIOR APPLICATION NUMBER: 60/088033  
 ;; PRIOR FILING DATE: 1998-06-04  
 ;; PRIOR APPLICATION NUMBER: 60/088326  
 ;; PRIOR FILING DATE: 1998-06-04  
 ;; PRIOR APPLICATION NUMBER: 60/088167  
 ;; PRIOR FILING DATE: 1998-06-05  
 ;; PRIOR APPLICATION NUMBER: 60/088202  
 ;; PRIOR FILING DATE: 1998-06-05  
 ;; PRIOR APPLICATION NUMBER: 60/088212  
 ;; PRIOR FILING DATE: 1998-06-05  
 ;; PRIOR APPLICATION NUMBER: 60/088217  
 ;; PRIOR FILING DATE: 1998-06-05  
 ;; PRIOR APPLICATION NUMBER: 60/088655  
 ;; PRIOR FILING DATE: 1998-06-09  
 ;; PRIOR APPLICATION NUMBER: 60/088734  
 ;; PRIOR FILING DATE: 1998-06-10  
 ;; PRIOR APPLICATION NUMBER: 60/088738  
 ;; PRIOR FILING DATE: 1998-06-10  
 ;; PRIOR APPLICATION NUMBER: 60/088742  
 ;; PRIOR FILING DATE: 1998-06-10  
 ;; PRIOR APPLICATION NUMBER: 60/088810  
 ;; PRIOR FILING DATE: 1998-06-10  
 ;; PRIOR APPLICATION NUMBER: 60/088824  
 ;; PRIOR FILING DATE: 1998-06-10  
 ;; PRIOR APPLICATION NUMBER: 60/088826  
 ;; PRIOR FILING DATE: 1998-06-10  
 ;; PRIOR APPLICATION NUMBER: 60/088858  
 ;; PRIOR FILING DATE: 1998-06-11  
 ;; PRIOR APPLICATION NUMBER: 60/088861  
 ;; PRIOR FILING DATE: 1998-06-11  
 ;; PRIOR APPLICATION NUMBER: 60/088876  
 ;; PRIOR FILING DATE: 1998-06-11  
 ;; PRIOR APPLICATION NUMBER: 60/089105  
 ;; PRIOR FILING DATE: 1998-06-12  
 ;; PRIOR APPLICATION NUMBER: 60/089440  
 ;; PRIOR FILING DATE: 1998-06-16  
 ;; PRIOR APPLICATION NUMBER: 60/089512  
 ;; PRIOR FILING DATE: 1998-06-16  
 ;; PRIOR APPLICATION NUMBER: 60/089514  
 ;; PRIOR FILING DATE: 1998-06-16  
 ;; PRIOR APPLICATION NUMBER: 60/089532  
 ;; PRIOR FILING DATE: 1998-06-17  
 ;; PRIOR APPLICATION NUMBER: 60/089538  
 ;; PRIOR FILING DATE: 1998-06-17  
 ;; PRIOR APPLICATION NUMBER: 60/089598  
 ;; PRIOR FILING DATE: 1998-06-17  
 ;; PRIOR APPLICATION NUMBER: 60/089599  
 ;; PRIOR FILING DATE: 1998-06-17  
 ;; PRIOR APPLICATION NUMBER: 60/089600  
 ;; PRIOR FILING DATE: 1998-06-17  
 ;; PRIOR APPLICATION NUMBER: 60/089653  
 ;; PRIOR FILING DATE: 1998-06-17  
 ;; PRIOR APPLICATION NUMBER: 60/089801  
 ;; PRIOR FILING DATE: 1998-06-18  
 ;; PRIOR APPLICATION NUMBER: 60/089907  
 ;; PRIOR FILING DATE: 1998-06-18  
 ;; PRIOR APPLICATION NUMBER: 60/089908  
 ;; PRIOR FILING DATE: 1998-06-18  
 ;; PRIOR APPLICATION NUMBER: 60/089947  
 ;; PRIOR FILING DATE: 1998-06-19  
 ;; PRIOR APPLICATION NUMBER: 60/089948

PRIOR FILING DATE: 1998-06-19  
 PRIOR APPLICATION NUMBER: 60/089952  
 PRIOR FILING DATE: 1998-06-19  
 PRIOR APPLICATION NUMBER: 60/090246  
 PRIOR FILING DATE: 1998-06-22  
 PRIOR APPLICATION NUMBER: 60/090252  
 PRIOR FILING DATE: 1998-06-22  
 PRIOR APPLICATION NUMBER: 60/090254  
 PRIOR FILING DATE: 1998-06-22  
 PRIOR APPLICATION NUMBER: 60/090349  
 PRIOR FILING DATE: 1998-06-23  
 PRIOR APPLICATION NUMBER: 60/090355  
 PRIOR FILING DATE: 1998-06-23  
 PRIOR APPLICATION NUMBER: 60/090429  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090431  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090435  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090444  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090445  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090472  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090535  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090540  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090542  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090557  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090676  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090678  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090690  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090694  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090695  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090696  
 PRIOR FILING DATE: 1998-06-25  
 PRIOR APPLICATION NUMBER: 60/090862  
 PRIOR FILING DATE: 1998-06-26  
 PRIOR APPLICATION NUMBER: 60/090863  
 PRIOR FILING DATE: 1998-06-26  
 PRIOR APPLICATION NUMBER: 60/091360  
 PRIOR FILING DATE: 1998-07-01  
 PRIOR APPLICATION NUMBER: 60/091478  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091544  
 PRIOR FILING DATE: 1998-07-01  
 PRIOR APPLICATION NUMBER: 60/091519  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091626  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091633  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091978  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Query Match 95.2%; Score 852; DB 10; Length 870;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-271;  
 Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

44 CTCGCCCTCAATGGAGCGCTGGGACTAAAGCATAGACCAAGGCTGAGTATC 103

|||||  
 1 CTCGCCCTCAATGGAGCGCTGGGACTAAAGCATAGACCAAGGCTGAGTATC 60  
 QY 104 CTCGCTGATGATATCCCGAGGATCAGAGCTCCAGAGGAACTTCATTATTTT 163  
 Db 61 CTCGCTGATGATATCCCGAGGATCAGAGCTCCAGAGGAACTTCATTATTTT 120  
 QY 164 TCAGCACTTACAGTGCACCGACAGTTGCGATGAAAGTTCTATCTCTCCCTCC 223  
 Db 121 TCAGCACTTACAGTGCACCGACAGTTGCGATGAAAGTTCTATCTCTCCCTCC 180  
 QY 224 TGTGTGCTGCTATTAAGCTGATGATGATGATGATGATGATGATGATGATGAT 283  
 Db 181 TGTGTGCTGCTATTAAGCTGATGATGATGATGATGATGATGATGATGATGAT 240  
 QY 284 GAGGCCACAGGAGCCAGGAGCTTCTAGAGATGATGATGATGATGATGATGATGAT 343  
 Db 241 GAGGCCACAGGAGCCAGGAGCTTCTAGAGATGATGATGATGATGATGATGATGAT 300  
 QY 344 GTGAGTGCAAGATTGTTCTGTAGAGCCCGAGAGAAATTCATGACATGTTGGGC 403  
 Db 301 GTGAGTGCAAGATTGTTCTGTAGAGCCCGAGAGAAATTCATGACATGTTGGGC 360  
 QY 404 TGCCAAAGAGAGTCCCTCTGATCATTTCAAGGCAATGTGAAGAAACAGACACC 463  
 Db 361 TGCCAAAGAGAGTCCCTCTGATCATTTCAAGGCAATGTGAAGAAACAGACACC 420  
 QY 464 AAAGCCACACAGAAAGCCAAACATTCAGAGCTCCAGAGGAAATTCATGACAT 523  
 Db 421 AAAGCCACACAGAAAGCCAAACATTCAGAGCTCCAGAGGAAATTCATGACAT 480  
 QY 524 GTGAGTGCAAGATTGTTCTGTAGAGCTTGTAGAGCTTGTAGAGCTTGTAGAGCT 583  
 Db 481 GTGAGTGCAAGATTGTTCTGTAGAGCTTGTAGAGCTTGTAGAGCTTGTAGAGCT 540  
 QY 584 AACATTCAGCCAAAGAGAGTGCACACCTACCAAGACTCTTCTTCCACCTC 643  
 Db 541 AACATTCAGCCAAAGAGAGTGCACACCTACCAAGACTCTTCTTCCACCTC 600  
 QY 644 ACTCTCCAGCTGACACCCCTTAATTCATTCAGTGTCTCAAAAAGATGTTTCAA 703  
 Db 601 ACTCTCCAGCTGACACCCCTTAATTCATTCAGTGTCTCAAAAAGATGTTTCAA 660  
 QY 704 GATCATTTTGTGTTGCTCTCTCTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 763  
 Db 661 GATCATTTTGTGTTGCTCTCTCTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 720  
 QY 764 CTCGCCCTTACCCAGGCTTACGCTTAATTAATTCAGTGTCTCTCTCTCTCTCTCT 823  
 Db 721 CTCGCCCTTACCCAGGCTTACGCTTAATTAATTCAGTGTCTCTCTCTCTCTCTCT 780  
 QY 824 AGCTAGTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 883  
 Db 781 AGCTAGTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 840  
 QY 884 TTTTAAATGTC 895  
 Db 841 TTTTAAATGTC 852

RESULT 14  
 US-09-990-456-164  
 ; Sequence 164, Application US/09990456  
 ; Patent No. US20020137890A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnovers, Luc  
 ; APPLICANT: Baton, Dan L.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C22  
CURRENT APPLICATION NUMBER: US/09/990.456  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087609  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087759  
PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087827  
PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088025  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088026  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088028  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088029  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088030  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088033  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088326  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088167  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088202  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088212  
PRIOR FILING DATE: 1998-06-05  
PRIOR APPLICATION NUMBER: 60/088217  
PRIOR FILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 60/088655  
PRIOR FILING DATE: 1998-06-09  
PRIOR APPLICATION NUMBER: 60/088734  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088738  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088742  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088810  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088826  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088876  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089440  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089512  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089598  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089599  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089600  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089653  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089907  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089908  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089947  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089948  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/089952  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090246  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090252  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090254  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: 60/090349  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090355  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090429  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090431  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090435  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090444  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090445  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090472



```

? PRIOR FILING DATE: 1998-06-24
? PRIOR APPLICATION NUMBER: 60/090535
? PRIOR FILING DATE: 1998-06-24
? PRIOR APPLICATION NUMBER: 60/090540
? PRIOR FILING DATE: 1998-06-24
? PRIOR APPLICATION NUMBER: 60/090542
? PRIOR FILING DATE: 1998-06-24
? PRIOR APPLICATION NUMBER: 60/090557
? PRIOR FILING DATE: 1998-06-24
? PRIOR APPLICATION NUMBER: 60/090676
? PRIOR FILING DATE: 1998-06-25
? PRIOR APPLICATION NUMBER: 60/090678
? PRIOR FILING DATE: 1998-06-25
? PRIOR APPLICATION NUMBER: 60/090690
? PRIOR FILING DATE: 1998-06-25
? PRIOR APPLICATION NUMBER: 60/090694
? PRIOR FILING DATE: 1998-06-25
? PRIOR APPLICATION NUMBER: 60/090695
? PRIOR FILING DATE: 1998-06-25
? PRIOR APPLICATION NUMBER: 60/090696
? PRIOR FILING DATE: 1998-06-25
? PRIOR APPLICATION NUMBER: 60/090862
? PRIOR FILING DATE: 1998-06-26
? PRIOR APPLICATION NUMBER: 60/090863
? PRIOR FILING DATE: 1998-06-26
? PRIOR APPLICATION NUMBER: 60/091360
? PRIOR FILING DATE: 1998-07-01
? PRIOR APPLICATION NUMBER: 60/091478
? PRIOR FILING DATE: 1998-07-02
? PRIOR APPLICATION NUMBER: 60/091544
? PRIOR FILING DATE: 1998-07-01
? PRIOR APPLICATION NUMBER: 60/091519
? PRIOR FILING DATE: 1998-07-02
? PRIOR APPLICATION NUMBER: 60/091626
? PRIOR FILING DATE: 1998-07-02
? PRIOR APPLICATION NUMBER: 60/091633
? PRIOR FILING DATE: 1998-07-02
? PRIOR APPLICATION NUMBER: 60/091978
? PRIOR FILING DATE: 1998-07-07
? PRIOR APPLICATION NUMBER: 60/091982
? PRIOR FILING DATE: 1998-07-07
? PRIOR APPLICATION NUMBER: 60/092182
? PRIOR FILING DATE: 1998-07-09

Query Match          95.2%; Score 852; DB 10; Length 870;
Best Local Similarity 100.0%; Pred. No. 3.4e-271;
Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Db 361 TGCCAAAGAGCAGTGCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAACACACC 420
Oy 464 AAAGCAGACACAGAAAGCCAAACAGCATTCAGAGCCGTCCAGCAATTTTCAACACAT 523
Db 421 AAAGCAGACACAGAAAGCCAAACAGCATTCAGAGCCGTCCAGCAATTTTCAACACAT 480
Oy 524 GTACAGCTAAGAGCTTTGCTGCTTGTGTAGAGCTGTGAGCGCCACTTTCACAAATTA 583
Db 481 GTACAGCTAAGAGCTTTGCTGCTTGTGTAGAGCTGTGAGCGCCACTTTCACAAATTA 540
Oy 584 AACATTCTCAGCAAGAAAGAGAGTACACACCTTCCAGACACTTTCTTCCACACTC 643
Db 541 AACATTCTCAGCAAGAAAGAGAGTACACACCTTCCAGACACTTTCTTCCACACTC 600
Oy 644 ACTCTCCAGCTTACCCACCCCTTAATCATTCAGAGCTGTCCAAAAGAGATTTTTCAA 703
Db 601 ACTCTCCAGCTTACCCACCCCTTAATCATTCAGAGCTGTCCAAAAGAGATTTTTCAA 660
Oy 704 GATCATTTTGTGTTGCTCTCTCTAGTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 763
Db 661 GATCATTTTGTGTTGCTCTCTCTAGTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
Oy 764 CTCCTCTTACCCAGGCTTAGGCTTAATTAACCTGAAAGATTCAGGAAACTGTAGCTTCT 823
Db 721 CTCCTCTTACCCAGGCTTAGGCTTAATTAACCTGAAAGATTCAGGAAACTGTAGCTTCT 780
Oy 824 ACCTAGTGTCTTAACTTAATGCAATGCAAGAGTGAAGAGTGAAGAGTGAAGAGTGA 883
Db 781 ACCTAGTGTCTTAACTTAATGCAATGCAAGAGTGAAGAGTGAAGAGTGAAGAGTGA 840
Oy 884 TTTTAAATGTC 895
Db 841 TTTTAAATGTC 852

RESULT 15
US-09-989-721-164
; Sequence 164, Application US/09989721
; Patent No. US20020142961A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC55
; CURRENT APPLICATION NUMBER: US/09/989,721
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250

```



;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 95.2%; Score 852; DB 10; Length 870;

Best Local Similarity 100.0%; Pred. No. 3.4e-271; Mismatches 0; Indels 0; Gaps 0;

Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 CTCGCCCTCAAAATGGGACGCTGGCCTGGGACTAAAGCATAGACACACAGGCTGAGTATC 103  
DB 1 CTCGCCCTCAAAATGGGACGCTGGCCTGGGACTAAAGCATAGACACACAGGCTGAGTATC 60  
QY 104 CTGACCTGATCATCCCGAGGATCGAGGCTCCCGACAGGGAACCTTCATTATATTTCT 163  
DB 61 CTGACCTGATCATCCCGAGGATCGAGGCTCCCGACAGGGAACCTTCATTATATTTCT 120  
QY 164 TCAAGCAATTCACGTGACGACGACAGTGGCGATGAAAGTCTAATCTCTCCCTCTCC 223  
DB 121 TCAAGCAATTCACGTGACGACGACAGTGGCGATGAAAGTCTAATCTCTCCCTCTCC 180  
QY 224 TGTGTGCTGCCTAATGCTGATGTCATGTCATGCTCTAGACGCTGAATCCAGGGGTGCCA 283  
DB 181 TGTGTGCTGCCTAATGCTGATGTCATGTCATGCTCTAGACGCTGAATCCAGGGGTGCCA 240  
QY 284 GAGGGCACAGGGGACGAGGCGCTTCAGAGATGGCTCCAGGAAGGGCGCCAGAAAT 343  
DB 241 GAGGGCACAGGGGACGAGGCGCTTCAGAGATGGCTCCAGGAAGGGCGCCAGAAAT 300  
QY 344 GTGAGTCAAAAGATTGTTCTCTGAGAGCCCGAGAGAAATTCATGACAGTGTGGGC 403  
DB 301 GTGAGTCAAAAGATTGTTCTCTGAGAGCCCGAGAGAAATTCATGACAGTGTGGGC 360  
QY 404 TGCCTAAAGAGAGTGCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAAGACAC 463  
DB 361 TGCCTAAAGAGAGTGCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAAGACAC 420  
QY 464 AAAGGACACAGAAAGCCCAACATTCAGAGCTGCGAGCAATTTCTCAAAACAAT 523  
DB 421 AAAGGACACAGAAAGCCCAACATTCAGAGCTGCGAGCAATTTCTCAAAACAAT 480  
QY 524 GTGAGTCAAAAGATTGTTCTCTGAGAGCCCGAGAGAAATTCATGACAGTGTGGGC 583  
DB 481 GTGAGTCAAAAGATTGTTCTCTGAGAGCCCGAGAGAAATTCATGACAGTGTGGGC 540  
QY 584 AACATTCTAGCCACAGAGACAGTGAACACCTACAGACACTCTTCTCTCCACCTC 643  
DB 541 AACATTCTAGCCACAGAGACAGTGAACACCTACAGACACTCTTCTCTCCACCTC 600  
QY 644 ACTCTCCACCTGACCCACCTTAATTCATTCAGAGCTCTCAAAAAAGCATGTTTTTCAA 703  
DB 601 ACTCTCCACCTGACCCACCTTAATTCATTCAGAGCTCTCAAAAAAGCATGTTTTTCAA 660  
QY 704 GATCATTTTGTGTTGCT 763  
DB 661 GATCATTTTGTGTTGCT 720  
QY 764 CTCGCCCTCAAAATGGGCTTAAATTAACCTGAAGATTCAGGAACCTGATGCTTCT 823

DB 721 CTCGCCCTCAAAATGGGCTTAAATTAACCTGAAGATTCAGGAACCTGATGCTTCT 780  
QY 824 AGCTAGTGCATTTAATGCAATCAGGAAGTGAACAGAGTCAATTAATA 883  
DB 781 AGCTAGTGCATTTAATGCAATCAGGAAGTGAACAGAGTCAATTAATA 840  
QY 884 TTTTAAATGTC 895  
DB 841 TTTTAAATGTC 852

Search completed: October 10, 2003, 05:45:44  
Job time : 258.83 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2003, 13:25:26 ; Search time 58.3306 Seconds

(without alignments)  
6772.395 Million cell updates/sec

Title: US-09-700-770-5

Perfect score: 895  
Sequence: 1 ctaactcttaagtaacagc.....ataaataatttaaatgltc 895

Scoring table: IDENTITY\_NDC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PCRTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	852	95.2	870	4	US-09-996-243-164
2	525.8	58.7	533	4	US-09-702-705-113
3	525.8	58.7	533	4	US-09-736-457-113
4	312	34.9	312	4	US-09-702-705-43
5	312	34.9	312	4	US-09-736-457-43
6	56.8	6.3	7218	1	US-08-232-463-14
7	38.6	4.3	7218	1	US-08-232-463-14
8	33.8	3.8	289	3	US-09-007-005-17
9	33.8	3.8	289	3	US-09-244-796-17
10	33.2	3.7	3701	4	US-09-220-132-57
11	32.8	3.7	445	4	US-09-247-155-53
12	32.8	3.7	2686	4	US-09-228-986-3
13	32.8	3.7	12001	1	US-08-458-568A-11
14	32.8	3.7	1664976	4	US-08-916-421B-1
15	32.4	3.6	4466	4	US-09-410-551B-20
16	32.4	3.6	4478	4	US-09-410-551B-16
17	32.4	3.6	4571	4	US-09-410-551B-22
18	32.4	3.6	4571	4	US-09-410-551B-18
19	32.4	3.6	34185	4	US-09-545-481-3
20	32.4	3.6	77536	4	US-09-410-551B-1
21	32.4	3.6	1830121	4	US-09-557-884-1
22	32.4	3.6	1830121	4	US-09-643-990A-1
23	32.2	3.6	6755	3	US-08-931-999-4
24	32	3.6	5000	4	US-08-836-687B-35
25	31.8	3.6	1191	4	US-09-459-133-3
26	31.8	3.6	7608	4	US-09-221-017B-14
27	31.6	3.5	1146	3	US-08-596-684F-1

c	28	31.4	3.5	77536	4	US-09-410-551B-1	Sequence 1, Appl1
	29	31.2	3.5	1365	4	US-09-107-532A-1659	Sequence 1659, Ap
	30	31.2	3.5	2264	3	US-09-126-109-9	Sequence 9, Appl1
	31	31.2	3.5	2318	4	US-09-620-312D-916	Sequence 916, App
	32	31.2	3.5	4674	4	US-09-410-551B-26	Sequence 26, Appl
	33	31.2	3.5	4725	4	US-09-410-551B-24	Sequence 24, Appl
	34	31.2	3.5	4737	4	US-09-410-551B-30	Sequence 30, Appl
	35	31.2	3.5	4767	4	US-09-410-551B-28	Sequence 28, Appl
	36	31.2	3.5	4818	4	US-09-410-551B-32	Sequence 32, Appl
	37	31.2	3.5	50000	4	US-09-146-053-3	Sequence 3, Appl1
c	38	30.8	3.4	1698	1	US-08-592-126-62	Sequence 62, Appl
c	39	30.8	3.4	1698	4	US-09-168-595-62	Sequence 62, Appl
c	40	30.8	3.4	2062	1	US-08-073-383-5	Sequence 5, Appl1
c	41	30.8	3.4	2062	3	US-08-328-239A-3	Sequence 3, Appl1
c	42	30.8	3.4	2062	5	PCT-US94-06365-5	Sequence 5, Appl1
c	43	30.8	3.4	2062	5	PCT-US95-13661-3	Sequence 3, Appl1
c	44	30.8	3.4	13011	2	US-08-791-849A-14	Sequence 14, Appl
c	45	30.8	3.4	1230025	4	US-09-196-452A-1	Sequence 1, Appl1

#### ALIGNMENTS.

RESULT 1  
US-09-996-243-164  
; Sequence 164, Application US/09996243  
; Patent No. 6478825  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Bostein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C13  
; CURRENT APPLICATION NUMBER: US/09/996,243  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28



; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 95.2%; Score 852; DB 4; Length 870;  
Best Local Similarity 100.0%; Pred. No. 4,9e-267;  
Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 44 CTCGCCCTTAATGGAGCGCTGGCTGGAGCTAAAGCATAGACCCAGCGCTGAGTATC 103
DB 1 CTCGCCCTTAATGGAGCGCTGGCTGGAGCTAAAGCATAGACCCAGCGCTGAGTATC 60
QY 104 CTGACCTGATGATCCCGAGGGATCGAGAGCTCCAGCGGGAACTTCATATATTC 163
DB 61 CTGACCTGATGATCCCGAGGGATCGAGAGCTCCAGCGGGAACTTCATATATTC 120
QY 164 TCAGCACTTACAGCTGACCGACAGTTGCGATGAAGTTCTATCTCTCCCTCC 223
DB 121 TCAGCACTTACAGCTGACCGACAGTTGCGATGAAGTTCTATCTCTCTCCCTCC 180
QY 224 TGTGTGTCACATATGCTGATGTCATGCTCTCTAGCAGCTGAAATCCAGGGGTGCCA 283
DB 181 TGTGTGTCACATATGCTGATGTCATGCTCTCTAGCAGCTGAAATCCAGGGGTGCCA 240
QY 284 GAGGCCACAGGACCGGACCGAGCTTCTAGAGATGGCTCCAGAAAGGCGCCAGAAAT 343
DB 241 GAGGCCACAGGACCGGACCGAGCTTCTAGAGATGGCTCCAGAAAGGCGCCAGAAAT 300
QY 344 GTGATGCAAAAGTTGTTCTCTGAGAGCCCGAGAAAGAAATTCATGACAGTGTGGGC 403
DB 301 GTGATGCAAAAGTTGTTCTCTGAGAGCCCGAGAAAGAAATTCATGACAGTGTGGGC 360
QY 404 TGGCAAGAGAGAGTCCCTGTGATCATTTCAAGGGCAATGTGAAGAAACAGACACC 463
DB 361 TGGCAAGAGAGAGTCCCTGTGATCATTTCAAGGGCAATGTGAAGAAACAGACACC 420
QY 464 AAAGCACCACAGAAAGCCAAACAAAGCATTTCCAGAGCTCCAGCAATTTCTCAAAAT 523
DB 421 AAAGCACCACAGAAAGCCAAACAAAGCATTTCCAGAGCTCCAGCAATTTCTCAAAAT 480
QY 524 GTGAGTAAGAGCTTGTCTGTGCTCTTGTAGAGCTGTGAGCGCCACTCTTCAATTA 583
DB 481 GTGAGTAAGAGCTTGTCTGTGCTCTTGTAGAGCTGTGAGCGCCACTCTTCAATTA 540
QY 584 AACATCTGAGCAAGAGAGAGAGAGTGGACAGCTTACAGACACTCTTCTTCCACCTC 643
DB 541 AACATCTGAGCAAGAGAGAGAGAGTGGACAGCTTACAGACACTCTTCTTCCACCTC 600
QY 644 ACTCTCCACAGTACCCACCCCTTAATCATTCAGAGCTCTCAAAAAGCATGTTTTCAA 703
DB 601 ACTCTCCACAGTACCCACCCCTTAATCATTCAGAGCTCTCAAAAAGCATGTTTTCAA 660
QY 704 GATCATTTGTTGTTGCTCTCTAGAGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 763
DB 661 GATCATTTGTTGTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
QY 764 CTCGCCCTTAATGGAGCTTATATACCTGAAGATTTCCAGGAACTGTAGCTTCT 823
DB 721 CTCGCCCTTAATGGAGCTTATATATTCCTGAAGATTTCCAGGAACTGTAGCTTCT 780
QY 824 AGCTAGTGTCTTAATCTTAATGCAATCAGAAAGTGAAGAAAGTCAATTAATA 883
DB 781 AGCTAGTGTCTTAATCTTAATGCAATCAGAAAGTGAAGAAAGTCAATTAATA 840
QY 884 TTTTAAATGTC 895
DB 841 TTTTAAATGTC 852
```

RESULT 2

US-09-702-705-113  
; Sequence 113, Application US/09702705  
; Patent No. 6504010  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tonglong  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Lodges, Michael A.  
; APPLICANT: Fanger, Gary  
; APPLICANT: Vedvick, Tom  
; APPLICANT: Carter, Darrick  
; APPLICANT: Retter, Marc  
; APPLICANT: Mannion, Jane  
; APPLICANT: Fan, Liqun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.478C14  
; CURRENT APPLICATION NUMBER: US/09/702,705  
; CURRENT FILING DATE: 2000-10-30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 113  
; LENGTH: 533  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-702-705-113

Query Match 58.7%; Score 525.8; DB 4; Length 533;  
Best Local Similarity 99.6%; Pred. No. 4,9e-161;  
Matches 527; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 179 CTGACCGAGAGTGGATGAAAGTTCTATCTTCCCTCTCTCTCTCTCTCTCTCTCA 238
DB 1 CTGACCGAGAGTGGATGAAAGTTCTATCTTCCCTCTCTCTCTCTCTCTCTCTCA 60
QY 239 TGTGTATGTCATGATGCTCTAGACAGCTGAAATCCAGGGGTGCCAGAGCGACAGGACC 298
DB 61 TGTGTATGTCATGATGCTCTAGACAGCTGAAATCCAGGGGTGCCAGAGCGACAGGACC 120
QY 299 GAGGCCAGGCTTGTAGAGATGGCTCCAGAGAGGCGCCAAAGATGTGATGCAAGAT 358
DB 121 GAGGCCAGGCTTGTAGAGATGGCTCCAGAGAGGCGCCAAAGATGTGATGCAAGAT 180
QY 359 GGTTCCTGAGAGCCCGAGAGAAATTCATGACAGTGTCTGGCTGCCAAAGACAGT 418
DB 181 GGTTCCTGAGAGCCCGAGAGAAATTCATGACAGTGTCTGGCTGCCAAAGACAGT 240
QY 419 GCGCCCTGTATCTTTCAAGGGCAATGTGAAGAAACAAAGACCAAGGACACAGAA 478
DB 241 GCGCCCTGTATCTTTCAAGGGCAATGTGAAGAAACAAAGACCAAGGACACAGAA 300
QY 479 AGCCAAACAAGCATTTCCAGAGCTTGCAGCAATTTCAAAAGATGCAAGCTAAGAGCT 538
DB 301 AGCCAAACAAGCATTTCCAGAGCTTGCAGCAATTTCAAAAGATGCAAGCTAAGAGCT 360
QY 539 TTGCTGTGCTTGTAGAGCTTGTAGCGCCACTCTTCAATTAACATTTCTACAGCA 598
DB 361 TTGCTGTGCTTGTAGAGCTTGTAGCGCCACTCTTCAATTAACATTTCTACAGCA 420
QY 599 GAAGAGAGTGAACACCTTACAGACACTTCTTCCACACTCTCTCCACTGTAC 658
DB 421 GAAGAGAGTGAACACCTTACAGACACTTCTTCCACACTCTCTCCACTGTAC 480
QY 659 CCAGCCCTTAATCATTCAGAGTGTCTCAAAAGCATGTTTCAAGATC 707
DB 481 CCAGCCCTTAATCATTCAGAGTGTCTCAAAAGCATGTTTCAAGATC 529
```

RESULT 3  
US-09-736-457-113  
; Sequence 113, Application US/09736457  
; Patent No. 6509448  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tonglong



```

; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 113
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-113

```

```

Query Match      58.7%; Score 525.8; DB 4; Length 533;
Best Local Similarity 99.6%; Pred. No. 4.9e-161;
Matches 527; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

OY 179 CTGCACCCAGCAAGTTCGATGAAAGTTCTAATCTCTCCCTCCTGTTGTCGCACCTAA 238
DB 1 CTGCACCCAGCAAGTTCGATGAAAGTTCTAATCTCTCCCTCCTGTTGTCGCACCTAA 60
OY 239 TGCATATGCAATGCTCTGCTAGCAGCCTGAATCCAGGGGTGGCCAGAGGCCACAGGACC 298
DB 61 TGCATATGCAATGCTCTGCTAGCAGCCTGAATCCAGGGGTGGCCAGAGGCCACAGGACC 120
OY 299 GAGGCCAGGCTTCTAGAGATGCTCCAGGAAGGGCCAGAAATGTAGTGCAGAAAGATT 358
DB 121 GAGGCCAGGCTTCTAGAGATGCTCCAGGAAGGGCCAGAAATGTAGTGCAGAAAGATT 180
OY 359 GGTTCCTGAGAGCCCGGAGAAATTCATGACAGTGTCTGGGCTGCCAAGAGACAGT 418
DB 181 GGTTCCTGAGAGCCCGGAGAAATTCATGACAGTGTCTGGGCTGCCAAGAGACAGT 240
OY 419 GCCCCTGTGATCATTTCAAGGGCAATGTGAAGAAACAGACACCAAGGACACAGAA 478
DB 241 GCCCCTGTGATCATTTCAAGGGCAATGTGAAGAAACAGACACCAAGGACACAGAA 300
OY 479 AGCCAAACAGCATTTCCAGAGCTGCGACAGCAATTTCTCAACAAATGTCAGCTAAGAACT 538
DB 301 AGCCAAACAGCATTTCCAGAGCTGCGACAGCAATTTCTCAACAAATGTCAGCTAAGAACT 360
OY 539 TTGCTGTGCTTTTGTAGAGAGCTGAGGGCCCACTCTTCAATTAACATTTCTAGCCAA 598
DB 361 TTGCTGTGCTTTTGTAGAGAGCTGAGGGCCCACTCTTCAATTAACATTTCTAGCCAA 420
OY 599 GAAGACAGTGAAGACACCTTACAGACACTTCTTCTCCACCTCACTCTCCACTGTAC 658
DB 421 GAAGACAGTGAAGACACCTTACAGACACTTCTTCTCCACCTCACTCTCCACTGTAC 480
OY 659 CCACCCCTTAATCATTTCCAGTGTCTTCAAAAAGCATTTTTCAGATC 707
DB 481 CCACCCCTTAATCATTTCCAGTGTCTTCAAAAAGCATTTTTCAGATC 529

```

```

RESULT 4
US-09-702-705-43
; Sequence 43, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
US-09-736-457-113

```

```

; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 312
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-43

```

```

Query Match      34.9%; Score 312; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.3e-91;
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 325 CAGGAAGGCGGCCAAGATGTAGTGCAGAAAGATTGTTCTGAGAGCCCGCAGAGAAA 384
DB 1 CAGGAAGGCGGCCAAGATGTAGTGCAGAAAGATTGTTCTGAGAGCCCGCAGAGAAA 60
OY 385 TTCAATGACAGTGTCTGGGCTGCCAAGAGCAGTGCCCTGTGATCATTTCAAGGGCAAT 444
DB 61 TTCAATGACAGTGTCTGGGCTGCCAAGAGCAGTGCCCTGTGATCATTTCAAGGGCAAT 120
OY 445 GTGAAGAAACAGACACCAAGGACACACAGAAAGCCAAACAGCATTCAGAGCCTGC 504
DB 121 GTGAAGAAACAGACACCAAGGACACACAGAAAGCCAAACAGCATTCAGAGCCTGC 180
OY 505 CAGCAATTTCCAAACATGTACACTTAAGAAAGTTTGTCTGCTTTGTAGAGCTTGA 564
DB 181 CAGCAATTTCCAAACATGTACACTTAAGAAAGTTTGTCTGCTTTGTAGAGCTTGA 240
OY 565 GCGCCCACTCTTCCAAATTAACATTTCCAGCAAGAGAGAGAGAGACACCTACAGAC 624
DB 241 GCGCCCACTCTTCCAAATTAACATTTCCAGCAAGAGAGAGAGAGACACCTACAGAC 300
OY 625 ACTCTTCTCTC 636
DB 301 ACTCTTCTCTC 312

```

```

RESULT 5
US-09-736-457-43
; Sequence 43, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 312
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-43

```

Query Match 34.9%; Score 312; DB 4; Length 312;  
Best Local Similarity 100.0%; Pred. No. 1.3e-91;  
Matches 312; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 325 CAGGAAGGGGCGCAAGAAATGTGAGTGCAGAAAGTTGGTTCTCTAGAGCCCGGAGAGAAA 384
   |||||||
Db 1 CAGGAAGGGGCGCAAGAAATGTGAGTGCAGAAAGTTGGTTCTCTAGAGCCCGGAGAGAAA 60
   |||||||
QY 385 TTCATGACAGAGTGTGGGCGCAAGAAAGAGTGGCCCTGTGATCATTTTCAAGGGCAAT 444
   |||||||
Db 61 TTCATGACAGAGTGTGGGCGCAAGAAAGAGTGGCCCTGTGATCATTTTCAAGGGCAAT 120
   |||||||
QY 445 GTGAAGAAAACAGACACCAAGAGCAACAGAGAAAGCCAAAGAGATTCAGAGGCTGC 504
   |||||||
Db 121 GTGAAGAAAACAGACACCAAGAGCAACAGAGAAAGCCAAAGAGATTCAGAGGCTGC 180
   |||||||
QY 505 CAGCAATTTCTCAAAATGTGAGTGCAGTAAGAACTTTGCTCTGCTTTGTAGAGCTCTGA 564
   |||||||
Db 181 CAGCAATTTCTCAAAATGTGAGTGCAGTAAGAACTTTGCTCTGCTTTGTAGAGCTCTGA 240
   |||||||
QY 565 GGGCCACCTCTTCAATTAACATTTCTGAGCCAGAGACAGTGAAGACACCTACAGAC 624
   |||||||
Db 241 GGGCCACCTCTTCAATTAACATTTCTGAGCCAGAGACAGTGAAGACACCTACAGAC 300
   |||||||
QY 625 ACTCTTCTCTC 636
   |||||||
Db 301 ACTCTTCTCTC 312

```

RESULT 6  
US-08-232-463-14  
Sequence 14, Application US/08232463  
Patent No. 5670367

GENERAL INFORMATION:

```

? APPLICANT: DORNER, F.
? APPLICANT: SCHEIFLINGER, F.
? APPLICANT: FALKNER, F. G.
? TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
? NUMBER OF SEQUENCES: 52
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Foley & Lardner
? STREET: 1800 Diagonal Road, Suite 500
? CITY: Alexandria
? STATE: VA
? COUNTRY: USA
? ZIP: 22313-0299
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/232,463
? FILING DATE:
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/07/935,313
? FILING DATE:
? APPLICATION NUMBER: EP 91 114 300.6
? FILING DATE: 26-AUG-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: BENT, Stephen A.
? REGISTRATION NUMBER: 29,768
? REFERENCE/DOCKET NUMBER: 30472/114 IMMU
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703)836-9300
? TELEFAX: (703)683-4109
? TELEX: 899149
? INFORMATION FOR SEQ ID NO: 14:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 7218 base pairs
? TYPE: nucleic acid

```

STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: PT29pt-FL5  
US-08-232-463-14

Query Match 6.3%; Score 56.8; DB 1; Length 7218;  
Best Local Similarity 8.8%; Pred. No. 8e-08;  
Matches 28; Conservative 170; Mismatches 122; Indels 0; Gaps 0;

```

QY 537 CTTTGCTGCGCTTTGTAGAGCTCTGAGCCGCCACTCTTCCATTAATTAATTCAGCC 596
   :::::
Db 1171 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1230
   :::::
QY 597 AAGAAGACAGTAGAGACACACACACACACACACACACACACACACACACACACAC 656
   : : : : :
Db 1231 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1290
   : : : : :
QY 657 ACCCACCCTTAATCATCTCAAGTCTGCAAAAAGCATGTTTCAAGATCATTTGT 716
   :::::
Db 1291 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1350
   :::::
QY 717 GTTGCTGCTGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 776
   :::::
Db 1351 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1410
   :::::
QY 777 GCGTAGCGTAACTAGCTGAAGATTCAGAACTGAGCTTCTCTCTCTCTCTCTCTCT 836
   :::::
Db 1411 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1470
   :::::
QY 837 TAACCTTAATGCAATCAGG 856
   |||||
Db 1471 GATAGGTAATTAACAGTAGTG 1490

```

RESULT 7  
US-08-232-463-14/C  
Sequence 14, Application US/08232463  
Patent No. 5670367

GENERAL INFORMATION:

```

? APPLICANT: DORNER, F.
? APPLICANT: SCHEIFLINGER, F.
? APPLICANT: FALKNER, F. G.
? TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
? NUMBER OF SEQUENCES: 52
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Foley & Lardner
? STREET: 1800 Diagonal Road, Suite 500
? CITY: Alexandria
? STATE: VA
? COUNTRY: USA
? ZIP: 22313-0299
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/232,463
? FILING DATE:
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/07/935,313
? FILING DATE:
? APPLICATION NUMBER: EP 91 114 300.6
? FILING DATE: 26-AUG-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: BENT, Stephen A.
? REGISTRATION NUMBER: 29,768
? REFERENCE/DOCKET NUMBER: 30472/114 IMMU
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703)836-9300
? TELEFAX: (703)683-4109

```

Query Match	3.8%	Score 33.8	DB 3	Length 289
Best Local Similarity	5.3%	Pred. No. 0.39		
Matches 11	Conservative 91	Mismatches 107	Indels 0	Gaps 0
624	CACTCTCTTCTCCGACGTCACATCTCCCACTGTACCCACACCCCTAAATCATTTCCAGTGCCTC 683			
11:	:	:	:	:

RESULT 10  
US-09-220-132-57  
; Sequence 57, Application US/09220132  
; Patent No. 6506607

```

1  GENERAL INFORMATION:
2  APPLICANT: Shyjan, Andrew W
3  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
4  TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
5  FILE REFERENCE: 07334-074001
6  CURRENT APPLICATION NUMBER: US/09/220,132
7  CURRENT FILING DATE: 1998-12-23
8  PRIOR APPLICATION NUMBER: US 60/079,303
9  PRIOR FILING DATE: 1998-03-25
10 PRIOR APPLICATION NUMBER: US 60/068,821
11 PRIOR FILING DATE: 1997-12-24
12 NUMBER OF SEQ ID NOS: 191
13 SOFTWARE: FastSeq for Windows Version 4.0
14 SEQ ID NO 57
15 LENGTH: 3701
16 TYPE: DNA
17 ORGANISM: Homo sapiens
18 US-09-220-132-57

```

```

Query Match 3.7%; Score 33.2; DB 4; Length 3701;
Best Local Similarity 50.6%; Pred. No. 2.6;
Matches 80; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 603 ACAGTGGACACCTTACGACGACACTCTCTCTCCGCCACGCGCCAGCTGTACCCAC 662
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2718 ACACTCTGTATTCATTCATCAATTCCTCAGTTTACACGCCCTCTTCGACACTGCACCTC 2777
      663 CCCTAAATCATTTCCAGTGTCTCTCAAAAAGCATGTTTTCAGATTCATTTGTTGTGCT 722
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2778 TCTGTATCATGTCGCCCTCTCTTTCATACAGAAAGGGGTATGTATTTGAAGGCTGTGGCT 2837
      723 CTCCTTAGTGTCTTCTTCTCTCGTCAGCTTTAGCGCTGT 760
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2838 TCAGGGAGTCTTTCGCAATCCTGTGGCCCTTAACATAT 2875

RESULT 11
US-09-247-155-53/C
Sequence 53, Application US/09247155A
Patent No. 6312922
GENERAL INFORMATION:
APPLICANT: Dumas Mline Edwards, Jean-Baptiste
APPLICANT: Duchet, Aymeric
APPLICANT: Bouquelerec, Lydie
TITLE OF INVENTION: Complementary DNAs
FILE REFERENCE: GENSET.021A
CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER FILING DATE: 1998-08-10
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
SOFTWARE: patent.pm
SEQ ID NO 53
LENGTH: 445
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 81..356
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 81..152
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 6.2
OTHER INFORMATION: seq ALLSTWALTTG/AL
FEATURE:
NAME/KEY: polyA_signal

```

```

; LOCATION: 406..411
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 429..445
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: n-a, g, c or t
US-09-247-155-53

```

	Query Match	3.7%	Score 32.8	DB 4	Length 445
	Best Local Similarity	53.0%	Pred. No. 1.1		
	Matches	70	Conservative	0	Mismatches 62; Indels 0; Gaps 0;
OY	207	AATCTCTTCCCTCCCTGTTGTCGCCACTATGCTGATGTCATGCAGTCTTAGCAGCCT	266		
Db	333	AGTGGGCTCGGGCCCTCTGTATCTGTGAGCTCGCGTGGGCGCTTCCTGCAGTAT	274		
OY	267	GAATCCAGGGGTTGGCCAGAGCCACAGGAGCCAGGCCCTTTAGAGATGGCTTCA	326		
Db	273	GAAAGTGGCCACAGATAGCCACAGTCCACAGGCGATAGCAGCGCGGACACACACA	214		
OY	327	GGAAGCGCGCCA	338		
Db	213	AGTAGCGCGGCA	202		

```

RESULT 12
US-09-228-986-3
; Sequence 3, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Tamothy
; APPLICANT: Neuenhulzen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2686
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-228-986-3

```

Query Match	3.7%	Score 32.8	DB 4	Length 2686
Best Local Similarity	45.9%	Pred. No. 2.9		
Matches 112	Conservative	0	Mismatches 132	Indels 0
				Gaps 0
QY	267	GAATCCAGGGGTGCGCAGAGGCCACAGAGGACCGAGGCCAGGCTTCTAGAGATGGCTCCA	326	
Db	2178	GAATTAATAGAGGTACCAAAACATAGAAAGAGATGCGCAGTTCTCTCAGATTGCCATG	2237	
QY	327	GGAAGGCCGCCAAGATGTGAGTGCAAAGATTGGTTCTGTGAGAGCCCCGAGAGAAATTT	386	
Db	2238	GCCTCGCGTGGTTACAGTGCCTGTATCCAGGGCCACAAATGCAGAGAGTGTTGTAAGATGATC	2297	
QY	387	CATGACATGTCTGTGGCTGCCAAAGACAGTGGCCCTGTGATCATTTCAAGGGCAATGT	446	
Db	2298	GAGCAGATGAGGCGACTTCCGAACACGACAGAGAAATAGACAACTCTTGATGATTAATCG	2357	
QY	447	GAAGAAACAAAGACACCAAGGACACAGAAAGCCAAACAGCATTCAGAGCCTGCCA	506	
Db	2358	AAAGATCTCAATGACAAATCTCTCCAGCAAGCACACAGAGACAGCACGCCACCCACAA	2417	
QY	507	GCAA 510		
Db	2418	GCAA 2421		

TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methano  
 Patent No. 6503729  
 TITLE OF INVENTION: jannaschii  
 FILE REFERENCE: PB2/5  
 CURRENT APPLICATION NUMBER: US/08/916,421B  
 CURRENT FILING DATE: 1997-08-22  
 PRIOR APPLICATION NUMBER: US 60/024,428  
 PRIOR FILING DATE: 1996-08-22  
 NUMBER OF SEQ ID NOS: 3  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 1  
 LENGTH: 1664976  
 TYPE: DNA  
 ORGANISM: Methanococcus jannaschii  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (28222)..(28222)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc\_feature  
 LOCATION: (28257)..(28258)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc\_feature  
 LOCATION: (84773)..(84773)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc\_feature  
 LOCATION: (84808)..(84808)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc\_feature  
 LOCATION: (84812)..(84812)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc\_feature  
 LOCATION: (98120)..(98120)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc\_feature  
 LOCATION: (98159)..(98159)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc\_feature  
 LOCATION: (98239)..(98239)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc\_feature  
 LOCATION: (98266)..(98266)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc\_feature  
 LOCATION: (98343)..(98343)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc\_feature  
 LOCATION: (103998)..(103998)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc\_feature  
 LOCATION: (148948)..(148948)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc\_feature  
 LOCATION: (163385)..(163385)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc\_feature  
 LOCATION: (191989)..(191989)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc\_feature  
 LOCATION: (191995)..(191995)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc\_feature  
 LOCATION: (231980)..(231980)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc\_feature  
 LOCATION: (234187)..(234187)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc\_feature  
 LOCATION: (234220)..(234220)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc\_feature  
 LOCATION: (234814)..(234814)  
 OTHER INFORMATION: n equals a, t, c, or g  
 NAME/KEY: misc\_feature

```

: OTHER INFORMATION: n equals a, t, c, or g
: NAME/KEY: misc_feature
: LOCATION: (1349473)..(1349473)
: OTHER INFORMATION: n equals a, t, c, or g
: NAME/KEY: misc_feature
: LOCATION: (1349491)..(1349491)
: OTHER INFORMATION: n equals a, t, c, or g
: NAME/KEY: misc_feature
: LOCATION: (1470091)..(1470091)
: OTHER INFORMATION: n equals a, t, c, or g
: NAME/KEY: misc_feature
: LOCATION: (1569020)..(1569020)
: OTHER INFORMATION: n equals a, t, c, or g
: NAME/KEY: misc_feature
: LOCATION: (1602912)..(1602912)
: OTHER INFORMATION: n equals a, t, c, or g
: NAME/KEY: misc_feature
: LOCATION: (1603734)..(1603734)
: OTHER INFORMATION: n equals a, t, c, or g
: NAME/KEY: misc_feature
: LOCATION: (1637998)..(1637998)
: OTHER INFORMATION: n equals a, t, c, or g
: NAME/KEY: misc_feature
: LOCATION: (1664854)..(1664855)
: OTHER INFORMATION: n equals a, t, c, or g
: US-08-916-421B-1

Query Match 3.7%; Score 32.8; DB 4; Length 1664976;
Best Local Similarity 59.8%; Pred. No. 93;
Matches 55; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 700 TCAGATCATTTTGTGTGCTCTCTCTAGTGTCTCTCTCGCAGCTTACGCTG 759
DB 571606 TCATGCGATTAGCTAGTGTCCCTCTCTCTATGCTCTTTTATTAACCTCTTAACTT 571665
QY 760 TGCCCTCCCTTACCAGGCTTAGGCTTAAT 791
DB 571666 TCACCTCAGCTTCTGGAGCTATGTTAAGT 571697

RESULT 15
US-09-410-551B-20
: Sequence 20, Application US/09410551B
: Patent No. 6503737
: GENERAL INFORMATION:
: APPLICANT: KOSAN BIOSCIENCES, Inc.
: APPLICANT: REEVES, CHRISTOPHER
: APPLICANT: CHU, DANIEL
: APPLICANT: KHOSLA, CHAITAN
: APPLICANT: SANTU, DANIEL
: APPLICANT: WU, KAI
: TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
: FILE OF INVENTION: CONSTRUCTS THEREFOR
: FILE REFERENCE: 30062-20026.00
: CURRENT APPLICATION NUMBER: US/09/410,551B
: CURRENT FILING DATE: 1999-10-01
: PRIOR APPLICATION NUMBER: US 60/139,650
: PRIOR FILING DATE: 1999-06-17
: PRIOR APPLICATION NUMBER: US 60/123,810
: PRIOR FILING DATE: 1999-03-11
: PRIOR APPLICATION NUMBER: US 60/102,748
: PRIOR FILING DATE: 1998-10-02
: NUMBER OF SEQ ID NOS: 72
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 20
: LENGTH: 4466
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: DNA encoding synthetic
: OTHER INFORMATION: PKS synthase fragment
: NAME/KEY: CDS

```





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2003, 13:25:26 ; Search time 134.258 Seconds  
(without alignments)  
6772.395 Million cell updates/sec

Title: US-09-700-770-3

Perfect score: 2060  
Sequence: 1 ctgagagctcctaact.....ttccattgaaaaaaaaaaaaa 2060

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA: \*  
1: /cgn2\_6/ptodata/2/1na/5A.COMB.seq: \*  
2: /cgn2\_6/ptodata/2/1na/5B.COMB.seq: \*  
3: /cgn2\_6/ptodata/2/1na/6A.COMB.seq: \*  
4: /cgn2\_6/ptodata/2/1na/6B.COMB.seq: \*  
5: /cgn2\_6/ptodata/2/1na/PCTUS.COMB.seq: \*  
6: /cgn2\_6/ptodata/2/1na/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2060	100.0	2061	3	US-09-008-271A-16
2	2058.4	99.9	2061	4	US-09-705-448-2
3	1356.8	65.9	1910	3	US-08-974-691-7
4	1199.2	58.2	1299	1	US-08-723-938-4
5	1199.2	58.2	1299	2	US-09-080-538-4
6	1199.2	58.2	1299	4	US-09-387-413-4
7	1142	55.4	1353	3	US-08-974-691-1
8	1122.6	54.5	1329	4	US-09-705-448-4
9	747	36.3	1651	3	US-08-974-691-5
10	502.8	24.4	693	4	US-09-280-116-36
11	462.4	22.4	663	4	US-09-392-184-33
12	339.6	16.5	466	4	US-09-705-448-9
13	316.6	15.4	2038	2	US-08-631-097-7
14	316.6	15.4	2038	3	US-08-810-712-11
15	316.6	15.4	2465	5	PCT-US92-08090-1
16	314.6	15.3	727	4	US-09-280-116-35
17	289.2	14.0	299	4	US-09-118-554-42
18	289.2	14.0	299	4	US-09-118-627-42
19	289.2	14.0	299	4	US-09-602-877A-42
20	249.6	12.1	262	4	US-09-280-116-53
21	249.2	12.1	289	4	US-09-705-448-9
22	241.6	11.7	264	4	US-09-016-434-292
23	216	10.5	227	4	US-09-705-448-6
24	201.4	9.8	226	4	US-09-016-434-563
25	198	9.6	249	4	US-09-016-434-163
26	186.8	9.1	215	4	US-09-705-448-8
27	184	8.9	186	4	US-09-705-448-5

28	168.2	8.2	1240	1	US-08-240-372-2	Sequence 2, Appl1
29	168.2	8.2	2073	3	US-09-032-523-6	Sequence 6, Appl1
30	168.2	8.2	2733	2	US-08-846-021A-6	Sequence 6, Appl1
31	167.8	8.1	2732	6	5217891-14	Patent No. 5217891
32	151.8	7.4	2875	1	US-08-328-314-1	Sequence 1, Appl1
33	151.8	7.4	2875	1	US-08-731-045-1	Sequence 1, Appl1
34	139.2	6.8	2454	3	US-09-079-415-1	Sequence 1, Appl1
35	139.2	6.8	1615	1	US-09-640-305-5	Sequence 5, Appl1
36	133.6	6.5	1615	1	US-08-360-673-5	Sequence 5, Appl1
37	130	6.3	160	4	US-09-705-448-7	Sequence 7, Appl1
38	123.6	6.0	2032	1	US-08-088-633-1	Sequence 1, Appl1
39	123.6	6.0	2032	1	US-08-245-756-1	Sequence 1, Appl1
40	123.6	6.0	2032	1	US-08-441-750-1	Sequence 1, Appl1
41	123.6	6.0	2032	2	US-08-441-751-1	Sequence 1, Appl1
42	123.6	6.0	2032	5	PCT-US92-02521-1	Sequence 1, Appl1
43	101	4.9	3230	4	US-08-961-527-703	Sequence 203, App
44	93.2	4.5	1191	4	US-09-328-352-509	Sequence 509, App
45	92	4.5	1383	4	US-09-252-991A-5684	Sequence 5684, Ap

## ALIGNMENTS

RESULT 1  
US-09-008-271A-16  
Sequence 16, Application US/09008271A  
Patent No. 6203979  
GENERAL INFORMATION:

APPLICANT: Bandman, Olga  
Hillman, Jennifer L.  
Yue, Henry  
Guegler, Karl J.  
Corley, Neil C.  
Tang, Tom Y.  
Shah, Purvi

TITLE OF INVENTION: HUMAN PROTEASE MOLECULES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESS: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/008,271A  
FILING DATE: 16-Jan-1998

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Mohan-Peterson, Sheela  
REGISTRATION NUMBER: 41,201

TELECOMMUNICATION INFORMATION:  
REFERENCE/DOCKET NUMBER: PF-0458 US  
TELEPHONE: 650-845-4166  
TELEFAX: 650-845-0555

INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:

LENGTH: 2061 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

IMMEDIATE SOURCE:  
LIBRARY: LUNCAST01

CLONE: 877617  
SEQUENCE DESCRIPTION: SEQ ID NO: 16 :

US-09-008-271A-16







|||||  
Db 1416 GGGCCCTGATGCAAGCATTGGGGGAATCCCTTGCTGCTGGGGAGTACATCATCTGTG 1475  
QY 1661 CTCGGAAATCCCAAAGCTCCCGAGTCTCTCTCTTTGGGGGGGTGGTTAACT 1720  
Db 1476 CTCGGAATCCCAAAGCTCCCGAGTCTCTCTCTTTGGGGGGGTGGTTAACT 1535  
QY 1721 CAGGGCCATGATTACTGATCAAGACTACTCGAAATGGCGTCCGCTGTGTCCG 1780  
Db 1536 CAGGGCCATGATTACTGATCAAGACTACTCGAAATGGCGTCCGCTGTGTCCG 1595  
QY 1781 TTTCAGGGCCCTGGATGCTCCCTCCGCTGAGAGGCCCTTGATCTCTGGTACGCTT 1840  
Db 1596 TTTCAGGGCCCTGGATGCTCCCTCCGCTGAGAGGCCCTTGATCTCTGGTACGCTT 1655  
QY 1841 CTTCGGGACGTATGTGCGCTCTTCGACCGCGGGGACATGAAGACAGCCCGGGTGG 1900  
Db 1656 CTTCGGGACGTATGTGCGCTCTTCGACCGCGGGGACATGAAGACAGCCCGGGTGG 1715  
QY 1901 CTTGGCGCGGCTCGCACTCGCGAGCGGACCTTCGATGGGGAGAGACTCGGAGCGCA 1960  
Db 1716 CTTGGCGCGGCTCGCACTCGCGAGCGGACCTTCGATGGGGAGAGACTCGGAGCGCA 1775  
QY 1961 GTTCCCGGGGTGACGCCCAAGTGAAGGCAATGGGACCGGGTGTCTCGGAGGTCTGCT 2020  
Db 1776 GTTCCCGGGGTGACGCCCAAGTGAAGGCAATGGGACCGGGTGTCTCGGAGGTCTGCT 1835  
QY 2021 ACCCAGTAAATCACTATTTTCATGTAATGAAAAA 2060  
Db 1836 ACCCAGTAAATCACTATTTTCATGTAATGAAAAA 1875

RESULT 4  
US-08-723-938-4  
; Sequence 4, Application US/08723938  
; Patent No. 5776759  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Coleman, Roger  
; TITLE OF INVENTION: TWO NOVEL HUMAN CATHESPIN PROTEINS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/723,938  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0125 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1299 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single

;;  
; TOPOLOGY: Linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; IMMEDIATE SOURCE:  
; LIBRARY: LUNGNOT02  
; CLONE: 312099  
; US-08-723-938-4

Query Match 58.2%; Score 1199.2; DB 1; Length 1299;  
Best Local Similarity 94.3%; Pred. No. 0;  
Matches 1286; Conservative 0; Mismatches 3; Indels 75; Gaps 1;

QY 697 ACGGCTCCCGACGATGCTCCACACCGGCTGCAACCCCTGTGTGTGCTG 756  
Db 3 ACGGCTCCCGACGATGCTCCACACCGGCTGCAACCCCTGTGTGTGCTG 62  
QY 757 TGCTGAATGTGAGCCTTCCGCGGCACTGATCCGCACTCTTCATGAGTCCAA 816  
Db 63 TGCTGAATGTGAGCCTTCCGCGGCACTGATCCGCACTCTTCATGAGTCCAA 122  
QY 817 CTGAGCAGAGACCTCTGACTGAGGGATGAGAGAACAGACAGACTCCCAAGT 876  
Db 123 CTGAGCAGAGATCTGAACTGAGGGATGAGAGAACAGACAGACTCCCAAGT 182  
QY 877 TGGGGGGCCCACTCCCTGGGGGCAAGCCATCTGTAACCTCTGCAACTACAGGATG 936  
Db 183 TGGGGGGCCCACTCCCTGGGGGCAAGCCATCTGTAACCTCTGCAACTACAGGATG 242  
QY 937 TGCAGTATTTGGGGAATTGGGCTGGGAACGCTCCACAAACTGCACTGTCCTTG 996  
Db 243 TGCAGTATTTGGGGAATTGGGCTGGGAACGCTCCACAAACTGCACTGTCCTTG 302  
QY 997 ACACTGCTCTCCAACTCTGGGTCCGCTCAGAGATGCACTTCTCAAGTGCCT 1056  
Db 303 ACACTGCTCTCCAACTCTGGGTCCGCTCAGAGATGCACTTCTCAAGTGCCT 362  
QY 1057 GCTGTTACACACGAGATTGATCCAAAGCCTTAGTCTCTCAGGCCAATGGAGCA 1116  
Db 363 GCTGTTACACACGAGATTGATCCAAAGCCTTAGTCTCTCAGGCCAATGGAGCA 422  
QY 1117 AGTTGGCATTCATATGGAACCTGGCGGTGAGATGGAATCTGAGGAGACAAGCTGA 1176  
Db 423 AGTTGGCATTCATATGGAACCTGGCGGTGAGATGGAATCTGAGGAGACAAGCTGA 482  
QY 1177 CTATTTGGAATCAAGGCTGATGATGATTTTCGGGGAGGCTCTGGAGCCCAAGC 1236  
Db 483 CTATTTGGAATCAAGGCTGATGATGATTTTCGGGGAGGCTCTGGAGCCCAAGC 542  
QY 1237 TGGTCTTCGCTTTGGCCATTTGATGGGATATGGGCTGGTTCCATCTGTCTG 1296  
Db 543 TGGTCTTCGCTTTGGCCATTTGATGGGATATGGGCTGGTTCCATCTGTCTG 602  
QY 1297 TGAAGAGATTCGCGCCCGATGATGATGATGAGACAGGGCTATTTGATTAAGCTG 1356  
Db 603 TGAAGAGATTCGCGCCCGATGATGATGATGAGACAGGGCTATTTGATTAAGCTG 662  
QY 1357 TCTTCTCTTTTACTCAACAGGACCTGGAAGGCTGATGAGAGAGAGCTGCTCTG 1416  
Db 663 TCTTCTCTTTTACTCAACAGGACCTGGAAGGCTGATGAGAGAGAGCTGCTCTG 722  
QY 1417 GGGGCTGGAGCCCGGACACTACATCCACCCCTGACCTTCTGTCAGTCAAGTCCCTG 1476  
Db 723 GGGGCTGGAGCCCGGACACTACATCCACCCCTGACCTTCTGTCAGTCAAGTCCCTG 782  
QY 1477 CCTACTGAGATCCACATGAGAGGTGAGAGGTGGGCCAGGGCTGACTTCTGTGCA 1536  
Db 783 CCTACTGAGATCCACATGAGAGGTGAGAGGTGGGCCAGGGCTGACTTCTGTGCA 842  
QY 1537 AGGGCTGTGCTGCATCTTGATACGGGACAGTCTCTCATCAGACCACTGAGAGAGA 1596



OY	1537	AGGCGTGGCGCCATCCCTGGATATGACGGGACGCTCCCTCATACAGAGACCCACTAGAGGA	1596
Db	843	AGGCGTGGCGCCATCCCTGGATATGACGGGACGCTCCCTCATACAGAGACCCACTAGAGGA	902
OY	1597	TCCGGGCGCTTCATCATGACGACCATTTGAGGGGAAATCCCTTGGCTGGCTGGGAGATACATATCC	1656
Db	903	TCCGGGCGCTTCATCATGACGACCATTTGAGGGGAAATCCCTTGGCTGGCTGGGAGATACATATCC	962
OY	1657	TGTGCTGGGAATCCCAAGTATCCCGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1716
Db	963	TGTGCTGGGAATCCCAAGTATCCCGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1022
OY	1717	ACCTCAGGGCCCATGATATAGTTCATATCCAGACTACTACGAAATGGGGTCCGCTCGCTGTGT	1776
Db	1023	ACCTCAGGGCCCATGATATAGTTCATATCCAGACTACTACGAAATGGGGTCCGCTCGCTGTGT	1062
OY	1777	CCGGTTTCCAGGCCCTGGATGTCTCCCTCCGCTGACAGGGCCCTTCTGATCTCGGTGACG	1836
Db	1063	-----TGACG	1063
OY	1837	TCTTCTTGGGAGACTATATGTGGCGCTCTTCACCCGCGGGGACATGAAAGCAGCGCCGGG	1896
Db	1068	TCTTCTTGGGAGACTATATGTGGCGCTCTTCACCCGCGGGGACATGAAAGCAGCGCCGGG	1127
OY	1897	TGGGCTTGGGCGCGGCTTCGACCTGCGGAGCGGACCTGATGGGGAGAGACTGCGCAGG	1956
Db	1128	TGGGCTTGGGCGCGGCTTCGACCTGCGGAGCGGACCTGATGGGGAGAGACTGCGCAGG	1187
OY	1957	CGCAGTTTCCCGGGGTGACGCCCAAGTGAAGCGCATGCGCAGCGGGTGGTTCGCGAGGTCC	2016
Db	1188	CGCAGTTTCCCGGGGTGACGCCCAAGTGAAGCGCATGCGCAGCGGGTGGTTCGCGAGGTCC	1247
OY	2017	TGCTACCCAGTAAATTCACATATTTCATTTGAAAAAATAAAAAA	2060
Db	1248	TGCTACCCAGTAAATTCACATATTTCATTTGAAAAAATAAAAAA	1291

RESULT 6  
US-09-387-413-4  
Sequence 4, Application US/09387413  
Patent No. 6475485  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
Coleman, Roger  
TITLE OF INVENTION: TWO NOVEL HUMAN CATHESPIN PROTEINS  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: PASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/387,413  
FILING DATE: 31-Aug-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/080,538  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0125 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166

```
? : TELEX: <Unknown>  
? : INFORMATION FOR SEQ ID NO: 4:  
? : SEQUENCE CHARACTERISTICS:  
? : LENGTH: 1299 base pairs  
? : TYPE: nucleic acid  
? : STRANDEDNESS: single  
? : TOPOLOGY: linear  
? : MOLECULE TYPE: cDNA  
? : HYPOTHEetical: NO  
? : ANTI-SENSE: NO  
? : FRAGMENT TYPE: <Unknown>  
? : ORIGINAL SOURCE:  
? : IMMEDIATE SOURCE:  
? : LIBRARY: LUNGNOT02  
? : CLONE: 312099  
? :  
? : SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-387-413-4
```

```
Query Match          58.2%; Score 1199.2; DB 4; Length 1299;  
Best Local Similarity    94.3%; Pred. No. 0;  
Matches 1286; Conservative   0; Mismatches   3; Indels   75; Gaps   1;
```

QY	697	ACGCGTCCCAAGCATGTCTTCACCACCGCTGCCTGCAACCCCCTCCTGCTGCTGCCCTC	756
Db	3	ACGGCTCCGAAGCATGTCTTCACACCGCTGCCTGCAACCCCCTCCTGCTGCTGCCCTC	62
QY	757	TGCTGAATGTGAGAACCTTTCCGGGGGSCAACAATGATCCGCATCCCTTCATCGATGCCAAAC	816
Db	63	TGCTGAATGTGAGAACCTTTCCGGGGGSCAACAATGATCCGCATCCGCATCCCTTCATCGATGCCAAAC	122
QY	817	CTGAGCACGAGAACCTTGTAACCTACTGAGGGGATGAGAAGAACGACAGAGCTCCCCAAGT	876
Db	123	CTGAGCACGAGAACCTTGTAACCTACTGAGGGGATGAGAAGAACGACAGAGCTCCCCAAGT	182
QY	877	TGGGGGGCCCATCCCTGGGGGACAAAGCCATCTCGTAGCTCTGTCCAACCTACAGGGATG	936
Db	183	TGGGGGGCCCATCCCTGGGGGACAAAGCCATCTGTGAGCTCTGTCCAACCTACAGGGATG	242
QY	937	TGCAGATTATTTTTGGGGAATAATGGGCTGGGAAAGCCCTCCACAAAACCTTCACTGTTCCTTTG	996
Db	243	TGCAGATTATTTTTGGGGAATAATGGGCTGGGAAAGCCCTCCACAAAACCTTCACTGTTCCTTTG	302
QY	997	ACATGTGGCTCTCCCAAATCTCTGGGCTCCCGTCAGAGAGATGCCACTTCTTCAAGTGTGCCCT	1056
Db	303	ACATGTGGCTCTCCCAAATCTCTGGGCTCCCGTCAGAGAGATGCCACTTCTTCAAGTGTGCCCT	362
QY	1057	GCTGGTTACACACACGCAATTTGATGCCAAAGCCTTAGCTCCCTTCAGAGCCAAATGGAGCA	1116
Db	363	GCTGGTTACACACACGCAATTTGATGCCAAAGCCTTAGCTCCCTTCAGAGCCAAATGGAGCA	422
QY	1117	AGTTTGCATTCAAATATGGAACCTGGGGGGGTAGATGAGAAATCCTTGAGGAGACAAGCTGA	1176
Db	423	AGTTTGCATTCAAATATGGAACCTGGGGGGGTAGATGAGAAATCCTTGAGGAGACAAGCTGA	482
QY	1177	CTATTGGGGAATCOAAGGTCATCAGATGATTTCCGGGAGGCGCTCGGGGAGGCCACGCC	1236
Db	483	CTATTGGGGAATCOAAGGTCATCAGATGATTTCCGGGAGGCGCTCGGGGAGGCCACGCC	542
QY	1237	TGGTCTTCGCTTTTGGCCATTTTGATGGGATATTTGGGCTCTCGATTTTCCATTTCTGTCGT	1296
Db	543	TGGTCTTCGCTTTTGGCCATTTTGATGGGATATTTGGGCTCTCGATTTTCCATTTCTGTCGT	602
QY	1297	TGGAAGGAGTTTCGGGCCCCCCATGATGTACTGTGTGTGAGACAGGGGCTATTTGATATAAGCTTG	1356
Db	603	TGGAAGGAGTTTCGGGCCCCCCATGATGTACTGTGTGTGAGACAGGGGCTATTTGATATAAGCTTG	662
QY	1357	TCTTCTCTCTTTTACCTCAACAGGAGACCTTGAAAGGCTGATGAGAGAGAGTGGTCTCGG	1416
Db	663	TCTTCTCTCTTTTACCTCAACAGGAGACCTTGAAAGGCTGATGAGAGAGAGTGGTCTCGG	722
QY	1417	GGGGCTCGAGACCGGGCACACTACATCCACCCTCTACCTTGTGTCCAGTCAGGTTCCCTG	1476
Db	723	GGGGCTCGAGACCGGGCACACTACATCCACCCTCTACCTTGTGTCCAGTCAGGTTCCCTG	782



```

QY      1477 CCTACATGGCAGATCCCATATGAGAGGTGTGAAGAAGGGGCCCGACGAGGCCTCACTCTGTGTGACA   1536
Db      783 CCTACTATGGCAGATCCCATATGAGAGGTGTGAAGAAGGGGCCCGACGAGGCCTCACTCTGTGTGACA   842
QY      1537 AGGGCTGTGCTGGCCATCTTGATATCGGGGCAAGCTTCATCACAGAACCCACTGAGAGA   1596
Db      843 AGGGCTGTGCTGGCCATCTTGATATCGGGGCAAGCTTCATCACAGAACCCACTGAGAGA   902
QY      1597 TCCGGGCCCCGTGATGACGACATTGGGGAAATCCCCTTGTGTGCTGGGGAGTATCATATCC   1656
Db      903 TTCGGGGCCCCGTGATGACGACATTGGGGAAATCCCCTTGTGTGCTGGGGAGTATCATATCC   962
QY      1657 TGATGCTGGGAATCCCAAAGTCCCGCAGATCTCTTCCTTTGCTTGGGGGGGTCTGGTTTA   1716
Db      963 TGATGCTGGGAATCCCAAAGTCCCGCAGATCTCTTCCTTTGCTTGGGGGGGTCTGGTTTA   1022
QY      1717 ACCTCACAGGCCCCATGATATTAGTCTCATCCAGACTCTGAAAATGCGCTCCGCCCTTGTGT   1776
Db      1023 ACCTCACAGGCCCCATGATATTAGTCTCATCCAGACTCTGAAA-----   1062
QY      1777 CCGGTTTCCAGGCCCTTGATATGTCCTTCGCCCTGACAGGCCCTTGTGATCTCGGTAGC   1836
Db      1063 -----TGACG   1067
QY      1837 TCTTCTTTGGGAGCATATGTGTGGCCGCTTTTCGACCGCGGGAGCATGAAGACGACGCCCGGG   1896
Db      1068 TCTTCTTTGGGAGCATATGTGTGGCCGCTTTTCGACCGCGGGAGCATGAAGACGACGCCCGGG   1127
QY      1897 TGGGCTGTGGCGCGGCTCGCATCTCGGAGCGGAGCGACTCGATGTGGGAGAGACTCGCAGG   1956
Db      1128 TTGGGCTGTGGCGCGGCTCGCATCTCGGAGCGGAGCGACTCGATGTGGGAGAGACTCGCAGG   1187
QY      1957 CGCAGTTTCCCCGGGTGAGCCCCAAGTAGAAGCGCATGCGCACCGGGGTGTGCGCGGAGATCC   2016
Db      1188 CGCAGTTTCCCCGGGTGAGCCCCAAGTAGAAGCGCATGCGCACCGGGGTGTGCGGAGATCC   1247
QY      2017 TGTATACCAGTAATAATTCACATATTTCATTTGAAAAA          2060
Db      1248 TGCTATCCAGTAATAATTCACATATTTCATTTGAAAAAAAA          1291

RESULT 7
US-08-974-691-1
; Sequence 1, Application us/08974691
; Patent No. 6225103
GENERAL INFORMATION:
APPLICANT: Keolsch, Gerald
APPLICANT: Lin, Xinli
APPLICANT: Tang, Jordan
TITLE OF INVENTION: Cloning and Characterization of Napsin
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patricia L. Pabst
STREET: 2800 One Atlantic Center, 1201 W. Peachtree
STREET: St.
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,691
FILING DATE: 20-NOV-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,196
FILING DATE: 20-NOV-1996
PRIOR APPLICATION DATA:

```

	APPLICATION NUMBER:	US 60/046,126
	FILING DATE:	09-MAY-1997
	ATTORNEY/AGENT INFORMATION:	
	NAME:	Pabst, Patricia L.
	REGISTRATION NUMBER:	31,284
	REFERENCE/DOCKET NUMBER:	OMR# 166
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE:	404-873-8794
	TELEFAX:	404-873-8795
	INFORMATION FOR SEQ ID NO:	1:
	SEQUENCE CHARACTERISTICS:	
	LENGTH:	1353 base pairs
	TYPE:	nucleic acid
	STRANDEDNESS:	single
	TOPOLOGY:	linear
	MOLECULE TYPE:	cDNA
	HYPOTHETICAL:	NO
	ANTI-SENSE:	NO
	ORIGINAL SOURCE:	
	ORGANISM:	Homo sapiens
	UN-08-974-691-1	
	Query Match	55.4%; Score 1142; DB 3; Length 1353;
	Best Local Similarity	90.9%; Pred. No. 4.1e-310;
	Matches 1227; Conservative	0; Mismatches 120; Indels 3; Gaps 1;
OY	711 ATGTCACACCACCGCTGCTGCACAACCCCTGTGCTGCTGCTGCTGCTGAATGTGGAG	770
Db	1 ATGTCACACCACCGCTGCTGCTAACCCTTGTGCTGCTGCTGCTGCTGAATGTGGAG	60
OY	771 CCTTCGGGGGCCAACACATCATCCTGCATCCCTTGATGAGTCAACCTCGAGGACGAGAC	830
Db	61 CCGTCGGGGGCCAACACTGATCCGATCCGATCCCTTTGTCAAGTCCACCCCTGGAGGACG	120
OY	831 CTGAACCTCACAGAGGGGATGAGAGAACACAGACAGCTCCCAAGTTGGGGCCCCATCC	890
Db	121 CTGAACCTCACAGAGGGGATGAGAGAAACACAGACAGCTCCCAAGTTGGGGCCCCATCC	180
OY	891 CCTGGGGCAAAGCCCATTTGTACTCTCTCGAATCACAGGATGTGCAATATTTTGGG	950
Db	181 CCTGGGGCAAAGCCCTGCTCGGTACCTCTCCAAATTCGAGATGCCCAGTAATTTTGGG	240
OY	951 GAAATGGGGCTGGGAAAGCTCTCCAAAATCTGTTGCTTTGACATGGCTCTCC	1010
Db	241 GAAATGGGGCTGGGAAAGCTCTCCAAAATCTGTTGCTTTGACATGGCTCTCC	300
OY	1011 AATCTGTGGTCCGCTCCAGAGATGCCATTTCTTAGTGTGCCCTGCTGTACACCAAC	1070
Db	301 AATCTGTGGTCCGCTCCAGAGATGCCATTTCTTAGTGTGCCCTGCTGTACACCAAC	360
OY	1071 CGATTGATGCCAAAGCCTTAGCTCCCTCCAGGCAATGGAGCAATTTGCCATTCAA	1130
Db	361 CGCTTCATCCCAATGCTTCCAAGTCTCTTCAAGCCCAATGGAGCAATTTGCCATTCAG	420
OY	1131 TATGAACTGGGCGGGTGAATGGAATCTCGACGAGAGCAAGCTGACTATTTGGTGAATC	1190
Db	421 TATGAACTGGGCGGGTGAATGGAATCTCGAGTGGAGCAAGCTGACTATTTGGTGAATC	480
OY	1191 AAGGTGATCAGTATTTTGGGGAGGCTCTGAGGAGCCCAAGCTGTGCTTGGCTTT	1250
Db	481 AAGGTGATCAGTATTTTGGGGAGGCTCTGAGGAGCTGAGCTGTGCTTCACTTT	540
OY	1251 GCCCATTTTGAATGGATATTTGGGCTCGGTTTTCCCATTTGCTGTGAGAAGATTTGG	1310
Db	541 TCCTGCGCCCGAATGGATATTTGGGCTCGGTTTTCCCATTTGCTGTGAGAAGATTTGG	600
OY	1311 CCCCGATGATGTAAGTGTGGAGACGGGGCTATTTGATTAAGCTGTCTCTCTTTTAC	1370
Db	601 CCCCGATGATGTAAGTGTGGAGACGGGGCTATTTGATTAAGCTGTCTCTCTTTTAC	660
OY	1371 CTCGAACAGGAGCCGAGAGACCTGATGGAAGAGAGCTGAGTCTGGGGGGCTCCGAGCCG	1430
Db	661 TTCGAACAGGAGCCGAGAGAGCTGATGGAAGAGAGCTGAGTCTGGGGGGCTCCGAGCCG	720



QY 1431 GCACACTACATCCACCCCTCAGCTTGTGTCAGTACAGGTCCTGCTACTGTCAGATC 1490  
 DB 721 GCACACTACATCCACCCCTCAGCTTGTGTCAGTACAGGTCCTGCTACTGTCAGATC 780  
 QY 1491 CACATGAGCGCTGTAAGTGGGCGCCAGGCTGACTCTCTGTCACCAAGGCTGTCTCC 1550  
 DB 781 CACATGAGCGCTGTAAGTGGGCGCCAGGCTGACTCTCTGTCACCAAGGCTGTCTCC 840  
 QY 1551 ATCTGTATGAGGAGCGCTCTCTATCATCAGACCCACTGAGAGATCCGGGCTGTAT 1610  
 DB 841 ATCTGTATGAGGAGCGCTCTCTATCATCAGACCCACTGAGAGATCCGGGCTGTAT 900  
 QY 1611 GCAGCCATGAGGAGATCCCTTGTGCTGGGAGTACATCATCTGTCTCGGAATC 1670  
 DB 901 GCAGCCATGAGGAGATCCCTTGTGCTGGGAGTACATCATCTGTCTCGGAATC 960  
 QY 1671 CCAAGCTCCCGGAGTCTCTCTTGTGGGGGGCTGTGTTAACTCAGCCCAT 1730  
 DB 961 CCAAGCTCCCGGAGTCTCTCTTGTGGGGGGCTGTGTTAACTCAGCCCAT 1020  
 QY 1731 GATTACGTATCAGACTACTGAAATGCGCTGCTGCTTGTCCGTTTCCAGGCC 1790  
 DB 1021 GATTACGTATCAGACTACTGAAATGCGCTGCTGCTTGTCCGTTTCCAGGCC 1080  
 QY 1791 CTGATGTCCTCCGCTGCAAGGGCCCTTGTGATCTGCTGACGCTTCTTGGGAGC 1850  
 DB 1081 TTGGACATCGCTGCTGCTGCAAGTACTGTGTGATCTGCTGAGACGTTTCTTGGGGAGC 1140  
 QY 1851 TATGTGCGCTCTTGTGACCGGGGGGACATGAAGACAGCCCGGGTGGCTGCGGCC 1910  
 DB 1141 TATGTGCGCTCTTGTGACCGGGGGGACATGAAGACAGCCCGGGTGGCTGCGGCC 1200  
 QY 1911 GCTGCACTCGCGGAGCGGACTGATGGGAGAGACTGCGACAGGCGAGTTCGCCGGG 1970  
 DB 1201 GCTGCACTCGCGGAGCGGACTGATGGGAGAGACTGCGACAGGCGAGTTCGCCGGG 1260  
 QY 1971 TGAGCCCAAGTGAAGCGCATGCGAGCGGCTGTGCGGAGGCTCTCTACCCAGTAA 2030  
 DB 1261 TGAGCCCAAGTGAAGCGCATGCGAGCGGCTGTGCGGAGGCTCTCTACCCAGTAA 1317  
 QY 2031 AATCCATATTTCATGAAAAA 2060  
 DB 1318 AATCCATATTTCATGAAAAA 1347

RESULT 8  
 US-09-705-448-4  
 ; Sequence 4, Application US/09705448  
 ; Patent No. 6432690  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, Hong  
 ; APPLICANT: Bruno, Sandra A.  
 ; APPLICANT: Eisenboss, Laura A.  
 ; APPLICANT: Fogliano, Michael  
 ; APPLICANT: Cohen, Victoria L.  
 ; APPLICANT: Bandman, Olga  
 ; TITLE OF INVENTION: HUMAN ASPARTIC PROTEASES  
 ; FILE REFERENCE: PF-0458-1 CIP  
 ; CURRENT APPLICATION NUMBER: US/09/705,448  
 ; CURRENT FILING DATE: 2000-11-02  
 ; PRIOR APPLICATION NUMBER: 09/116,641  
 ; PRIOR FILING DATE: 1998-07-16  
 ; PRIOR APPLICATION NUMBER: 09/008,271  
 ; PRIOR FILING DATE: 1998-01-16  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 4  
 ; LENGTH: 1329  
 ; TYPE: DNA  
 ; ORGANISM: HOMO SAPIENS  
 ; FEATURE:  
 ; OTHER INFORMATION: 2435410, EOSINOT03

US-09-705-448-4  
 Query Match 54.5%; Score 1122.6; DB 4; Length 1329;  
 Best Local Similarity 90.9%; Pred. No. 1,1e-304;  
 Matches 1194; Conservative 0; Mismatches 119; Indels 0; Gaps 0;  
 QY 697 ACGGCTCCCAAGCATGTCTCCACACCGCTGTCTGCAACCCCTGCTGTCTGCTGCTG 756  
 DB 17 ACGGCTCCCAAGCATGTCTCCACACCGCTGTCTGCAACCCCTGCTGTCTGCTGCTG 76  
 QY 757 TGCTGAATGTGAGCTCTCCGGGGGACACATGATCCGATCCCTTTATGAGTCAAC 816  
 DB 77 TGCTGAATGTGAGCTCTCCGGGGGACACATGATCCGATCCCTTTATGAGTCAAC 136  
 QY 817 CTGACGAGAGACCTGTAACCTACTGAGGGGATGAGAGAAACACAGAGCTCCCAAGT 876  
 DB 137 CTGACGAGAGACCTGTAACCTACTGAGGGGATGAGAGAAACACAGAGCTCCCAAGT 196  
 QY 877 TGGGGGGCCCATCCCTGCGGGGACAAGCCATCTTGTACTCTCTCTGCAATACAGGATG 936  
 DB 197 TGGGGGGCCCATCCCTGCGGGGACAAGCCATCTTGTACTCTCTCTGCAATACAGGATG 256  
 QY 937 TGCAATATTTTGGGAAATTTGGGCTGGGAGAGCCCTCCACAAATCTTCACTGTGCTT 996  
 DB 257 CCCAGTATTTTGGGAAATTTGGGCTGGGAGAGCCCTCCACAAATCTTCACTGTGCTT 316  
 QY 997 ACACGTGCTCCCAATCTCTGGTCCCGTCCAGAGATGACACTTCTTCACTGTGCTT 1056  
 DB 317 ACACGTGCTCCCAATCTCTGGTCCCGTCCAGAGATGACACTTCTTCACTGTGCTT 376  
 QY 1057 GCTGTTACACACCGATTTTGAATCCAAAGCCTCTAGCTCTCTTCCAGGCAATGGAGACA 1116  
 DB 377 GCTGTTACACACCGATTTTGAATCCAAAGCCTCTAGCTCTCTTCCAGGCAATGGAGACA 436  
 QY 1117 AGTTGCCATTCATATGAGTGGGCTGGGATGATGAAATCTGTAGGAGACAAGCTGA 1176  
 DB 437 AGTTGCCATTCATATGAGTGGGCTGGGATGATGAAATCTGTAGGAGACAAGCTGA 496  
 QY 1177 CTATGTGAGATCAAGGCTGATGATGATTTTGGGAGAGCTCTGTGGAGCCAGCC 1236  
 DB 497 CTATGTGAGATCAAGGCTGATGATGATTTTGGGAGAGCTCTGTGGAGATTCAGCC 556  
 QY 1237 TGGTCTTGCTTTGCCATTTTGAATGGAGATTTGGGCTGCGGTTTCCATCTGTCTG 1296  
 DB 557 TGGTCTTGCTTTGCCATTTTGAATGGAGATTTGGGCTGCGGTTTCCATCTGTCTG 616  
 QY 1297 TGGAGAGATTCGGGCGCCGATGATGATGATGATGATGATGATGATGATGATGATG 1356  
 DB 617 TGGAGAGATTCGGGCGCCGATGATGATGATGATGATGATGATGATGATGATGATG 676  
 QY 1357 TCTTCTCTTTTACCTCAAGAGACCTGAAAGACCTGATGAGAGAGAGTGTCTG 1416  
 DB 677 TCTTCTCTTTTACCTCAAGAGACCTGAAAGAGAGAGTGTGTGTGTGTGTGTGTGTGT 736  
 QY 1417 GGGGCTCGAGCCCGGACACTACATCCACCCCTGACCTTGTGCTGAGTCCGCTG 1476  
 DB 737 GGGGCTCGAGCCCGGACACTACATCCACCCCTGACCTTGTGCTGAGTCCGCTG 796  
 QY 1477 CCTACTGCAATTCACATGAGGCTGAGAGTGGGCGCCAGGCTGACTCTGTGCA 1536  
 DB 797 CCTACTGCAATTCACATGAGGCTGAGAGTGGGCGCCAGGCTGACTCTGTGCA 856  
 QY 1537 AGGCTGTGCTGCAATTCCTGATGAGGAGCTGCTCATACAGAGACCTGAGAG 1596  
 DB 857 AGGCTGTGCTGCAATTCCTGATGAGGAGCTGCTCATACAGAGACCTGAGAG 916  
 QY 1597 TCCGGGCTGCTGCAATTCCTGATGAGGAGATCCCTTGTGCTGAGAGTACATATCC 1656  
 DB 917 TCCGGGCTGCTGCAATTCCTGATGAGGAGATCCCTTGTGCTGAGAGTACATATCC 976  
 QY 1657 TGTGCTGGAATTCCAAAAGCTCCCGGAGTCTCTCTTCTTGGGGGGGCTGTTTA 1716  
 DB 977 GGTGCTGGAATTCCAAAAGCTCCCGGAGTCTCTCTTCTTGGGGGGGCTGTTTA 1036







SEQUENCE CHARACTERISTICS:  
LENGTH: 2038 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: Double  
TOPOLOGY: Linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: No. 5968816 applicable  
ORIGINAL SOURCE:  
ORGANISM: homo sapiens  
SPRAIN: not applicable  
INDIVIDUAL ISOLATE: not applicable  
DEVELOPMENTAL STAGE: not applicable  
HAPLOTYPE: not applicable  
TISSUE TYPE: blood  
CELL TYPE: Luecocyte  
CELL LINE: HeLa  
ORGANELLE: not applicable  
IMMEDIATE SOURCE:  
LIBRARY: not applicable  
CLONE: not applicable  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: not applicable  
MAP POSITION: not applicable  
UNITS: not applicable  
FEATURE:  
NAME/KEY: This is the DNA sequence  
NAME/KEY: claimed in 15(v1) as the Cathepsin gene in FIG. 15.  
LOCATION: not available  
IDENTIFICATION METHOD: experiment-  
OTHER INFORMATION: prevention of IFN-2  
OTHER INFORMATION: promoted cell death  
PUBLICATION INFORMATION: not available  
us-08-631-097-7

Query Match 15.4%; Score 316.6; DB 2; Length 2038;  
Best Local Similarity 57.9%; Pred. No. 1.1e-78;  
Matches 602; Conservative 0; Mismatches 404; Indels 33; Gaps 1;  
QY 878 GGGGGCCCCATCCCTGGGGAGAACCCATCTTGTACTCTCTGGAACCTACAGGAGT 937  
DB 222 GGGGGTCCAGCCGTGACCGAGGGGCCATTCGCCGAGGTCTCAAGAACTACATGAGCG 281  
QY 938 GCAGATTTTGGGAAATTGGGCTGGGAAGCGCTCCACAAAACCTACAGTTCCTTGA 997  
DB 282 CCAGTACTACGGGAGATTGGCATCGGAGACGCCGCCCGACATGCTTCAAGTCTTGA 341  
QY 998 CACTGGCTCCCAATCTCTGGGTCCTCCAGGAGATGCCACTTCTTCAAGTGCCTG 1057  
DB 342 CACGGGCTCCCAACCTGTGGTCCCTCCATCCATGCAAACTGTGGAGCATGCTG 401  
QY 1058 CTGTGTACACACCGATTGATCCCAAGCCTTACTGCTCTTCCAGGCGCATGGACCA 1117  
DB 402 CTGATTCACCAAGTACCAAGGAGGACAGCAAGTCAACGTAAGTAAGTAAGTCA 461  
QY 1118 GTTGGCATTCATATGGAAGTGGGCGGGTAGATGAATCTGAGCAGGACAACTGA- 1176  
DB 462 GTTGGACATCCACATATGCTGGGCGAGCCTCTCCGGTAGCTGAGCCAGGACATGCTC 521  
QY 1177 -----CTATTGTGTAATCAAGGGTGCATCACT 1204  
DB 522 GGTGGCCTGCAAGTCAAGCGTGTACGCTGACCTGACCTGTGGCGGTGTCAAAATGAGAGCA 581  
QY 1205 GATTTTGGGAGAGCTCTCTGGGAGCCAGCCTGGTCTTCTGCTTTGGCCATTTGATGG 1264  
DB 582 GGTCTTTGGGAGGCGCACCAAGCAGGATCACTTCAATCGCAGCCAAAGTTTGATGG 641  
QY 1265 GATATTGGGCGCTGGTTTCCATCTGTCTGTGGAAGAGTGGGCGCCCGATGGATGT 1324  
DB 642 CATCTGGGAGGAGGCTTACCCCGCATCTCCGTCAACAACGTGCTGCGCGTCTTGACAA 701

QY 1325 ACTGTGAGACGAGGGGCTATTGATTAAGCCTCTCTCTTTTAACTCAACAGGAGACC 1384  
DB 702 CCTGATGACGAGAAAGTGTGGAGCAAGACATCTTCTCTTCACTGACGAGGAGACC 761  
QY 1385 TGAAGAGCCTGATGGAGAGAGCTGTCTGGGGGGCTCGGACCGGACACTCATGCC 1444  
DB 762 AGATGCGAGCCTGGGGGTGAGCTGATCTGGGTGGGACACAGATCCAAAGTATTCAGAGG 821  
QY 1445 ACCCTCACCTTCTGTCGACGACGAGTCCCTGCTACTGAGGACATCCATGAGAGCTGT 1504  
DB 822 TTTCTGTCTTACCTGATGTCACCCGCAAGGCCCTACTGGACAGTCCACCTGGACAGT 881  
QY 1505 GAAGTGGGCGGAGGCTGACTCTCTGTGCAAGGGCTGTGCTGCATCTGGATACGGG 1564  
DB 882 GGAGGTGGCCAGCGGCTGACCCGTGTGCAAGAGGGCTGTGAGGCCATTTGGACACAGG 941  
QY 1565 CACGTCCTCATACAGAGACCCACAGAGAAATCCGGGCCCTGCACTGAGCATTTGGGG 1624  
DB 942 CACTTCCCTCATGTGGGCGCGGTGGATGAGGTGGCGCAGCTGCGAAGGCCATCGGGGC 1001  
QY 1625 AATCCCTTGTGCTGGGAGATCATCATCTGCTGCGAATCCCAAGCTCCCGC 1684  
DB 1002 CGTGCCGCTGATTCAGGGCGAGTACATATCCCTGTGAGAAAGTGTCCACCTTCGCCG 1061  
QY 1685 AGTCTCTTCTCTTGGGGGGGCTGTGTTAACTCAAGGCCCATGATTAAGTACATCA 1744  
DB 1062 GATCACACTGAAGCTGGGAGGCAAAAGGCTTACAGCTGTCCCAAGAGCTACAGCTCA 1121  
QY 1745 GACTACTGGAATGGCGCTCCGCTCTGTCTGTGCGGTTTCCAGGCGCTGATGTCCCTCC 1804  
DB 1122 GGTGTGCGAGCGCGGGAAGACCTCTGCTGAGCGGCTTCAATGGGATGAGCATGCCCGC 1181  
QY 1805 GCCTTCAGGCGCTTCTGATCTCTGTGAGCTCTTCTTGGGAGATGATGGCCGCTT 1864  
DB 1182 ACCACAGGGGCGACCTGTGATCTGTGGGAGCTTCTTCAATCGGCCCTACTACATGCTGT 1241  
QY 1865 CGACCGCGGGGACATGAAG 1883  
DB 1242 TGACGCTGACAAACACAGG 1260

RESULT 14  
US-08-810-712-11  
; Sequence 11, Application US/088107126  
; Patent No. 6160106  
; GENERAL INFORMATION:  
; APPLICANT: Yeda Research and Development Co. Ltd  
; TITLE OF INVENTION: Tumor Suppressor Genes, Proteins Encoded Thereby and  
; FILE REFERENCE: sequence list  
; CURRENT APPLICATION NUMBER: US/08/810,7126  
; CURRENT FILING DATE: 1997-03-03  
; EARLIER APPLICATION NUMBER: PCT/US94/11598  
; EARLIER FILING DATE: 1994-10-12  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 2038  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
us-08-810-712-11  
Query Match 15.4%; Score 316.6; DB 3; Length 2038;  
Best Local Similarity 57.9%; Pred. No. 1.1e-78;  
Matches 602; Conservative 0; Mismatches 404; Indels 33; Gaps 1;  
QY 878 GGGGGCCCCATCCCTGGGGAGAACCCATCTTGTACTCTCTGGAACCTACAGGAGT 937  
DB 222 GGGGGTCCAGCCGTGACCGAGGGGCCATTCGCCGAGGTCTCAAGAACTACATGAGCG 281  
QY 938 GCAGATTTTGGGAAATTGGGCTGGGAAGCGCTCCACAAAACCTACAGTTCCTTGA 997  
DB 282 CCAGTACTACGGGAGATTGGCATCGGAGACGCCGCCCGACATGCTTCAAGTCTTGA 341

```

QY 998 CACTGCTCTCCATCTCTGGGTCGCCGACAGAGATGCCATCTTCACTGTGCTG 1057
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 342 CACGGGCTCCCAACCTGGGTCCCTCCATCCATCGCAAACTGCTGACATCGCTG 401
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1058 CTGGTTACACCGAATTGTGATCCCAAGGCTCTAGCTCTCTCCAGGCAATGGACCA 1117
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 402 CTGGATCCACCAAGATACACAGCGAGCAAGTCCAGACCTAGCTGAAGAAATGGTAC 461
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1118 GTTTCATTCATATATGAACTGGCGGGATGATGATGATCTGAGCAGCAAGCTGA- 1176
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 462 GTTTCATTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 521
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1177 -----CTATTGTGGAATCAAGGGTGCATCACT 1204
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 522 GTTTCATTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 581
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1205 GATTTTGGGGAGGCTCTGGGAGCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1264
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 582 GGTCTTTGGGGAGGCTCTGGGAGCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 641
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1265 GATATTTGGGGAGGCTCTGGGAGCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1324
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 642 CATCTCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 701
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1325 ACTGTGTGAGCAGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1384
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 702 CTTGATCAGCAGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 761
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1385 TGAAGAGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1444
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 762 AGATGAGCAGCTGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 821
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1445 ACCCTTCCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1504
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 822 TTTCTGTCTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 881
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1505 GAAGTGTGGGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1564
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 882 GGAAGTGTGGGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 941
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1565 CAGTGTCTCTATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1624
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 942 CACTTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1001
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1625 AATTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1684
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1002 CGTGTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1061
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1685 AGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1744
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1062 GATTCACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1121
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1745 GACTTACTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1804
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1122 GGTGTGTGCAAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1181
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1805 GCTGTGAGGCGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1864
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1182 ACCAGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1241
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1865 CGAGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1883
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1242 TGACCGGTGACACACACAGG 1260
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 100 Peachtree Street
; City: Atlanta
; STATE: Georgia
; COUNTRY: U.S.
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/08090
; FILING DATE: 19920922
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRF129
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-572-6508
; TELEFAX: 404-572-6555
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2465 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapien
; TISSUE TYPE: Epithelial
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..6
; OTHER INFORMATION: /note= "Restriction site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2460..2465
; OTHER INFORMATION: /note= "Restriction site"
PCT-US92-08090-1
Query Match 15.4%; Score 316.6; DB 5; Length 2465;
Best Local Similarity 57.9%; Pred. No. 1.2e-78;
Matches 602; Conservative 0; Mismatches 404; Indels 33; Gaps 1;
QY 878 GGGGGCCCCATCCCTGGGGAGCAAGCCCATCTTGTACCTCTCTCGAAGTACAGGATGT 937
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1391 GCGGCTGCGCCAGCGGTGACGAGAGGGGCCCATTCCTCAAGAGTACATGAGAGCG 1450
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 938 GCAGTATTTGGGGAATTTGGGCTGGGAGCGCTCCACAAATTCATCTGTTGCTTGA 997
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1451 CCAGTACTAGGGGAGATTGCAATCGGAGAGCGCCGCCCAAGTGTACAGTCTGTTGCA 1510
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 998 CACTGGCTCTCAATCTGCTGGGCTCCCGTCCAGAGATGCAATCTTCTGAGTGGCCCTG 1057
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1511 CACGGGCTCTCCAACTGTGGGTGCCCTCCTCAATCCATCGAAACTCTGACATCGCTTG 1570
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1058 CTGGTTACACCGAATTGTGATCCCAAGGCTCTAGCTCTTCCAGGCGCAATGGAGCA 1117
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1571 CTGGATCCACCAAGTACACAGCGACAAAGTCCAGCACCTTACGTAAAGATGTACTTC 1630
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1118 GTTTCATTCATATGAACTGGCGGGATGATGATGATGATGATGATGATGATGATGATG 1176
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1631 GTTTCATTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1690
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1177 -----CTATTGTGGAATCAAGGGTGCATCACT 1204
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1691 GTTTCATTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1750
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 15
PCT-US92-08090-1
; Sequence 1, Application PC/RUS9208090
; GENERAL INFORMATION:
; APPLICANT: Tang, J. N.
; TITLE OF INVENTION: Fusion Protein Genes for Treatment of
; TITLE OF INVENTION: Aids

```







GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OK nucleic - nucleic search, using sw model

Run on: October 9, 2003, 12:41:16 ; Search time 264.117 Seconds

(without alignments)  
9147.448 Million cell updates/sec

Title: US-09-700-770-5

Perfect score: 895  
Sequence: 1 ctaactcgttaacgtaacagc.....aataaataatttaaatgctc 895

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

N.Geneseq.19Jun03.\*  
1: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.\*  
2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.\*  
3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.\*  
4: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.\*  
5: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.\*  
6: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.\*  
7: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.\*  
8: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.\*  
9: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.\*  
10: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.\*  
11: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.\*  
12: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.\*  
13: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.\*  
14: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.\*  
15: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.\*  
16: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.\*  
17: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.\*  
18: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.\*  
19: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.\*  
20: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.\*  
21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.\*  
22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.\*  
23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*  
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*  
25: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	895	100.0	895	21	AAZ29726
2	895	100.0	895	22	AAH77949
3	895	100.0	1171	22	AAH77951
4	858	95.9	870	21	AAZ98202
5	856.4	95.7	1148	22	ABA09257
6	852	95.2	870	21	AAZ65001
7	852	95.2	870	22	AAZ45994
8	852	95.2	870	22	AAZ92070

9	852	95.2	870	22	AAZ44147
10	852	95.2	870	24	ABV73914
11	852	95.2	870	24	ABV74390
12	852	95.2	870	25	ACA57752
13	852	95.2	870	25	ACA58822
14	852	95.2	870	25	ACA60375
15	852	95.2	870	25	ACA63385
16	852	95.2	870	25	ABX98222
17	852	95.2	870	25	ABX98724
18	852	95.2	870	25	ACA05769
19	852	95.2	870	25	ABX97813
20	852	95.2	870	25	ABX80232
21	852	95.2	870	25	ABX80736
22	852	95.2	870	25	ABX81119
23	852	95.2	870	25	ABX90209
24	852	95.2	870	25	ABX77820
25	852	95.2	870	25	ABX78597
26	852	95.2	870	25	ABX79416
27	852	95.2	870	25	ABX75610
28	852	95.2	870	25	ABX76815
29	852	95.2	870	25	ABX64055
30	852	95.2	870	25	ABX16655
31	852	95.2	870	25	ABX17019
32	699	78.1	849	21	AAA08343
33	630	70.4	654	21	AAZ59829
34	525.8	58.7	533	22	AAZ68195
35	525.8	58.7	533	24	ABL64634
36	525.8	58.7	533	25	AAZ04354
37	525.8	58.7	533	25	ABX99386
38	445.2	49.7	511	19	AAZ69618
39	438.4	49.0	30709	24	ABK87217
40	414.8	46.3	419	24	ABL64634
41	362.4	40.5	365	20	AAZ04354
42	357	39.9	357	21	AAA08344
43	312	34.9	312	22	AAZ68125
44	312	34.9	312	24	ABK38036
45	312	34.9	312	25	ACA10365

#### ALIGNMENTS

RESULT 1  
AAZ29726  
ID AAZ29726 standard; DNA; 895 BP.  
XX  
AC AAZ29726;  
XX  
DT 27-MAR-2000 (first entry)  
XX  
DE Human lung specific gene-3.  
XX  
DE Human lung specific gene-3.  
XX  
KW Lung Specific Gene; LSG; human; diagnostic marker;  
XX prognosticate; lung cancer; diagnosis; ds.  
XX  
XX Homo sapiens.  
XX  
XX WO9960160-A1.  
XX  
XX 25-NOV-1999.  
PD  
XX  
XX 12-MAY-1999; 99WO-US10344.  
PF  
XX  
XX 21-MAY-1998; 98US-0086212.  
PR  
XX  
XX (DIAD-) DIADEXUS LLC.  
PA  
XX Yang F, Macina RA, Sun Y;  
PI  
XX WPI; 2000-116320/10.  
DR  
XX  
XX A new method for diagnosing, monitoring and staging lung cancer  
PT  
XX



```

QY 181 GCACCGACAGCTTCCGATGAAAGTCTAATCTCTCCCTCTCTCTGTGCTGCCACTAATG 240
    |||
DB 181 GCACCGACAGCTTCCGATGAAAGTCTAATCTCTCCCTCTCTCTGTGCTGCCACTAATG 240
QY 241 CTGATGTCATGCTCTCTAGCAGCCGTAATCCAGGGGTGCCAGAGGCCACAGGGCCGA 300
    |||
DB 241 CTGATGTCATGCTCTCTAGCAGCCGTAATCCAGGGGTGCCAGAGGCCACAGGGCCGA 300
QY 301 GGCAGAGCTTCTAGAGATGCTCCAGGAAGCGCCCAAGAAATGTAGTCAAGATTTGG 360
    |||
DB 301 GGCAGAGCTTCTAGAGATGCTCCAGGAAGCGCCCAAGAAATGTAGTCAAGATTTGG 360
QY 361 TTCCTGAGAGCCCGGAGAAAGAAATTCATGACAGTGTCTGGGCTGCCAAAGAGAGTGC 420
    |||
DB 361 TTCCTGAGAGCCCGGAGAAAGAAATTCATGACAGTGTCTGGGCTGCCAAAGAGAGTGC 420
QY 421 CCCTGTGATCATTTTCAAGGGCAATGTGAAGAAACACCAAGAGCCACAGCAAGAG 480
    |||
DB 421 CCCTGTGATCATTTTCAAGGGCAATGTGAAGAAACACCAAGAGCCACAGCAAGAG 480
QY 481 CCAAAACAGCATTTCCAGAGCCTGCGCAACAATTTCTCAACAATGTGAGCTAAGAAAGCTTT 540
    |||
DB 481 CCAAAACAGCATTTCCAGAGCCTGCGCAACAATTTCTCAACAATGTGAGCTAAGAAAGCTTT 540
QY 541 GCTCTGCTTTTGTAGAGCTCTGAGCGCCCACTCTTCAATTAACTTCAAGCTTCAAGCAAGA 600
    |||
DB 541 GCTCTGCTTTTGTAGAGCTCTGAGCGCCCACTCTTCAATTAACTTCAAGCTTCAAGCAAGA 600
QY 601 AGCAGCTGAGCACTTACCAAGACACTCTTCTCTCCACCTCCACTCTCCACTGTACCC 660
    |||
DB 601 AGCAGCTGAGCACTTACCAAGACACTCTTCTCTCCACCTCCACTCTCCACTGTACCC 660
QY 661 ACCCCCTAAATTCATTCAGTGTCTCTCAAAAAGCATGTTTTCAGATCATTTTGTGTTG 720
    |||
DB 661 ACCCCCTAAATTCATTCAGTGTCTCTCAAAAAGCATGTTTTCAGATCATTTTGTGTTG 720
QY 721 CTCTCTCTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
    |||
DB 721 CTCTCTCTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
QY 781 TAGGCTTAATTCCTGAAGATTCAGGAAGCTGTAGCTTCCAGTAGTGTGATTTAAC 840
    |||
DB 781 TAGGCTTAATTCCTGAAGATTCAGGAAGCTGTAGCTTCCAGTAGTGTGATTTAAC 840
QY 841 CTTAAATGCAATTCAGGAAGTACCAAGTCAATTAATTTTAAATGTC 895
    |||
DB 841 CTTAAATGCAATTCAGGAAGTACCAAGTCAATTAATTTTAAATGTC 895

RESULT 3
AAH77951
ID AAH77951 standard; DNA; 1171 BP.
AC AAH77951;
XX
XX 13-NOV-2001 (first entry)
DE Nucleotide sequence of a human Lng104 polypeptide.
XX
XX Human; Lung cancer specific gene; LSG; Lng104; Lung cancer; SS.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT 217..576
XX FT /tag= a
XX FT /product= "Lng104"
XX
XX PD 23-AUG-2001.
XX
XX PF 20-FEB-2001; 2001MO-US05674.

```

```

XX 17-FEB-2000; 2000US-0183188.
PR
XX
XX (DIAD-) DIADEXUS INC.
PA
XX
XX Chen S, Sun Y, MacIra RA;
PI
XX
XX WPI; 2001-529917/58.
DR
XX
XX P-PSDB; AAG63977.
PT
XX
XX New Lung cancer specific gene for the treatment and diagnosis of Lung
XX cancer -
XX
XX Claim 1: Page 117; 119pp; English.
CC
XX
XX The present sequence represents a human lung cancer specific gene
CC (LSG), and encodes a polypeptide designated Lng104. LSGs are useful
CC in the treatment and diagnosis of lung cancer. The treatment of lung
CC cancer comprises the administration of a molecule which down regulates
CC the expression of an LSG. An immune response can be mounted against a
CC target cell expressing an LSG. Identification of potential therapeutic
CC agents for use in imaging and treating lung cancer which comprises
CC screening molecules for an ability to bind to or decrease expression
CC of an LSG relative to LSG in the absence of the agent where the ability
CC of a molecule to bind to the LSG or decrease expression of the LSG is
CC indicative of the molecule being useful in imaging and treating lung
CC cancer.
XX
SQ Sequence 1171 BP; 333 A; 320 C; 225 G; 293 T; 0 other;
Query Match 100.0%; Score 895; DB 22; Length 1171;
Best Local Similarity 100.0%; Pred. No. 1.8e-270;
Matches 895; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTATATCTGTACCTAAACAGACAGACAGCTACCTGCTGTCGCCCTCAATAGGA 60
    |||
DB 22 CTATATCTGTACCTAAACAGACAGACAGCTACCTGCTGTCGCCCTCAATAGGA 81
QY 61 AGCCTGCGCTGGGACATAAAGACATAGACACACAGAGCTGAGATTCAGCTCATCTATCC 120
    |||
DB 82 AGCCTGCGCTGGGACATAAAGACATAGACACACAGAGCTGAGATTCAGCTCATCTATCC 141
QY 121 CAGGATTCAGAGAGCTTCAGCAGAGGAACTTCATTATATTTCTCAAGCAACTTACAGCT 180
    |||
DB 142 CAGGATTCAGAGAGCTTCAGCAGAGGAACTTCATTATATTTCTCAAGCAACTTACAGCT 201
QY 181 GCACCGACAGCTTCCGATGAAAGTCTAATCTCTCCCTCTCTCTGTGCTGCCACTAATG 240
    |||
DB 202 GCACCGACAGCTTCCGATGAAAGTCTAATCTCTCCCTCTCTCTGTGCTGCCACTAATG 261
QY 241 CTGATGTCATGCTCTCTAGCAGCCGTAATCCAGGGGTGCCAGAGGCCACAGGGCCGA 300
    |||
DB 262 CTGATGTCATGCTCTCTAGCAGCCGTAATCCAGGGGTGCCAGAGGCCACAGGGCCGA 321
QY 301 GGCAGAGCTTCTAGAGATGCTCCAGGAAGCGCGCAAGAAATGTAGTCAAGATTTGG 360
    |||
DB 322 GGCAGAGCTTCTAGAGATGCTCCAGGAAGCGCGCAAGAAATGTAGTCAAGATTTGG 381
QY 361 TTCCTGAGAGCCCGGAGAAAGAAATTCATGACAGTGTCTGGGCTGCCAAAGAGAGTGC 420
    |||
DB 382 TTCCTGAGAGCCCGGAGAAAGAAATTCATGACAGTGTCTGGGCTGCCAAAGAGAGTGC 441
QY 421 CCCTGTGATCATTTTCAAGGGCAATGTGAAGAAACACCAAGAGCCACAGCAAGAG 480
    |||
DB 442 CCCTGTGATCATTTTCAAGGGCAATGTGAAGAAACACCAAGAGCCACAGCAAGAG 501
QY 481 CCAAAACAGCATTTCCAGAGCCTGCGCAACAATTTCTCAACAATGTGAGCTAAGAAAGCTTT 540
    |||
DB 502 CCAAAACAGCATTTCCAGAGCCTGCGCAACAATTTCTCAACAATGTGAGCTAAGAAAGCTTT 561
QY 541 GCTCTGCTTTTGTAGAGCTCTGAGCGCCCACTCTTCAATTAACTTCAAGCTTCAAGCAAGA 600
    |||
DB 562 GCTCTGCTTTTGTAGAGCTCTGAGCGCCCACTCTTCAATTAACTTCAAGCTTCAAGCAAGA 621

```



|||||  
 Db 661 TTTCAGATCATTTGTTGGTCTCTAGTCTTCTCTCTGCACTTACGCC 720  
 OY 758 TGTGGCTTCCCTTACCCAGGCTTACCTTAACTGAAAGTCCAGAACTGAG 817  
 Db 721 TGTGGCTTCCCTTACCCAGGCTTACCTTAACTGAAAGTCCAGAACTGAG 780  
 OY 818 CTTCCTAGCTAGTGTCTTAACTTAAATGCAATCAGAAAGTCAAGATCA 877  
 Db 781 CTTCCTAGCTAGTGTCTTAACTTAAATGCAATCAGAAAGTCAAGATCA 840  
 OY 878 TAAATATTTTAAATGTC 895  
 Db 841 TAAATATTTTAAATGTC 858  
 RESULT 5  
 ABA09257  
 ID ABA09257 standard; cDNA, 1148 BP.  
 XX ABA09257;  
 AC  
 DT 11-JAN-2002 (first entry)  
 XX  
 DE Human TGC-440 homologue-encoding cDNA, SEQ ID NO:1033.  
 XX  
 KW Human; cytokine; cell proliferation; cell differentiation; growth factor;  
 KW haematopoiesis regulation; tissue growth; immunomodulator; actlyin;  
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;  
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;  
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;  
 KW chronic inflammatory condition; proliferative retinopathy;  
 KW atherosclerosis; coronary heart disease; arterial ischaemia;  
 KW bone disorder; osteoporosis; vascular growth disorder;  
 KW tissue regeneration; wound healing; infection; immune disorder;  
 KW cell culture; drug screening; gene therapy; antiinflammatory;  
 KW antiasthmatic; antiarthritis; haemostatic; antiatherosclerotic;  
 KW cytoskeletal; osteopathic; vasotropic; cardiant; virucide; antibacterial;  
 KW antifungal; vulnerary; antilucer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157188-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 05-FEB-2001; 2001WO-US03800.  
 XX  
 PR 03-FEB-2000; 2000US-0496914.  
 PR 27-APR-2000; 2000US-0560875.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Dymnac RT;  
 XX  
 DR WPI: 2001-457740/49.  
 DR P-PSDB: ABB12013.  
 XX  
 PT Human proteins and DNA encoding sequences useful for preventing,  
 PT treating or ameliorating a medical condition in a mammalian subject  
 PT e.g. arthritis and cancer -  
 PS  
 PS  
 XX Claim 1; Page 867-868; 1963bp; English.  
 CC Sequences ABA010981-ABA12330 represent 1350 novel human polypeptides, and  
 CC sequences ABA08225-ABA0574 represent nucleic acids encoding them. The  
 CC invention also relates to vectors and recombinant host cells comprising a  
 CC nucleotide of the invention, methods of producing the novel polypeptides,  
 CC antibodies against the polypeptides, methods of detecting the nucleotides  
 CC or polypeptides in a sample, and methods of identifying compounds which  
 CC bind to polypeptides of the invention. Although novel, many of the  
 CC polypeptides of the invention have homology to known proteins, thereby  
 CC giving an insight into their probable biological activities, and hence

potential therapeutic applications. The polypeptides of the invention may  
 CC have various activities, including cytokine, cell proliferation or cell  
 CC differentiation activities; stem cell growth factor activity;  
 CC haematopoiesis regulatory activity; tissue growth activity;  
 CC immunomodulatory activity; actlyin- or inhibin-related activities;  
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or  
 CC thrombolytic activities; receptor or ligand activities; or may be  
 CC involved in oncogenesis, cancer cell proliferation or metastasis.  
 CC Depending on their biological activities, polypeptides and nucleotides of  
 CC the invention are useful for preventing, treating or ameliorating medical  
 CC conditions, e.g., by protein or gene therapy. Such conditions include  
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell  
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),  
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,  
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal  
 CC vascular growth. Polypeptides involved with tissue regeneration and  
 CC repair (or nucleic acids encoding them) may be used to promote wound  
 CC healing (e.g., of burns, incisions and ulcers), while those with  
 CC immunomodulatory activities may be used in the treatment of viral,  
 CC bacterial and fungal infections in addition to immune disorders.  
 CC Polypeptides with growth factor activity may be used in cell cultures to  
 CC promote cell growth. For example, such polypeptides may be used to  
 CC manipulate stem cells in culture to give rise to neuroepithelial cells  
 CC that can be used to augment or replace cells damaged by illness,  
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides  
 CC may also be used in the diagnosis of the above conditions, and in drug  
 CC screening techniques. The present sequence represents a cDNA encoding a  
 CC novel human polypeptide of the invention.  
 XX  
 SQ Sequence 1148 BP; 328 A; 309 C; 222 G; 289 T; 0 other;

Query Match 95.7%; Score 856.4; DB 22; Length 1148;  
 Best local Similarity 99.9%; Pred. No. 2,5e-258;  
 Matches 857; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 38 CCTGTTCTGCGCCCTCAATGGAAGCGCTGCGACTTAAGATGACCAAGCGCTG 97  
 Db 23 CCTGTTCTGCGCCCTCAATGGAAGCGCTGCGACTTAAGATGACCAAGCGCTG 82  
 OY 98 AGTATCCGACCTGATGATCCCGCAGGGGATGAGAGCCCTCCAGCGGGAACCTTCATTA 157  
 Db 83 AGTATCCGACCTGATGATCCCGCAGGGGATGAGAGCCCTCCAGCGGGAACCTTCATTA 142  
 OY 158 TATTCCTCAAGCACTTACAGCTGCACGACAGTTGCGATGAAATTCATCTCTCC 217  
 Db 143 TATTCCTCAAGCACTTACAGCTGCACGACAGTTGCGATGAAATTCATCTCTCC 202  
 OY 218 TCTCTCTGTTGCTGCACTAATGCTGATGCTCTAGCAGCTGAATCCAGGGG 277  
 Db 203 TCTCTCTGTTGCTGCACTAATGCTGATGCTCTAGCAGCTGAATCCAGGGG 262  
 OY 278 TCGCCAGAGCCAGAGGGGACGAGCGAGCTTTCAGAGAGAGTCCAGAAAGCGGCG 337  
 Db 263 TCGCCAGAGCCAGAGGGGACGAGCGAGCTTTCAGAGAGAGTCCAGAAAGCGGCG 322  
 OY 338 AAGAATGTGATGCAAAAGATTGTTCTCTAGAGCCCGGAGAAATTCATGACAGTGT 397  
 Db 323 AAGAATGTGATGCAAAAGATTGTTCTCTAGAGCCCGGAGAAATTCATGACAGTGT 382  
 OY 398 CTGGGCTGCAAAAGAGCAGTGCCCTGTGATCATTTCAAGGGCATGTGAAGAAACNA 457  
 Db 383 CTGGGCTGCAAAAGAGCAGTGCCCTGTGATCATTTCAAGGGCATGTGAAGAAACNA 442  
 OY 458 GACACCAAAAGGCACACAGAAAGCAAAACAGCATTTCCAGAGCTGCCAGCAATTTCTCA 517  
 Db 443 GACACCAAAAGGCACACAGAAAGCAAAACAGCATTTCCAGAGCTGCCAGCAATTTCTCA 502  
 OY 518 AACATGTGAGTAGAAGCTTGTGCTGCTTTCAGAGAGTGTGAGGCGCCACACTTC 577  
 Db 503 AACATGTGAGTAGAAGCTTGTGCTGCTTTCAGAGAGTGTGAGGCGCCACACTTC 562  
 OY 578 CAATTAAACATTTCTGAGCCAGAAAGACAGTGAACACACTTACAGACACTTCTTCTCC 637  
 Db 562 CAATTAAACATTTCTGAGCCAGAAAGACAGTGAACACACTTACAGACACTTCTTCTCC 637



PR 11-AUG-1998; 98US-0096143.  
 PR 11-AUG-1998; 98US-0096146.  
 PR 12-AUG-1998; 98US-0096329.  
 PR 17-AUG-1998; 98US-0096757.  
 PR 17-AUG-1998; 98US-0096766.  
 PR 17-AUG-1998; 98US-0096768.  
 PR 17-AUG-1998; 98US-0096773.  
 PR 17-AUG-1998; 98US-0096791.  
 PR 17-AUG-1998; 98US-0096867.  
 PR 17-AUG-1998; 98US-0096891.  
 PR 17-AUG-1998; 98US-0096894.  
 PR 17-AUG-1998; 98US-0096895.  
 PR 17-AUG-1998; 98US-0096897.  
 PR 18-AUG-1998; 98US-0096949.  
 PR 18-AUG-1998; 98US-0096950.  
 PR 18-AUG-1998; 98US-0096959.  
 PR 18-AUG-1998; 98US-0096960.  
 PR 18-AUG-1998; 98US-0097022.  
 PR 19-AUG-1998; 98US-0097141.  
 PR 20-AUG-1998; 98US-0097218.  
 PR 24-AUG-1998; 98US-0097651.  
 PR 26-AUG-1998; 98US-0097951.  
 PR 26-AUG-1998; 98US-0097952.  
 PR 26-AUG-1998; 98US-0097954.  
 PR 26-AUG-1998; 98US-0097955.  
 PR 26-AUG-1998; 98US-0097971.  
 PR 26-AUG-1998; 98US-0097974.  
 PR 26-AUG-1998; 98US-0097978.  
 PR 26-AUG-1998; 98US-0097979.  
 PR 26-AUG-1998; 98US-0097986.  
 PR 26-AUG-1998; 98US-0098014.  
 PR 31-AUG-1998; 98US-0098525.  
 PR 16-SEP-1998; 98US-0100634.  
 PR 12-JAN-1999; 99US-0115565.  
 XX  
 PA (GENE) GENENTECH INC.  
 XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
 PI Wood WI, Yuan J;  
 XX  
 DR WPI: 2000-072883/06.  
 DR P-PSDB: AAY66668.  
 XX  
 PS Membrane-bound proteins and related nucleotide sequences -  
 XX Claim 2; Fig 98; 822pp; English.

CC The invention provides membrane-bound PRO polypeptides and  
 CC polynucleotides encoding them. The PRO sequences of the invention were  
 CC identified based on extracellular domain homology screening. The PRO  
 CC sequences have homology with proteins including LDL receptors, the  
 CC ligands and various enzymes. The membrane-bound proteins and receptor  
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
 CC immunoadhesins, for instance, can be used as therapeutic agents to block  
 CC receptor-ligand interactions. The membrane-bound proteins can also be  
 CC employed for screening of potential peptide or small molecule inhibitors  
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
 CC are useful as hybridization probes, in chromosome and gene mapping and in  
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
 CC will also be useful for the preparation of PRO polypeptides, especially  
 CC by recombinant techniques.

XX Sequence 870 BP; 251 A; 237 C; 176 G; 206 T; 0 other;

Query Match 95.2%; Score 852; DB 21; Length 870;

Best Local Similarity 100.0%; Pred. No. 5.1e-257; Mismatches 0; Indels 0; Gaps 0;

QY 44 CTCGCCCTCAATGGAACGCTGGCTGAGCTAAAGATACACACGAGCTGAGTATC 103  
 DB 1 CTCGCCCTCAATGGAACGCTGGCTGAGCTAAAGATACACACGAGCTGAGTATC 60  
 QY 104 CTGACCTGATCATCCCAAGGATACAGAGCTCCAGCAGGAACTTCATTATTTCT 163

DB 61 CTGACCTGATCATCCCAAGGATACAGAGCTCCAGCAGGAACTTCATTATTTCT 120  
 QY 164 TCACGAACCTTACAGCTGACGACGACAGTGGATGAAGTTTATTCCTCCCTCC 223  
 DB 121 TCACGAACCTTACAGCTGACGACGACAGTGGATGAAGTTTATTCCTCCCTCC 180  
 QY 224 TGTGTGCTGACCTAATGCTGATGTCATGCTCCTAGCAGCTGATCCAGGGTCGCA 283  
 DB 181 TGTGTGCTGACCTAATGCTGATGTCATGCTCCTAGCAGCTGATCCAGGGTCGCA 240  
 QY 284 GAGCCACAGGACCGAGGCGCAGCTTCTAGAGATGCTCAGAGAAAGGCGCAAGAT 343  
 DB 241 GAGCCACAGGACCGAGGCGCAGCTTCTAGAGATGCTCAGAGAAAGGCGCAAGAT 300  
 QY 344 GTGAGTGCAGAAATGCTGCTCCGAGAGCCCCAGAGAAAGAAATTCATGACGTCTGGGC 403  
 DB 301 GTGAGTGCAGAAATGCTGCTCCGAGAGCCCCAGAGAAAGAAATTCATGACGTCTGGGC 360  
 QY 404 TGCAGAAAGAGCAGTGCCTGCTGATCATTTCAAGGGCAATGTGAAGAAACAGACACC 463  
 DB 361 TGCAGAAAGAGCAGTGCCTGCTGATCATTTCAAGGGCAATGTGAAGAAACAGACACC 420  
 QY 464 AAAGCAGCAGAGAAAGCCAAACAGCATTCAGAGCCTGCAGCAATTTCTCAACAAT 523  
 DB 421 AAAGCAGCAGAGAAAGCCAAACAGCATTCAGAGCCTGCAGCAATTTCTCAACAAT 480  
 QY 524 GTGAGTGCAGAAATGCTGCTCCGAGAGCCCCAGAGAAAGAAATTCATGACGTCTGGGC 583  
 DB 481 GTGAGTGCAGAAATGCTGCTCCGAGAGCCCCAGAGAAAGAAATTCATGACGTCTGGGC 540  
 QY 584 AACATTCTCAGCCAGAAAGACAGTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 643  
 DB 541 AACATTCTCAGCCAGAAAGACAGTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 600  
 QY 644 ACTCTCCACGCTACCCACCTTAATCATTCACAGTCTCTCAAAAAGCATGTTTTCAA 703  
 DB 601 ACTCTCCACGCTACCCACCTTAATCATTCACAGTCTCTCTCAAAAAGCATGTTTTCAA 660  
 QY 704 GATCATTTGTTGTTGCTCTCTCTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 763  
 DB 661 GATCATTTGTTGTTGCTCTCTCTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720  
 QY 764 CTCGCCCTTACCCAGGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 823  
 DB 721 CTCGCCCTTACCCAGGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 780  
 QY 824 ACCTAGTGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 883  
 DB 781 ACCTAGTGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 840  
 QY 884 TTTTAAATGTC 895  
 DB 841 TTTTAAATGTC 852

RESULT 7

AA545994 standard; cDNA; 870 BP.

AA545994;

18-DEC-2001 (first entry)

Human DNA encoding PRO polypeptide sequence #70.

PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;  
 dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
 blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
 adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;  
 PCR primer.  
 Homo sapiens.



XX WO200168848-A2.  
 XX  
 XX 20-SEP-2001.  
 XX  
 XX 28-FEB-2001; 2001WO-US06520.  
 XX  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 03-MAR-2000; 2000US-187202P.  
 PR 06-MAR-2000; 2000US-186968P.  
 PR 14-MAR-2000; 2000US-189320P.  
 PR 15-MAR-2000; 2000US-189328P.  
 PR 21-MAR-2000; 2000US-190828P.  
 PR 21-MAR-2000; 2000US-191007P.  
 PR 21-MAR-2000; 2000US-191048P.  
 PR 28-MAR-2000; 2000US-191314P.  
 PR 29-MAR-2000; 2000US-192655P.  
 PR 29-MAR-2000; 2000US-193032P.  
 PR 30-MAR-2000; 2000US-193053P.  
 PR 04-APR-2000; 2000WO-US08439.  
 PR 04-APR-2000; 2000US-194449P.  
 PR 11-APR-2000; 2000US-195975P.  
 PR 11-APR-2000; 2000US-196000P.  
 PR 11-APR-2000; 2000US-196187P.  
 PR 11-APR-2000; 2000US-196690P.  
 PR 18-APR-2000; 2000US-198121P.  
 PR 18-APR-2000; 2000US-198585P.  
 PR 25-APR-2000; 2000US-199397P.  
 PR 25-APR-2000; 2000US-199550P.  
 PR 03-MAY-2000; 2000US-199634P.  
 PR 03-MAY-2000; 2000US-201516P.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14941.  
 PR 30-MAY-2000; 2000WO-US15264.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 05-JUN-2000; 2000US-209832P.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 22-AUG-2000; 2000US-0644848.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000WO-US34956.  
 XX  
 PA (GENENTECH INC.  
 XX  
 PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL,  
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 WI: 2001-602746/68.  
 DR P-PSDB; AAU29093.  
 XX  
 PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
 PT presence of tumours, such as prostate and breast tumours, in mammals and  
 PT to screen for modulators of the compounds -  
 XX  
 XX Claim 2; Fig 139; 774pp; English.  
 PS  
 CC Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR  
 CC primers for PRO polypeptides of the invention. The sequences of the  
 CC invention can be used to detect the presence of a tumour in a mammal by  
 CC comparing the level of expression of a PRO polypeptide in a test sample  
 CC of cells from the animal and a control sample of normal cells, whereby a  
 CC higher level of expression in the test sample indicates the presence of a  
 CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,  
 CC pigs, goats and rabbits but are preferably human. The polypeptides can be  
 CC used to stimulate tumour necrosis factor (TNF) alpha release from human  
 CC blood, when contacted with it. A specific polypeptide can be used to  
 CC stimulate the proliferation or differentiation of chondrocyte cells. The  
 CC PRO proteins can be used to determine the presence of tumours and also

CC susceptibility to tumour development, particularly adrenal, lung, colon,  
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
 CC can be used for genetic analysis of individuals with genetic disorders.  
 XX  
 SQ Sequence 870 BP; 251 A; 237 C; 176 G; 206 T; 0 other;

Query Match 95.28; Score 852; DB 22; Length 870;  
 Best Local Similarity 100.00; Pred. No. 5.1e-257;  
 Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

44 CTCGCCCTCAAAATGGGAACGCTGCGCTGGAGCTAAACATAGACACAGGCTGAGATC 103  
 1 CTCGCCCTCAAAATGGGAACGCTGCGCTGGAGCTAAACATAGACACAGGCTGAGATC 60  
 QY 104 CTGACCTGAGTCATCCCGAGGATCAGAGCCTCCAGCAGGAACTTCCATTATATTC 163  
 DB 61 CTGACCTGAGTCATCCCGAGGATCAGAGCCTCCAGCAGGAACTTCCATTATATTC 120  
 QY 164 TCAAGCACTTACAGCTGACACCGACAGTGCATGGAAGTTCTATCTTCCCTCC 223  
 DB 121 TCAAGCACTTACAGCTGACACCGACAGTGCATGGAAGTTCTATCTTCCCTCC 180  
 QY 224 TGTTCCTGCACTAATGCTGATGTCATGCTCTCTAGACCTGAAATCCAGGGGTGCC 283  
 DB 181 TGTTCCTGCACTAATGCTGATGTCATGCTCTCTAGACCTGAAATCCAGGGGTGCC 240  
 QY 284 GAGGCCACAGGACCGGACGCTTGAAGATGCTCCAGAGGCGCCAGAAAT 343  
 DB 241 GAGGCCACAGGACCGGACGCTTGAAGATGCTCCAGAGGCGCCAGAAAT 300  
 QY 344 GTGAGTGCAGAAAGATTGTTCTCTGAGAGCCCCGGAAGAAATCATAGACAGTCTGGGC 403  
 DB 301 GTGAGTGCAGAAAGATTGTTCTCTGAGAGCCCCGGAAGAAATCATAGACAGTCTGGGC 360  
 QY 404 TGCCTAAAGAGAGTGCCTGATCATTTCAAGGCAATGGAAGAAACAAGACAC 463  
 DB 361 TGCCTAAAGAGAGTGCCTGATCATTTCAAGGCAATGGAAGAAACAAGACAC 420  
 QY 464 AAAGGACACAGAAAGGCAACAAACAGCTTCCAGACCTGCGCAATTTCTCAAAAT 523  
 DB 421 AAAGGACACAGAAAGGCAACAAACAGCTTCCAGACCTGCGCAATTTCTCAAAAT 480  
 QY 524 GTGAGTGAAGAACTTGTCTGCTCTTGTAGAGCTGAGGCGCCACTTCCAAATTA 583  
 DB 481 GTGAGTGAAGAACTTGTCTGCTCTTGTAGAGCTGAGGCGCCACTTCCAAATTA 540  
 QY 584 AACATTCTAGCCAAAGACAGTGCACACCTACACACTCTTCTCCACCTC 643  
 DB 541 AACATTCTAGCCAAAGACAGTGCACACCTACACACTCTTCTCCACCTC 600  
 QY 644 ACTCTCCACTGACACCCCTAAATCATTCAGTCCAGTCTCAAAAGATTTTTC 703  
 DB 601 ACTCTCCACTGACACCCCTAAATCATTCAGTCCAGTCTCAAAAGATTTTTC 660  
 QY 704 GATCATTTTGTGTTGCTCTCTCTAGAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 763  
 DB 661 GATCATTTTGTGTTGCT 720  
 QY 764 CTCGCCCTCAAAATGGGAACGCTGCGCTGGAGCTAAACATAGACACAGGCTGAGATC 823  
 DB 721 CTCGCCCTCAAAATGGGAACGCTGCGCTGGAGCTAAACATAGACACAGGCTGAGATC 780  
 QY 824 ACCTAGTGCATTTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 883  
 DB 781 ACCTAGTGCATTTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 840  
 QY 884 TTTTAAATGTC 895  
 DB 841 TTTTAAATGTC 852

RESULT 8



AA92070  
ID AAF92070 standard; cDNA; 870 BP.  
XX  
AC AAF92070;  
XX  
DT 15-MAY-2001 (first entry)  
XX  
DE Human PRO842 cDNA.  
XX  
KW Human; PRO protein; mapping; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200116318-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 24-AUG-2000; 2000MO-US23328.  
XX  
PR 01-SEP-1999; 99MO-US20111.  
PR 15-SEP-1999; 99MO-US21090.  
PR 07-DEC-1999; 99US-0169495.  
PR 09-DEC-1999; 99US-0170262.  
PR 11-JAN-2000; 2000US-0175481.  
PR 18-FEB-2000; 2000MO-US04341.  
PR 22-FEB-2000; 2000MO-US04342.  
PR 01-MAR-2000; 2000MO-US05601.  
PR 03-MAR-2000; 2000US-0187202.  
PR 25-APR-2000; 2000US-0199397.  
PR 22-MAY-2000; 2000MO-US14042.  
PR 05-JUN-2000; 2000US-0209832.  
XX  
XX  
PA (GENE) GENENTECH INC.  
XX  
PI Eaton DL, Flivatroff E, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi CJ, Gunney AL, Malanade CK, Wood WI;  
XX  
DR WPI; 2001-183260/18.  
DR P-PSDB; AAB87538.  
XX  
XX  
PT Eighty four nucleic acids encoding PRO polypeptides, useful in  
PT molecular biology, including use as hybridization probes, and in  
PT chromosome and gene mapping.  
XX  
PS Claim 2; Fig 25; 278bp; English.  
XX  
CC The present sequence is the coding sequence for a human PRO polypeptide  
CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO  
CC antagonists or anti-PRO antibodies are useful for preparation of a  
CC medicament useful in the treatment of a condition which is responsive to  
CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO  
CC protein may also be employed as molecular weight markers for protein  
CC electrophoresis. The PRO coding sequence has applications in molecular  
CC biology, including use as hybridisation probes, and in chromosome and  
CC gene mapping.  
XX  
SQ Sequence 870 BP; 251 A; 237 C; 176 G; 206 T; 0 other;

Query Match 95.2%; Score 852; DB 22; Length 870;  
Best Local Similarity 100.0%; Pred. No. 5.1e-257;  
Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 CTCGCCCTCAATGTGGAACGCTGGCTGGACTAAGCATAGACACAGCGCTGAGTATC 103  
DB 1 CTCGCCCTCAATGTGGAACGCTGGCTGGACTAAGCATAGACACAGCGCTGAGTATC 60  
QY 104 CTGACCTGAGTATCCAGGAGATCAGAGCCTCCAGCAGGAGACCTTCATTATATCT 163  
DB 61 CTGACCTGAGTATCCAGGAGATCAGAGCCTCCAGCAGGAGACCTTCATTATATCT 120  
QY 164 TCAAGCACTTACAGCTGACGACGAGATGTCGATGAAGTTCTTATCTTCCCTCTCC 223

DB 121 TCAAGCACTTACAGCTGACGACGAGATGTCGATGAAGTTCTTATCTTCCCTCTCC 180  
QY 224 TGTTCCTGCTCAATATGCTGATGTCATGCTGTCTAGACGCTGATCCAGGGGTCCCA 283  
DB 181 TGTTCCTGCTCAATATGCTGATGTCATGCTGTCTAGACGCTGATCCAGGGGTCCCA 240  
QY 284 GAGGCCACAGGAGCAGGAGCCAGGCTTCTAGAGATGCTCCAGGAGGCGCCCAAGAT 343  
DB 241 GAGGCCACAGGAGCAGGAGCCAGGCTTCTAGAGATGCTCCAGGAGGCGCCCAAGAT 300  
QY 344 GTGAGTGCAGAAATGTTGTTCTCTGAGACGCCCGCAGAAAGAAATTCATGACGTCTGGGC 403  
DB 301 GTGAGTGCAGAAATGTTGTTCTCTGAGAGGCCCGCAGAAAGAAATTCATGACGTCTGGGC 360  
QY 404 TGCCTAAGAGAGAGTGCCTGCTGATTCATTTCAAGGGCAATGTGAAGAAAGAACAGCACC 463  
DB 361 TGCCTAAGAGAGAGTGCCTGCTGATTCATTTCAAGGGCAATGTGAAGAAAGAACAGCACC 420  
QY 464 AAGGACACACAGAAAGCCAAACAGCATTCAGAGCCTGCCAGCAATTTCTCAACAAT 523  
DB 421 AAGGACACACAGAAAGCCAAACAGCATTCAGAGCCTGCCAGCAATTTCTCAACAAT 480  
QY 524 GTGAGCTAAGAAAGCTTTGCTGCTGCTTTGTAGAGCTGTGAGCCGCCACTCTTCCAATTA 583  
DB 481 GTGAGCTAAGAAAGCTTTGCTGCTGCTTTGTAGAGCTGTGAGCCGCCACTCTTCCAATTA 540  
QY 584 AACATTTCTCAGGCAAGAAAGAGTGTGAGCAGCAGCTCCAGACCTCTCTCCCAACCTC 643  
DB 541 AACATTTCTCAGGCAAGAAAGAGTGTGAGCAGCAGCTCCAGACCTCTCTCCCAACCTC 600  
QY 644 ACTCTCCACAGTGTACCCACCCCTTAATCATTCAGTGTCTCTCAAAAAGCATGTTTTTCA 703  
DB 601 ACTCTCCACAGTGTACCCACCCCTTAATCATTCAGTGTCTCTCTCAAAAAGCATGTTTTTCA 660  
QY 704 GATCATTTTGTGTTGCTGCTCTCTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 763  
DB 661 GATCATTTTGTGTTGCTGCTCTCTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720  
QY 764 CTCGCCCTTACCCAGGCTTGTGCTTAAATCTGTAAGATTCAGGAAACTGTAGCTGCT 823  
DB 721 CTCGCCCTTACCCAGGCTTGTGCTTAAATCTGTAAGATTCAGGAAACTGTAGCTGCT 780  
QY 824 ACCTAGTGTCTTAACTTAAATGCAATCAGAGAAAGTGAAGAGATCAATTAATA 883  
DB 781 ACCTAGTGTCTTAACTTAAATGCAATCAGAGAAAGTGAAGAGATCAATTAATA 840  
QY 884 TTTTAAATGTC 895  
DB 841 TTTTAAATGTC 852

RESULT 9  
AAF44147  
ID AAF44147 standard; cDNA; 870 BP.  
XX  
AC AAF44147;  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE Human PRO842 (UNQ473) nucleotide sequence SEQ ID NO:164.  
XX  
KW Human; secreted and transmembrane protein; PRO; cytosolic;  
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
KW diagnostic assay; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200073454-A1.  
XX  
PD 07-DEC-2000.  
XX  
PF 30-MAR-2000; 2000MO-US08439.

```

PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 17-AUG-1999; 99US-0148396.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 08-OCT-1999; 99US-0158663.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
XX
XX (GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
PI Ferrara N, Fong S, Gerber H, Gertlisen ME, Goddard A, Godowski PJ,
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NP,
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
XX Zhang Z;
XX WPI: 2001-032160/04.
XX P-PSDB; AAB65191.
XX
XX PRO polynucleotides used to produce polypeptides used to target
XX PT bioactive molecules such as toxins, radiolabels or antibodies, to
XX PT specific cells, to cause targeted cell death -
XX
XX Claim 2; Fig 98; 935pp; English.
XX
XX The present invention describes human secreted and transmembrane PRO
XX CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
XX CC can be used for targeted delivery of bioactive molecules, such as
XX CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
XX CC sequences, and their fragments, can be used as hybridisation probes, in
XX CC chromosomal and gene mapping, and in the generation of anti-sense RNA
XX CC and DNA. They may also be used to produce transgenic animals which are
XX CC used to develop and screen therapeutically useful reagents. The PRO
XX CC nucleotide and protein sequence can be used for tissue typing and in
XX CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
XX CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
XX CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
XX CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
XX CC sequences given in the exemplification of the present invention.
XX
XX Sequence 870 BP; 251 A; 237 C; 176 G; 206 T; 0 other;
XX
XX Query Match 95.28; Score 852; DB 22; Length 870;
XX Best Local Similarity 100.0%; Pred. No. 5,1e-257;
XX Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 44 CTGGCCCTCAAAATGGGAGACGCTGGGACCTAAAGCATAGACCAAGGCTGAGTATC 103
XX 1 CTGGCCCTCAAAATGGGAGACGCTGGGACCTAAAGCATAGACCAAGGCTGAGTATC 60
XX
XX 104 CTGACCTGATCATCCCGAGGATCGAGACCTCCAGCAGGGAACCTTCATTATTTCT 163
XX 61 CTGACCTGATCATCCCGAGGATCGAGACCTCCAGCAGGGAACCTTCATTATTTCT 120
XX
XX 164 TCAGCACTTACAGCTGCAGCAGACGTTGCATGAAGTTCTTATCTTCCCTCTCC 223
XX

```

```

Db 121 TCAAGCACTTACAGCTGCAGCAGACGAGTGGCATGAAGTTCTTCTTCCCTCC 180
QY 224 TGTTCGTCCCACTTAATGCTGATGTCATAGTCTCTAGCAGCTGAATCCAGGGTCCCA 283
Db 181 TGTTCGTCCCACTTAATGCTGATGTCATAGTCTCTAGCAGCTGAATCCAGGGTCCCA 240
QY 284 GAGCCACAGGAGCCAGGAGCCAGGCTTCTAGGATGCTCCAGGAAGGGGGCCAGAAAT 343
Db 241 GAGCCACAGGAGCCAGGAGCCAGGCTTCTAGGATGCTCCAGGAAGGGGGCCAGAAAT 300
QY 344 GTGAGTCAAGATTTGCTCTGAGAGCCCGGAGAGAAAATTCATGACAGTGTGAGGC 403
Db 301 GTGAGTCAAGATTTGCTCTGAGAGCCCGGAGAGAAAATTCATGACAGTGTGAGGC 360
QY 404 TGCCAAAGAGCAGTGGCCCGTGTGATCATTTCAAGGCGCATGTGAGAGAAAACAGACACC 463
Db 361 TGCCAAAGAGCAGTGGCCCGTGTGATCATTTCAAGGCGCATGTGAGAGAAAACAGACACC 420
QY 464 AAAGGACACAGAGAAAGCCAAACAGCATTCAGAGCTCCAGCAATTTCTCAACAAAT 523
Db 421 AAAGGACACAGAGAAAGCCAAACAGCATTCAGAGCTCCAGCAATTTCTCAACAAAT 480
QY 524 GTGAGCTAAGAGCTTTGCTCTGCTGCTTTGAGAGCTGTGAGGCCACCTTCAATTA 583
Db 481 GTGAGCTAAGAGCTTTGCTCTGCTTTGAGAGCTGTGAGGCCACCTTCAATTA 540
QY 584 AACATTCACAGCCAGAGACAGTGAAGACACCTTACAGACATCTTCTTCCACCTC 643
Db 541 AACATTCACAGCCAGAGACAGTGAAGACACCTTACAGACATCTTCTTCCACCTC 600
QY 644 AGCTCTCCAGCTGACCCACCCCTTAATTCATTCAGTGTCTCAAAAGATGTTTCA 703
Db 601 AGCTCTCCAGCTGACCCACCCCTTAATTCATTCAGTGTCTCAAAAGATGTTTCA 660
QY 704 GATCATTTTGTGTGTGCTCTCTCTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 763
Db 661 GATCATTTTGTGTGTGCTCTCTCTAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
QY 764 CTCCCTTACCCAGGCTTGAAGCTTAATTCCTGAAGATTCAGGAAGCTTGAAGCTCT 823
Db 721 CTCCCTTACCCAGGCTTGAAGCTTAATTCCTGAAGATTCAGGAAGCTTGAAGCTCT 780
QY 824 AGCTAGTGTCAATTAACCTTAATGAATCAGAGAAAGTGAAGCAAGAGTCAATTAATA 883
Db 781 AGCTAGTGTCAATTAACCTTAATGAATCAGAGAAAGTGAAGCAAGAGTCAATTAATA 840
QY 884 TTTTAAATGTC 895
Db 841 TTTTAAATGTC 852
XX
XX RESULT 10
XX ABV73914
XX ID ABV73914 standard; cDNA; 870 BP.
XX
XX AC ABV73914;
XX
XX 08-JAN-2003 (first entry)
XX
XX Human cytokine PRO842 (CK27) cDNA.
XX
XX PRO842; CK27; chemokine; human; antiinflammatory; dermatological;
XX KW hepatotropic; antiallergic; antiaesthetic; immunosuppressive;
XX KW antithyroid; antidiabetic; antinaemic; haemostatic; antipsoriatic;
XX KW antirheumatic; antiarthritic; nephrotropic; gene therapy; gene; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 153..512
XX FT
XX FT
XX sig_peptide 153..218

```



Human CDNA encoding secreted/transmembrane protein PRO842.  
 Human; ss; gene; secreted protein; transmembrane protein; antirheumatic;  
 anarthritic; osteopathic; sports-related joint problem;  
 articular cartilage defect; osteoarthritis; rheumatoid arthritis.  
 Homo sapiens.  
 US2002119130-A1.  
 29-AUG-2002.  
 06-DEC-2001; 2001US-0006867.  
 29-OCT-1997; 97US-063435P.  
 29-OCT-1997; 97US-064215P.  
 22-APR-1998; 98US-082797P.  
 29-APR-1998; 98US-083495P.  
 15-MAY-1998; 98US-085579P.  
 10-JUN-1998; 98US-088811P.  
 10-JUN-1998; 98US-088824P.  
 10-JUN-1998; 98US-088825P.  
 11-JUN-1998; 98US-089105P.  
 12-JUN-1998; 98US-089105P.  
 16-JUN-1998; 98US-089514P.  
 16-SEP-1998; 98WO-US19330.  
 08-MAR-1999; 99WO-US05028.  
 14-MAY-1999; 99WO-US10733.  
 02-JUN-1999; 99WO-US12252.  
 01-SEP-1999; 99WO-US20111.  
 15-SEP-1999; 99WO-US21050.  
 15-SEP-1999; 99WO-US21194.  
 22-DEC-1999; 99WO-US30720.  
 18-FEB-2000; 2000WO-US04341.  
 18-FEB-2000; 2000WO-US04342.  
 30-MAR-2000; 2000WO-US08439.  
 22-MAY-2000; 2000WO-US14042.  
 02-JUN-2000; 2000WO-US15264.  
 23-AUG-2000; 2000WO-US23352.  
 24-AUG-2000; 2000WO-US23352.  
 10-NOV-2000; 2000WO-US30873.  
 01-DEC-2000; 2000WO-US32378.  
 20-DEC-2000; 2000WO-US34956.  
 28-FEB-2001; 2001WO-US06520.  
 20-JUN-2001; 2001WO-US19652.  
 29-JUN-2001; 2001WO-US21066.  
 09-JUL-2001; 2001WO-US21735.  
 (GETH ) GENENTECH INC.  
 Eaton DL, Flivartoff E, Gerritsen ME, Goddard A, Godowski PJ;  
 Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
 P-PSDB; ABG95863.  
 PFI; 2002-731348/79.  
 New isolated secreted and transmembrane PRO polypeptide useful for  
 modulating biological activity of a cell, or for treating  
 sports-related joint problems, osteoarthritis or rheumatoid arthritis  
 Claim 2; Fig 25; 39pp: English.

or D/I polypeptide conjugate in the sample, where the formation of the  
 conjugate is indicative of the presence of an A, B, C or D polypeptide  
 in the sample, where A is a PRO10272 polypeptide, B is a PRO20110  
 polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide,  
 E is a PRO5801 polypeptide, F is a PRO1 polypeptide, G is a PRO1890  
 polypeptide, H is a PRO20233 polypeptide and I is a PRO1890  
 polypeptide. The sample comprises a cell suspected of expressing the A,  
 B, C or D polypeptide. The E, F, G, H or I polypeptide is labeled with  
 a detectable label or is attached to a solid support. The proteins are  
 useful for linking a bioactive molecule to a cell expressing a  
 polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive  
 molecule is a toxin, a radiolabel or an antibody. The bioactive molecule  
 causes death of the cell. A, B, C, D, E, F, G, H, or I, or antibodies  
 against them are useful for modulating a biological activity of a cell  
 expressing a polypeptide designated as A, B, C or D or E, F, G, H, or  
 I. The cell is killed. The proteins are useful for identifying  
 agonists or antagonists, for the preparation of a medicament useful in  
 the treatment of a condition which is responsive to the proteins, as  
 molecular weight markers for protein electrophoresis purposes, and as  
 therapeutic agents for treating sports-related joint problems,  
 articular cartilage defects, osteoarthritis or rheumatoid arthritis.  
 Nucleic acids encoding the proteins are useful as hybridisation probes,  
 in chromosome and gene mapping, in the generation of anti-sense RNA and  
 DNA, for the preparation of the proteins, to generate transgenic or  
 knockout animals which are useful in the development and screening of  
 therapeutic useful reagents, for chromosome identification, and in gene  
 therapy. The antibody is useful as a therapeutic agent, in a diagnostic  
 assay and for affinity purification of the protein from recombinant  
 cell culture natural sources. The present sequence encodes a novel  
 secreted or transmembrane protein of the invention.  
 Sequence 870 BP; 251 A; 237 C; 176 G; 206 T; 0 other;  
 Query Match 95.2%; Score 852; DB 24; Length 870;  
 Best Local Similarity 100.0%; Pred. NO. 5.1e-257;  
 Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 44 CTCGCCCTCAATGGGAACGCTGGCTGGGACCTAAGCATAGACACAGCTGAGTATC 103  
 DB 1 CTCGCCCTCAATGGGAACGCTGGCTGGGACCTAAGCATAGACACAGCTGAGTATC 60  
 QY 104 CTGACCTGATCATCCCGAGGATCAGAGACCTCCAGAGGAACTTCATTATATCT 163  
 DB 61 CTGACCTGATCATCCCGAGGATCAGAGACCTCCAGAGGAACTTCATTATATCT 120  
 QY 164 TCAAGCACTTACAGCTGCACGACAGTTCGATGGAAGTTCTAATCTTCCCTCC 223  
 DB 121 TCAAGCACTTACAGCTGCACGACAGTTCGATGGAAGTTCTAATCTTCCCTCC 180  
 QY 224 TGTTCCTGACCTAATGCTGATGTCATGCTCTAGACACCTGAATCCAGGGGTGCCA 283  
 DB 181 TGTTCCTGACCTAATGCTGATGTCATGCTCTAGACACCTGAATCCAGGGGTGCCA 240  
 QY 284 GAGGCCACAGGACCCGAGGCTTCTAGAGATGCTCCAGAGGCGGCAAGAT 343  
 DB 241 GAGGCCACAGGACCCGAGGCTTCTAGAGATGCTCCAGAGGCGGCAAGAT 300  
 QY 344 GTGAGTGCAGAAAGTTGCTTCTGAGAGCCCGAGAGAAATTCATGACAGTGTGGGC 403  
 DB 301 GTGAGTGCAGAAAGTTGCTTCTGAGAGCCCGAGAGAAATTCATGACAGTGTGGGC 360  
 QY 404 TGCAGAAAGAGAGTGCCTGTGATCATTTCAAGGCGCATGTGAAGAAACAAGACACC 463  
 DB 361 TGCAGAAAGAGAGTGCCTGTGATCATTTCAAGGCGCATGTGAAGAAACAAGACACC 420  
 QY 464 AAAGGCACACAGAGAAAGCAACAGACATTCAGAGCTCCAGCAATTTCTCAACAT 523  
 DB 421 AAAGGCACACAGAGAAAGCAACAGACATTCAGAGCTCCAGCAATTTCTCAACAT 480  
 QY 524 GTGAGTGAAGAACCTTGTGCTGCTGCTTGTAGAGAGCTCAGAGCCACTCTTCAATTA 583  
 DB 481 GTGAGTGAAGAACCTTGTGCTGCTGCTTGTAGAGAGCTCAGAGCCACTCTTCAATTA 540

PR	08-NOV-2000	2000MC-US30952
PR	01-DEC-2000	2000MC-US32678
PR	20-DEC-2000	2000MC-US34356
PR	28-FEB-2001	2001MC-US065620
PR	01-MAR-2001	2001MC-US178600
PR	20-JUN-2001	2001MC-US192160
PR	28-JUN-2001	2001MC-US210666
PR	09-AUG-2001	2001MC-US217099
PR	28-SEP-2001	2001MC-US270795
PR	18-SEP-1997	97US-0592853P
PR	18-SEP-1997	97US-0592856P
PR	17-OCT-1997	97US-0622520P
PR	21-OCT-1997	97US-063486P
PR	24-OCT-1997	97US-063120P
PR	24-OCT-1997	97US-063121P
PR	28-OCT-1997	97US-063540P
PR	28-OCT-1997	97US-063541P
PR	28-OCT-1997	97US-063544P
PR	28-OCT-1997	97US-063554P
PR	29-OCT-1997	97US-063734P
PR	31-OCT-1997	97US-063870P
PR	31-OCT-1997	97US-064103P
PR	13-NOV-1997	97US-065311P

## ACA57752

AC ACA57752;

Human PRO842 cDNA

KW differentiation; tumour; gene therapy; ss.

PN US2003036143-A1

PF 02-JUL-2002; 2002US-0187600.

PR 16-SEP-1998; 98WO-US193330.

PR 01-DEC-1998: 98WO-US25108

14-MAY-1999: 99WO-ITS10733

01-SEP-1999: 99WQ-11S20111

PR 01-DEC-1999: 99WO-NS28301

PR	02-DEC-1999;	99WO-US28531.
30-DEC-1999:		99WO-US31374
PR		

PR 03-JAN-2000; 2000WO-US00219.  
DB 18-FEB-2000; 2000FO-FS04341

PR 18-FEB-2000; 2000WO-US04342.

PR 24-FEB-2000; 2000WO-US05004.

PR 02-MAR-2000; 2000WO-US05841.

PR 30-MAR-2000; 2000WO-US08439.

PR 22-MAY-2000; 2000WO-US14042.

PR 02-JUN-2000; 2000WO-US15264.

PR : 24-AUG-2000; 2000WO-US233328.

PR : 24-AUG-2000; 2000WO-US23328.

PR 04-JUN-1998; 98US-088029P.  
 PR 04-JUN-1998; 98US-088033P.  
 PR 04-JUN-1998; 98US-088326P.  
 PR 05-JUN-1998; 98US-088167P.  
 PR 05-JUN-1998; 98US-088202P.  
 PR 05-JUN-1998; 98US-088212P.  
 PR 05-JUN-1998; 98US-088217P.  
 PR 09-JUN-1998; 98US-088535P.  
 PR 10-JUN-1998; 98US-088722P.  
 PR 10-JUN-1998; 98US-088738P.  
 PR 10-JUN-1998; 98US-088740P.  
 PR 10-JUN-1998; 98US-088811P.  
 PR 10-JUN-1998; 98US-088824P.  
 PR 10-JUN-1998; 98US-088825P.  
 PR 10-JUN-1998; 98US-088826P.  
 PR 11-JUN-1998; 98US-088861P.  
 PR 11-JUN-1998; 98US-088863P.  
 PR 11-JUN-1998; 98US-088909P.  
 PR 12-JUN-1998; 98US-088976P.  
 PR 12-JUN-1998; 98US-089090P.  
 PR 12-JUN-1998; 98US-089105P.  
 PR 16-JUN-1998; 98US-089512P.  
 PR 16-JUN-1998; 98US-089514P.  
 PR 17-JUN-1998; 98US-089538P.  
 PR 17-JUN-1998; 98US-089598P.  
 PR 18-JUN-1998; 98US-089653P.  
 PR 18-JUN-1998; 98US-089908P.  
 PR 19-JUN-1998; 98US-089952P.  
 PR 22-JUN-1998; 98US-090246P.  
 PR 22-JUN-1998; 98US-090252P.  
 PR 22-JUN-1998; 98US-090254P.  
 PR 24-JUN-1998; 98US-090429P.  
 PR 24-JUN-1998; 98US-090435P.  
 PR 24-JUN-1998; 98US-090444P.  
 PR 24-JUN-1998; 98US-090461P.  
 PR 24-JUN-1998; 98US-090535P.  
 PR 25-JUN-1998; 98US-090540P.  
 PR 25-JUN-1998; 98US-090676P.  
 PR 25-JUN-1998; 98US-090678P.  
 PR 25-JUN-1998; 98US-090688P.  
 PR 25-JUN-1998; 98US-090690P.  
 PR 25-JUN-1998; 98US-090694P.  
 PR 25-JUN-1998; 98US-090695P.  
 PR 25-JUN-1998; 98US-090696P.  
 PR 26-JUN-1998; 98US-090863P.  
 PR 26-JUN-1998; 98US-090863P.  
 PR 01-JUL-1998; 98US-091010P.  
 PR 01-JUL-1998; 98US-091359P.  
 PR 02-JUL-1998; 98US-091544P.  
 PR 02-JUL-1998; 98US-091478P.  
 PR 02-JUL-1998; 98US-091486P.  
 PR 02-JUL-1998; 98US-091628P.  
 PR 02-JUL-1998; 98US-091628P.  
 PR 02-JUL-1998; 98US-091632P.  
 PR 24-JUL-1998; 98US-094006P.  
 PR 04-AUG-1998; 98US-095282P.  
 PR 10-AUG-1998; 98US-095998P.  
 PR 10-AUG-1998; 98US-096012P.  
 PR 17-AUG-1998; 98US-09612P.  
 PR 17-AUG-1998; 98US-096757P.  
 PR 17-AUG-1998; 98US-096766P.  
 PR 17-AUG-1998; 98US-096867P.  
 PR 17-AUG-1998; 98US-096891P.  
 PR 17-AUG-1998; 98US-096897P.  
 PR 18-AUG-1998; 98US-096949P.  
 PR 18-AUG-1998; 98US-096959P.  
 PR 18-AUG-1998; 98US-097022P.  
 PR 26-AUG-1998; 98US-097952P.  
 PR 26-AUG-1998; 98US-097954P.  
 PR 26-AUG-1998; 98US-097955P.  
 PR 26-AUG-1998; 98US-097971P.  
 PR 26-AUG-1998; 98US-097974P.  
 PR 26-AUG-1998; 98US-098014P.  
 PR 01-SEP-1998; 98US-098716P.  
 PR 01-SEP-1998; 98US-098723P.

PR 02-SEP-1998; 98US-098803P.  
 PR 02-SEP-1998; 98US-098821P.  
 PR 02-SEP-1998; 98US-098843P.  
 PR 09-SEP-1998; 98US-099602P.  
 PR 10-SEP-1998; 98US-099741P.  
 PR 10-SEP-1998; 98US-099754P.  
 PR 10-SEP-1998; 98US-099763P.  
 PR 10-SEP-1998; 98US-099812P.  
 Query Match 95.2%; Score 852; DB 25; Length 870;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-257;  
 Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 44 CTCGCCCTCAATGGAAAGCTGGCTGGGACTAAAGCATAGACACAGGCTAGATTC 103  
 1 CTCGCCCTCAATGGAAAGCTGGCTGGGACTAAAGCATAGACACAGGCTAGATTC 60  
 104 CTGACCTGATCATCCCGAGGATCAGAGGCTCCAGCAGGAGGAACTTCATATATTC 163  
 61 CTGACCTGATCATCCCGAGGATCAGAGGCTCCAGCAGGAGGAACTTCATATATTC 120  
 164 TCAAGCACTTACAGCTGACCGACGAGTGGGATGAAAGTTCTAATCTTCCCTCC 223  
 121 TCAAGCACTTACAGCTGACCGACGAGTGGGATGAAAGTTCTAATCTTCCCTCC 180  
 224 TGTGCTGCCACTATGCTGATGTCATGGTCTCTACAGGCTGAATCCAGGGGTCC 283  
 181 TGTGCTGCCACTATGCTGATGTCATGGTCTCTACAGGCTGAATCCAGGGGTCC 240  
 284 GAGGCCACAGGAGCCAGGCCAGGCTCTAGAGATGGCTCCAGAGGCGCCAAAT 343  
 241 GAGGCCACAGGAGCCAGGCCAGGCTCTAGAGATGGCTCCAGAGGCGCCAAAT 300  
 344 GTGAGTCAAAAGATTGGTTCTCTGAGACCCCGAAGAAATTTATACAGTGTGGC 403  
 301 GTGAGTCAAAAGATTGGTTCTCTGAGACCCCGAAGAAATTTATACAGTGTGGC 360  
 404 TGCCAAAGAAAGCAATGGCCCTGTGATCATTTTCAAGGCAATGTGAAGAAACAGAC 463  
 361 TGCCAAAGAAAGCAATGGCCCTGTGATCATTTTCAAGGCAATGTGAAGAAACAGAC 420  
 464 AAAGGCAACAGAAAGCCAAACAGATTCAGAGGCTCCAGCAATTTCTCAACAT 523  
 421 AAAGGCAACAGAAAGCCAAACAGATTCAGAGGCTCCAGCAATTTCTCAACAT 480  
 524 GTGAGTCAAAAGATTGGTTCTCTGAGACCCCGAAGAAATTTATACAGTGTGGC 583  
 481 GTGAGTCAAAAGATTGGTTCTCTGAGACCCCGAAGAAATTTATACAGTGTGGC 540  
 584 AACATTCTCAGCAAGAGACAGTGAAGACCTACAGACACTCTTCTCCACATTC 643  
 541 AACATTCTCAGCAAGAGACAGTGAAGACCTACAGACACTCTTCTCCACATTC 600  
 644 ACTCTCCACTGTAACCCACCCCTAATCATTCAGTGTCTCAAAAAGCATGTTTTCA 703  
 601 ACTCTCCACTGTAACCCACCCCTAATCATTCAGTGTCTCAAAAAGCATGTTTTCA 660  
 704 GATCATTTTGTGTTGCTGCTGCTAGTGTCTCTCTCGACAGTCTTAGGCTGGC 763  
 661 GATCATTTTGTGTTGCTGCTGCTAGTGTCTCTCTCGACAGTCTTAGGCTGGC 720  
 764 CTCGCCCTTACCAAGGCTTAGGCTTAATTAACCTGAAGATTCAGAGAACTGATTC 823  
 721 CTCGCCCTTACCAAGGCTTAGGCTTAATTAACCTGAAGATTCAGAGAACTGATTC 780  
 824 AGCTAGTGTATTTAACTTAATGAATGAGAAAGTAGCAAAAGAGTCAATAATA 883  
 781 AGCTAGTGTATTTAACTTAATGAATGAGAAAGTAGCAAAAGAGTCAATAATA 840  
 884 TTTTAAATGTC 895  
 841 TTTTAAATGTC 852

RESULT 13  
ACAS8822  
ID ACAS8822 standard; cDNA; 870 BP.  
XX  
AC ACAS8822;  
XX  
DT 10-JUN-2003 (first entry)  
XX  
DE cDNA encoding human secreted polypeptide PR0842.  
XX  
KW Human; ss; gene; gene therapy; tumour; cancer.  
XX  
OS Homo sapiens.  
XX  
PN US2003013855-A1.  
XX  
PD 16-JAN-2003.  
XX  
PF 03-MAY-2002; 2002US-0063616.  
XX  
PR 30-DEC-1998; 98KR-0062142.  
PR 08-MAR-1999; 99WO-US05028.  
PR 14-MAY-1999; 99WO-US10733.  
PR 30-DEC-1999; 99WO-US31274.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 01-MAR-2000; 2000WO-US05601.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 14-MAY-1999; 99US-0311832.  
PR 25-AUG-1999; 99US-0380137.  
PR 25-AUG-1999; 99US-0380138.  
PR 25-AUG-1999; 99US-0380139.  
PR 25-AUG-1999; 99US-0380142.  
PR 15-SEP-1999; 99US-0397342.  
PR 18-OCT-1999; 99US-0403297.  
PR 12-NOV-1999; 99US-0423844.  
PR 22-AUG-2000; 2000US-0644848.  
PR 18-SEP-2000; 2000US-0664610.  
PR 08-NOV-2000; 2000US-0709238.  
PR 20-DEC-2000; 2000US-0747259.  
PR 22-MAR-2001; 2001US-0816744.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 30-MAY-2001; 2001US-0870574.  
PR 05-JUN-2001; 2001US-0874503.  
PR 29-JUN-2001; 2001US-0869599.  
PR 18-JUL-2001; 2001US-0908827.  
PR 06-DEC-2001; 2001US-0906867.  
XX  
PA (GENE ) GENENTECH INC.  
XX  
PI Baton DL, Flivaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
XX  
DR MPI; 2003-330485/31.  
XX  
P-PSDB; AB071518.  
XX  
PT New isolated antibody specifically binding a PRO polypeptide, useful  
PT aberrant expression or activity of a medicament for treating disorders with the  
PT conditions and cancer -  
XX  
PS Example 4; Page 92-93; 406pp; English.

XX The invention relates to an antibody that binds to a polypeptide with a  
CC fully defined sequence given in the specification. The methods and  
CC compositions (containing antibodies that specifically bind a PRO  
CC polypeptide) of the present invention are useful for the preparation of a  
CC medicament for the treatment of disorders associated with the aberrant  
CC expression or activity of the PRO polypeptide, such as tumour conditions  
CC and cancer. They can also be used to generate transgenic or knockout  
CC animals useful in the development and screening of therapeutically useful  
CC reagents. The PRO polypeptides and encoding nucleic acids can be used as  
CC molecular weight markers for protein electrophoresis, chromosome  
CC identification and tissue typing. The PRO polypeptides are useful to  
CC induce angiogenesis e.g wound healing. In the treatment of sports-related  
CC joint problems, articular cartilage defects, osteoarthritis or rheumatoid  
CC arthritis; diabetes; hyperinsulinaemia and hypoinulinaemia. The  
CC antibodies may be used in various diagnostic, competitive binding and/or  
CC immunoprecipitation assays. The present sequence represents a cDNA  
XX encoding a PRO polypeptide of the invention.

SQ Sequence 870 BP; 251 A; 237 C; 176 G; 206 T; 0 other;

Query Match 95.2%; Score 852; DB 25; Length 870;  
Best Local Similarity 100.0%; Pred. No. 5.1e-257;  
Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 CTCGCCCTCAATGGGAGCGTGGCCCTGGGACTAAAGCATAGACACAGCGCTGAGTATC 103  
DB 1 CTCGCCCTCAATGGGAGCGTGGCCCTGGGACTAAAGCATAGACACAGCGCTGAGTATC 60  
QY 104 CTGACCTGATGATATCCCGAGGATCGAGAGCTCCAGCAGGAGACCTTCATTATATCT 163  
DB 61 CTGACCTGATGATATCCCGAGGATCGAGAGCTCCAGCAGGAGACCTTCATTATATCT 120  
QY 164 TCAGCACTTACAGTGCAGCAGCGAGTGCAGTGAAGTCAATCTGCTCCCTCC 223  
DB 121 TCAGCACTTACAGTGCAGCAGCGAGTGCAGTGAAGTCAATCTGCTCCCTCC 180  
QY 224 TGTGCTGCACATATGCTGATGCTCATGCTCTAGACGCTGAATCCAGGGGTGCCA 283  
DB 181 TGTGCTGCACATATGCTGATGCTCATGCTCTAGACGCTGAATCCAGGGGTGCCA 240  
QY 284 GAGGCCACAGGAGCCAGGCGGAGCTTCAGAGATAGGCTCCAGGAGGCGGCAAGAT 343  
DB 241 GAGGCCACAGGAGCCAGGCGGAGCTTCAGAGATAGGCTCCAGGAGGCGGCAAGAT 300  
QY 344 GTGAGTGCAGAGATGTTGTTCTGAGAGCCCGAGAGAAATTCATGACAGTGTGGC 403  
DB 301 GTGAGTGCAGAGATGTTGTTCTGAGAGCCCGAGAGAAATTCATGACAGTGTGGC 360  
QY 404 TGCAGAAAGACAGTGCCTGTGATCATTTCAAGGCAATGAGAAACAAAGACACC 463  
DB 361 TGCAGAAAGACAGTGCCTGTGATCATTTCAAGGCAATGAGAAACAAAGACACC 420  
QY 464 AAAGGACACAGAGAAAGCCAAAGACATTCAGAGCTCCAGCAATTTCTAAACAAT 523  
DB 421 AAAGGACACAGAGAAAGCCAAAGACATTCAGAGCTCCAGCAATTTCTAAACAAT 480  
QY 524 GTGAGTGAAGAGCTTGTGCTGCTGTTGAGAGAGTGAAGGCGCCAGCTCCCAATTA 583  
DB 481 GTGAGTGAAGAGCTTGTGCTGCTGTTGAGAGAGTGAAGGCGCCAGCTCCCAATTA 540  
QY 584 AACATTCAGCCAGCAAGAGACAGTGAACACACTTACAGACACTTCTTCTCCACCTC 643  
DB 541 AACATTCAGCCAGCAAGAGACAGTGAACACACTTACAGACACTTCTTCTCCACCTC 600  
QY 644 ACTCTCCCACTGACACACCCCTTAATCATTCAGTGTCTCAAAAAGCATGTTTCAA 703  
DB 601 ACTCTCCCACTGACACACCCCTTAATCATTCAGTGTCTCAAAAAGCATGTTTCAA 660  
QY 704 GATCATTTGTTGTTGCTCTCTCTGAGTGTCTCTCTCGACATTTAGCTGTGGC 763  
DB 661 GATCATTTGTTGTTGCTCTCTCTGAGTGTCTCTCTCGACATTTAGCTGTGGC 720



QY 764 CTCGCCCTTACCCAGGCTTAGGCTTAATTACTGTAAGAAATCCAGAAAGTGTAGCTCCT 823  
DB 721 CTCGCCCTTACCCAGGCTTAGGCTTAATTACTGTAAGAAATCCAGAAAGTGTAGCTCCT 780  
QY 824 AGCTAGTGCATTTAACTTAATGCAATCAGAGAAAGTGTGCAAGAAAGTCAATTAATA 883  
DB 781 AGCTAGTGCATTTAACTTAATGCAATCAGAGAAAGTGTGCAAGAAAGTCAATTAATA 840  
QY 884 TTTTAAATGTC 895  
DB 841 TTTTAAATGTC 852

## RESULT 14

AC60375  
ID ACA60375 standard; cDNA; 870 BP.

AC60375;  
XX

DT 11-JUN-2003 (first entry)  
XX

DE Novel human secreted and transmembrane protein PRO842 cDNA.  
XX

Human; secreted and transmembrane polypeptide; gene; ss.  
XX

chromosome mapping; gene mapping; transgenic animal; knockout animal;  
therapeutic agent screening; chromosome identification; tissue typing;  
gene therapy.  
XX

Homo sapiens.  
OS

US2003018183-A1.  
PN

23-JAN-2003.  
PD

01-MAY-2002; 2002US-0063512.  
PE

06-DEC-2001; 2001US-0006867.  
PR

(GENH ) GENENTECH INC.  
PA

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ,  
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WZ;  
XX

WPI; 2003-330984/31.  
DR P-PSDB; ABU71964.

New secreted and transmembrane PRO polypeptides and nucleic acid  
PT molecules encoding the polypeptides, useful in gene therapy or  
PT preparing a medicament for treating a condition that is responsive to  
PT the PRO polypeptide or antibody -  
XX

Disclosure; Fig 25; 409pp; English.  
PS

The invention describes novel isolated PRO polypeptides. The PRO  
CC polypeptides or anti-PRO antibodies are useful in preparing a medicament  
CC for treating a condition that is responsive to the PRO polypeptide or  
CC antibody. The PRO nucleotide sequences may be used as hybridisation  
CC probes in chromosome and gene mapping, or in generating antisense RNA  
CC and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides,  
CC in assays to identify other proteins or molecules involved in binding  
CC reaction, to generate transgenic animals or knockout animals, which in  
CC turn are useful in the development and screening of therapeutically  
CC useful reagents, for chromosome identification, and tissue typing. The  
CC PRO polypeptides and nucleic acid molecules are also useful in gene  
CC therapy, and as molecular weight markers for protein electrophoresis  
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for  
CC PRO, or for the affinity purification of PRO from recombinant cell  
CC culture or natural sources. This sequence encodes a novel human  
CC secreted and transmembrane PRO polypeptide.  
XX

Sequence 870 BP; 251 A; 237 C; 176 G; 206 T; 0 other;  
XX

Query Match 95.2%; Score 852; DB 25; Length 870;

Best Local Similarity 100.0%; Pred. No. 5.1e-257;  
Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 CTCGCCCTTAAATGGGAACGCTGGCCCTGGGACTAAAGCATGACACACAGGCTAGATTC 103  
DB 1 CTCGCCCTTAAATGGGAACGCTGGCCCTGGGACTAAAGCATGACACACAGGCTAGATTC 60  
QY 104 CTGACCTAGTCATCCCGAGGAGTCCAGAGGCTCCAGCAGGAACTTCCATTAATATCT 163  
DB 61 CTGACCTAGTCATCCCGAGGAGTCCAGAGGCTCCAGCAGGAACTTCCATTAATATCT 120  
QY 164 TCAAGCAACTTACAGCTGACCGACGAGTGGGATGAAAGTCTATCTCTTCCCTCCTCC 223  
DB 121 TCAAGCAACTTACAGCTGACCGACGAGTGGGATGAAAGTCTATCTCTTCCCTCCTCC 180  
QY 224 TGTTCGTCGCTATGCTGATGTCATATGCTCTAGACGCTTATCCAGGAGGCTGCGCA 283  
DB 181 TGTTCGTCGCTATGCTGATGTCATATGCTCTAGACGCTTATCCAGGAGGCTGCGCA 240  
QY 284 GAGGCGACAGGAGACCGAGCCAGGCTTCTAGAGATGCTCCAGAGGCGCCAGAAAT 343  
DB 241 GAGGCGACAGGAGACCGAGGCGGAGCTTCTAGAGATGCTCCAGAGGCGCCAGAAAT 300  
QY 344 GTGAGTGCMAAGATTGGTCTCTGAGAGCCCGAGAGAAATTCATGACATGCTGTGGC 403  
DB 301 GTGAGTGCMAAGATTGGTCTCTGAGAGCCCGAGAGAAATTCATGACATGCTGTGGC 360  
QY 404 TGCCAAAGAAAGACTGCCCTGTGATCATTTTCAAGGGCAATGTGAAGAAACAGACACC 463  
DB 361 TGCCAAAGAAAGACTGCCCTGTGATCATTTTCAAGGGCAATGTGAAGAAACAGACACC 420  
QY 464 AAAGGACACAGAAAGCCAAACAGCATTCGAGGCTGCGCAATTTCTCAACAAAT 523  
DB 421 AAAGGACACAGAAAGCCAAACAGCATTCGAGGCTGCGCAATTTCTCAACAAAT 480  
QY 524 GTGAGCTAAGAAAGCTTGTGCTGTGCTTGTAGAGAGCTGTAGGCGCCACTCTCAATTA 583  
DB 481 GTGAGCTAAGAAAGCTTGTGCTGTGCTTGTAGAGAGCTGTAGGCGCCACTCTCAATTA 540  
QY 584 AACATTCGAGCCCAAGAAAGACATGAGACACACTTACAGACACTTCTTCCACCTTC 643  
DB 541 AACATTCGAGCCCAAGAAAGACATGAGACACACTTACAGACACTTCTTCCACCTTC 600  
QY 644 ACTCTCCACTGTACCCACCCCTAAATCATTTCCAGTGTCTCAAAAGCATGTTTTCAA 703  
DB 601 ACTCTCCACTGTACCCACCCCTAAATCATTTCCAGTGTCTCAAAAGCATGTTTTCAA 660  
QY 704 GATCATTGTTGTTGTTGCTCTCTAGTGTCTTCTCTGCTAGCTTAAAGCTTGGC 763  
DB 661 GATCATTGTTGTTGTTGCTCTCTAGTGTCTTCTCTGCTAGCTTAAAGCTTGGC 720  
QY 764 CTCGCCCTTACCCAGGCTTAGGCTTAATTACTGTAAGAAATCCAGAAAGTGTAGCTCCT 823  
DB 721 CTCGCCCTTACCCAGGCTTAGGCTTAATTACTGTAAGAAATCCAGAAAGTGTAGCTCCT 780  
QY 824 AGCTAGTGCATTTAACTTAATGCAATCAGAGAAAGTGTGCAAGAAAGTCAATTAATA 883  
DB 781 AGCTAGTGCATTTAACTTAATGCAATCAGAGAAAGTGTGCAAGAAAGTCAATTAATA 840  
QY 884 TTTTAAATGTC 895  
DB 841 TTTTAAATGTC 852

## RESULT 15

AC63385  
ID ACA63385 standard; cDNA; 870 BP.

AC63385;  
XX

DT 13-JUN-2003 (first entry)  
XX

CDNA encoding human PRO polypeptide #13.  
DE



XX Human: PRO polypeptide; secreted and transmembrane protein;  
 KW anti-PRO antibody; diagnostic assay; gene expression; gene; ss.  
 OS Homo sapiens.  
 XX US2003023042-A1.  
 XX 30-JAN-2003.  
 XX 01-MAY-2002; 2002US-0063502.  
 XX 06-DEC-2001; 2001US-0006867.  
 XX (GETH ) GENENTECH INC.  
 XX Eaton DL, Fillaroff E, Gerritsen ME, Goddard A, Godowski PJ,  
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;  
 XX WPI; 2003-331484/31.  
 DR P-PSDB; AB072121.  
 XX Novel monoclonal antibody that binds to secreted and transmembrane  
 PT polypeptide, useful for detecting and purifying the polypeptide and  
 PT also for treating conditions responsive to the antibody -  
 PS Disclosure; Fig 25; 408pp; English.  
 XX The present invention relates to the isolation of novel human PRO  
 CC polypeptides, and the polynucleotide sequences encoding them. The  
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO  
 CC polypeptides and polynucleotides are useful for preparing a  
 CC medicament useful in the treatment of a condition responsive to  
 CC anti-PRO antibody. Anti-PRO antibodies are useful in diagnostic  
 CC assays for PRO, by detecting its expression in specific cells,  
 CC tissues or serum, and for affinity purification of PRO from  
 CC recombinant cell culture or natural sources. ACA63373-ACA63456  
 CC represent cDNA sequences encoding the human PRO polypeptides of  
 CC the invention.  
 XX  
 SQ Sequence 870 BP; 251 A; 237 C; 176 G; 206 T; 0 other;  
 Query Match 95.2%; Score 852; DB 25; Length 870;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-257;  
 Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 44 CTGCGCCTCAAAATGGGAAGCGTGGCTGGGACTAAAGCATAGACACAGGCTGATATC 103  
 Db 1 CTGCGCCTCAAAATGGGAAGCGTGGCTGGGACTAAAGCATAGACACAGGCTGATATC 60  
 QY 104 CTGACCTGAGTCATCCGACGAGATCAGAGCCTCCAGCAGGGAACCTTCCATTATATCT 163  
 Db 61 CTGACCTGAGTCATCCGACGAGATCAGAGCCTCCAGCAGGGAACCTTCCATTATATCT 120  
 QY 164 TCAAGCAACTTACAGCTGCACCGACAGTGGGATGGAAGTCTTATCTCTTCCCTCC 223  
 Db 121 TCAAGCAACTTACAGCTGCACCGACAGTGGGATGGAAGTCTTATCTCTTCCCTCC 180  
 QY 224 TGTGCTGCCACTATGCTGATGTCATGCTCTAGAGCCTGAATCCAGGGGTGGCA 283  
 Db 181 TGTGCTGCCACTATGCTGATGTCATGCTCTAGAGCCTGAATCCAGGGGTGGCA 240  
 QY 284 GAGGCCACAGGAGCAGGCGGCTTCTAGAGATGCTCCAGGAAGGCGGCAAGAT 343  
 Db 241 GAGGCCACAGGAGCAGGCGGCTTCTAGAGATGCTCCAGGAAGGCGGCAAGAT 300  
 QY 344 GTGAGTCAAAAGATTGTTCTGTAGAGCCCCGAGAAGAAATTCATGACAGTGTGGGC 403  
 Db 301 GTGAGTCAAAAGATTGTTCTGTAGAGCCCCGAGAAGAAATTCATGACAGTGTGGGC 360  
 QY 404 TGCCAAAGAAAGCATGGCCCTGTATCATTTCAAGGGCAATGTGAAGAAACAAGACACC 463  
 Db 361 TGCCAAAGAAAGCATGGCCCTGTATCATTTCAAGGGCAATGTGAAGAAACAAGACACC 420

QY 464 AAAGCACACAGAAAGCCAAACAGATTCAGAGCCTGCCAGCAATTTCTCAAGCAT 523  
 Db 421 AAAGCACACAGAAAGCCAAACAGATTCAGAGCCTGCCAGCAATTTCTCAAGCAT 480  
 QY 524 GTCACTTAAGAAAGCTTGTGCTGCTTTGTATGAGAGCTGTAGGCGCCACTTTCCAAATTA 583  
 Db 481 GTCACTTAAGAAAGCTTGTGCTGCTTTGTATGAGAGCTGTAGGCGCCACTTTCCAAATTA 540  
 QY 584 AACATTCACAGCAAGAAAGACAGTGAAGACACTACAGACACTTTCTTCCACCTC 643  
 Db 541 AACATTCACAGCAAGAAAGACAGTGAAGACACTACAGACACTTTCTTCCACCTC 600  
 QY 644 ACTCTCCACTGTACCCACCCCTAAATCATTCAGTGTCTCAAAAAGCATGTTTTTCAA 703  
 Db 601 ACTCTCCACTGTACCCACCCCTAAATCATTCAGTGTCTCAAAAAGCATGTTTTTCAA 660  
 QY 704 GATCATTTTGTGTTGTGCTCTCTAGTGTCTTCTCTCTGTACAGTGTAGCTGTGCCC 763  
 Db 661 GATCATTTTGTGTTGTGCTCTCTAGTGTCTTCTCTCTGTACAGTGTAGCTGTGCCC 720  
 QY 764 CTCCCTTACCCAGGCTTAGGCTTAATTAATCTGAAGATTCAGAAACCTGATGCTTCC 823  
 Db 721 CTCCCTTACCCAGGCTTAGGCTTAATTAATCTGAAGATTCAGAAACCTGATGCTTCC 780  
 QY 824 AGCTAGTGTCAATTAACCTTAATGCAATTCAGAAAGTACGAAACAGAAATCAATTAATA 883  
 Db 781 AGCTAGTGTCAATTAACCTTAATGCAATTCAGAAAGTACGAAACAGAAATCAATTAATA 840  
 QY 884 TTTTAAATGTC 895  
 Db 841 TTTTAAATGTC 852

Search completed: October 9, 2003, 13:55:36  
 Job time : 267.117 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2003, 12:42:26 ; Search time 3445.74 Seconds

(without alignments)  
10625.902 Million cell updates/sec

Title: US-09-700-770-5

Perfect score: 895

Sequence: 1 ctaactctgtacgtacagc.....ataaataattttaaatgtc 895

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: gb\_da:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_da:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_in:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rod:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vtl:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	895	100.0	895	6	AX224644 Sequence
2	895	100.0	1171	6	AX224648 Sequence
3	852	95.2	870	6	AR325494 Sequence
4	852	95.2	870	6	AX092294 Sequence
5	852	95.2	870	6	AX376072 Sequence
6	852	95.2	870	6	AX403277 Sequence
7	852	95.2	870	6	AX675218 Sequence
8	525.8	58.7	533	6	AR272401 Sequence
9	525.8	58.7	533	6	AR275982 Sequence
10	525.8	58.7	533	6	AX062486 Sequence
11	525.8	58.7	533	6	AX367403 Sequence
12	481	53.7	481	6	BD107982 Sequence
13	475	53.1	626	6	AX182041 Sequence
14	445.2	49.7	511	6	BD082607 Sequence
15	438.4	49.0	168586	9	AC011497 Sequence
16	414.8	46.3	419	6	AX332462 Sequence
17	362.4	39.9	357	6	BD076801 Sequence
18	357	39.9	357	6	E40581 Sequence
19	312	34.9	312	6	AR272331 Sequence
20	312	34.9	312	6	AR275912 Sequence
21	312	34.9	312	6	AX062416 Sequence
22	312	34.9	312	6	AX367333 Sequence
23	291	32.5	291	6	E40584 Sequence
24	254.2	28.4	808	10	BC024561 Sequence
25	245.6	27.4	357	6	E40583 Sequence
26	230	25.7	235	6	BD076800 Sequence
27	228	25.5	357	6	E40582 Sequence
28	200.4	22.4	291	6	E40586 Sequence
29	190	21.2	44332	9	AC005794 Sequence
30	189.2	21.1	291	6	E40585 Sequence
31	138.2	15.4	40520	9	AC011513 Sequence
32	118.4	13.2	43593	2	AC022516 Sequence
33	78.8	8.8	190860	2	AC073803 Sequence
34	78.8	8.8	215234	2	AC073745 Sequence
35	73.4	8.2	218925	2	AX182077 Sequence
36	66.4	7.4	218925	2	AX109038 Sequence
37	66.4	7.4	229745	2	AC121639 Sequence
38	66.4	7.4	242596	2	AC134759 Sequence
39	56.8	6.3	7218	6	I66494 Sequence
40	45.8	5.1	518	6	AX185599 Sequence
41	45.2	5.1	179378	2	AC141011 Sequence
42	44.6	5.0	51	6	E40591 Sequence
43	44	4.9	125020	9	AF429315 Sequence
44	44	4.9	209887	2	AC079424 Sequence
45	43.6	4.9	125020	9	AF429315 Sequence

# ALIGNMENTS

RESULT 1  
AX224644  
LOCUS AX224644 895 bp DNA linear PAT 10-SHP-2001  
DEFINITION Sequence 2 from Patent WO0161055.  
ACCESSION AX224644  
VERSION AX224644.1 GI:15554773  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1  
AUTHORS Chen, S.Y., Sun, Y. and Macina, R.A.  
TITLE Methods for diagnosing, monitoring, staging, imaging and treating lung cancer via lung cancer specific genes

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: WO 0161055-A 2 23-AUG-2001;  
diadexus, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..895  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 245 a 250 c 183 g 217 t  
ORIGIN  
Query Match 100.0%; Score 895; DB 6; Length 895;  
Best Local Similarity 100.0%; Pred. No. 3,7e-264;  
Matches 895; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTAATCTGTACGTAACAGACAAGAGCGTCACTCACTGCTTCGCGCTCAATAGGA 60  
Db 1 CTAATCTGTACGTAACAGACAAGAGCGTCACTCACTGCTTCGCGCTCAATAGGA 60  
QY 61 ACAGTGGCTGGGACTAAAGATAGACCAAGCGTGAATTCCTGACCTGATCC 120  
Db 61 ACAGTGGCTGGGACTAAAGATAGACCAAGCGTGAATTCCTGACCTGATCC 120  
QY 121 CAGGATCAGAGAGCTCCAGCAGGAGAACTTCATTAATCTCAAGCAACTTACAGCT 180  
Db 121 CAGGATCAGAGAGCTCCAGCAGGAGAACTTCATTAATCTCAAGCAACTTACAGCT 180  
QY 181 GCACCGACAGTGGCGATGAAGAAATCTTAATCTCTCCCTCTGTTGCTGCCACTAATG 240  
Db 181 GCACCGACAGTGGCGATGAAGAAATCTTAATCTCTCCCTCTGTTGCTGCCACTAATG 240  
QY 241 CTGATGTCAGATGGCTCTAGAGCGCTGAATCCAGAGGGTCCGACAGGCGACAGGACCGA 300  
Db 241 CTGATGTCAGATGGCTCTAGAGCGCTGAATCCAGAGGGTCCGACAGGCGACAGGACCGA 300  
QY 301 GGGCAGGCTTCTAGAGATGGCTCCAGAGAGCGCGCCAGAAATGTGATCAAGATTGG 360  
Db 301 GGGCAGGCTTCTAGAGATGGCTCCAGAGAGCGCGCCAGAAATGTGATCAAGATTGG 360  
QY 361 TTCTGTAGAGCCCCGAGAAATTTATGACAGTGTCTGGCTGCCAAAGACAGTGC 420  
Db 361 TTCTGTAGAGCCCCGAGAAATTTATGACAGTGTCTGGCTGCCAAAGACAGTGC 420  
QY 421 CCTGTATCATTTTCAAGGGCAATGTGAAGAAACAAAGCAAGAGCGACCAAGAG 480  
Db 421 CCTGTATCATTTTCAAGGGCAATGTGAAGAAACAAAGCAAGAGCGACCAAGAG 480  
QY 481 CCAAAACAAGCATTCAGAGAGCTGCCAGCAATTTCTCAACAAATGTGATGAAGCTTT 540  
Db 481 CCAAAACAAGCATTCAGAGAGCTGCCAGCAATTTCTCAACAAATGTGATGAAGCTTT 540  
QY 541 GCTCTGCTTTGTAGAGAGCTCTAGAGCGCCACACTCTTCCAAATTAACATTCAGCCAGA 600  
Db 541 GCTCTGCTTTGTAGAGAGCTCTAGAGCGCCACACTCTTCCAAATTAACATTCAGCCAGA 600  
QY 601 AGACATGAGACACCTTACAGACACTCTTCTCCACACTCAGCTCCCACTGTAACCC 660  
Db 601 AGACATGAGACACCTTACAGACACTCTTCTCCACACTCAGCTCCCACTGTAACCC 660  
QY 661 ACCCGTAATTCATTCAGAGTGTCTCAAAAAGCAATGTTTTTCAAGATCATTTTGTGTTG 720  
Db 661 ACCCGTAATTCATTCAGAGTGTCTCAAAAAGCAATGTTTTTCAAGATCATTTTGTGTTG 720  
QY 721 CTCTCTGATGCTCTTCTCTCTGTCAGTCTTAAAGCTTGGCTTCCCTTACCCAGGCT 780  
Db 721 CTCTCTGATGCTCTTCTCTCTGTCAGTCTTAAAGCTTGGCTTCCCTTACCCAGGCT 780  
QY 781 TAGGCTTAATTAAGTAAGATTCAGAGAACTGTAGTTCCTAGCTAGTCAATTAAAC 840  
Db 781 TAGGCTTAATTAAGTAAGATTCAGAGAACTGTAGTTCCTAGCTAGTCAATTAAAC 840  
QY 841 CTTAAATGCAATCAGAGAAATAGCAAAAGCAAGACTCAATTAATTTTAAATGTC 895  
Db 841 CTTAAATGCAATCAGAGAAATAGCAAAAGCAAGACTCAATTAATTTTAAATGTC 895

RESULT 2  
AX224648  
LOCUS  
DEFINITION Sequence 6 from Patent WO0161055.  
AX224648  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE  
1  
AUTHORS Chen, S.Y., Sun, Y. and Macina, R.A.  
TITLE Methods for diagnosing, monitoring, staging, imaging and treating  
lung cancer via lung cancer specific genes  
JOURNAL Patent: WO 0161055-A 6 23-AUG-2001;  
diadexus, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..1171  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 333 a 320 c 225 g 293 t  
ORIGIN  
Query Match 100.0%; Score 895; DB 6; Length 1171;  
Best Local Similarity 100.0%; Pred. No. 3.8e-264;  
Matches 895; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTAATCTGTACGTAACAGACAAGAGCGTCACTCACTGCTTCGCGCTCAATAGGA 60  
Db 22 CTAATCTGTACGTAACAGACAAGAGCGTCACTCACTGCTTCGCGCTCAATAGGA 81  
QY 61 ACAGTGGCTGGGACTAAAGATAGACCAAGCGTGAATTCCTGACCTGATCC 120  
Db 82 ACAGTGGCTGGGACTAAAGATAGACCAAGCGTGAATTCCTGACCTGATCC 141  
QY 121 CAGGATCAGAGAGCTCCAGCAGGAGAACTTCATTAATCTCAAGCAACTTACAGCT 180  
Db 142 CAGGATCAGAGAGCTCCAGCAGGAGAACTTCATTAATCTCAAGCAACTTACAGCT 201  
QY 181 GCACCGACAGTGGCGATGAAGAAATCTTAATCTCTCCCTCTGTTGCTGCCACTAATG 240  
Db 202 GCACCGACAGTGGCGATGAAGAAATCTTAATCTCTCCCTCTGTTGCTGCCACTAATG 261  
QY 241 CTGATGTCAGATGGCTCTAGAGCGCTGAATCCAGAGGGTCCGACAGGCGACAGGACCGA 300  
Db 262 CTGATGTCAGATGGCTCTAGAGCGCTGAATCCAGAGGGTCCGACAGGCGACAGGACCGA 321  
QY 301 GGGCAGGCTTCTAGAGATGGCTCCAGAGAGCGCGCCAGAAATGTGATCAAGATTGG 360  
Db 322 GGGCAGGCTTCTAGAGATGGCTCCAGAGAGCGCGCCAGAAATGTGATCAAGATTGG 381  
QY 361 TTCTGTAGAGCCCCGAGAAATTTATGACAGTGTCTGGCTGCCAAAGACAGTGC 420  
Db 382 TTCTGTAGAGCCCCGAGAAATTTATGACAGTGTCTGGCTGCCAAAGACAGTGC 441  
QY 421 CCTGTATCATTTTCAAGGGCAATGTGAAGAAACAAAGCAAGAGCGACCAAGAG 480  
Db 442 CCTGTATCATTTTCAAGGGCAATGTGAAGAAACAAAGCAAGAGCGACCAAGAG 501  
QY 481 CCAAAACAAGCATTCAGAGAGCTGCCAGCAATTTCTCAACAAATGTGATGAAGCTTT 540  
Db 502 CCAAAACAAGCATTCAGAGAGCTGCCAGCAATTTCTCAACAAATGTGATGAAGCTTT 561  
QY 541 GCTCTGCTTTGTAGAGAGCTCTAGAGCGCCACACTCTTCCAAATTAACATTCAGCCAGA 600  
Db 562 GCTCTGCTTTGTAGAGAGCTCTAGAGCGCCACACTCTTCCAAATTAACATTCAGCCAGA 621  
QY 601 AGACATGAGACACCTTACAGACACTCTTCTCCACACTCAGCTCCCACTGTAACCC 660

```

DB      622 AGACAGTGCACACTACACAGACTCTTCTTCCCACTACTCTCCCACTGACC 681
OY      661 ACCCTTAATCATTCACAGTCTCTCMAAAGCATGTTTTTCAAGATCATTTTGTGTG 720
DB      682 ACCCTTAATCATTCACAGTCTCTCMAAAGCATGTTTTTCAAGATCATTTTGTGTG 741
OY      721 CTCCTCTAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
DB      742 CTCCTCTAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 801
OY      761 TAGGCTTAATTCAGAAAGATTCAGAAAGATTCAGAAAGATTCAGAAAGATTCAGAA 840
DB      802 TAGGCTTAATTCAGAAAGATTCAGAAAGATTCAGAAAGATTCAGAAAGATTCAGAA 861
OY      841 CTAAATGCAATCAGAAAGATTCAGAAAGATTCAGAAAGATTCAGAAAGATTCAGAA 895
DB      862 CTAAATGCAATCAGAAAGATTCAGAAAGATTCAGAAAGATTCAGAAAGATTCAGAA 916

RESULT 3
AR252494      870 bp      DNA      linear      PAT 20-DEC-2002
LOCUS      AR252494
DEFINITION      Sequence 164 from patent US 6478825.
ACCESSION      AR252494
VERSION      AR252494.1 GI:27300402
KEYWORDS
SOURCE
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 870)
AUTHORS      Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
TITLE      Implant, method of making same and use of the implant for the
JOURNAL      Patent: US 6478825-A 164 12-NOV-2002;
FEATURES
source      1. 870
              Location/Qualifiers
BASE COUNT      251 a 237 c 176 g 206 t
ORIGIN
Query Match      95.2%; Score 852; DB 6; Length 870;
Best Local Similarity 100.0%; Pred. No. 6.6e-251;
Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      44 CTCGCCCTCAATGGGAACGCTGGCTGGACTAAAGCATAGACACAGCGCTGATATC 103
DB      1 CTCGCCCTCAATGGGAACGCTGGCTGGACTAAAGCATAGACACAGCGCTGATATC 60
OY      104 CTGACCTGATCATCCCAAGGATCAGAGCCTCCAGCAGGAGACCTTCATTAATATCT 163
DB      61 CTGACCTGATCATCCCAAGGATCAGAGCCTCCAGCAGGAGACCTTCATTAATATCT 120
OY      164 TCAACCAACTTACAGCTGACCGACGATGGATGATGAATGATTAATCTCTCTCTCTCT 223
DB      121 TCAACCAACTTACAGCTGACCGACGATGGATGATGAATGATTAATCTCTCTCTCTCT 180
OY      224 TGTTCCTGCACTAATGCTGATGTCATGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 283
DB      181 TGTTCCTGCACTAATGCTGATGTCATGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
OY      284 GAGGCCACAGGAGCGGAGCGGAGCTTCTAGAGATGCTGCTCAGAGAGGCGGCAAGAT 343
DB      241 GAGGCCACAGGAGCGGAGCGGAGCTTCTAGAGATGCTGCTCAGAGAGGCGGCAAGAT 300
OY      344 GTGATGCAAAAGATGTTCTCTGAGAGCCCGGAGAAAGAAATTCATGACAGTCTGGGC 403
DB      301 GTGATGCAAAAGATGTTCTCTGAGAGCCCGGAGAAAGAAATTCATGACAGTCTGGGC 360
OY      404 TSCCAAGAGAGAGTGCCTCTGATCATTTCAAGGGCAATGAGAAAGCAAGACACC 463
DB      361 TSCCAAGAGAGAGTGCCTCTGATCATTTCAAGGGCAATGAGAAAGCAAGACACC 420
OY      464 AAAGCACCACAGAAAGCCAAAGCAAGCATTCAGAGCCCTGCGACGAATTTCTCAACAT 523

```

```

DB      421 AAAGCACCACAGAAAGCCAAAGCAATTCAGAGCCCTGCGAGCAATTCACAAACAT 480
OY      524 GTGAGTAAAGAGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 583
DB      481 GTGAGTAAAGAGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
OY      584 AACATTCACAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 643
DB      541 AACATTCACAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
OY      644 ACTCTCCACAGTACCCACCCCTTAATCATTCAGAGTCTCTCAAAAAGCATGTTTTCAA 703
DB      601 ACTCTCCACAGTACCCACCCCTTAATCATTCAGAGTCTCTCAAAAAGCATGTTTTCAA 660
OY      704 GATCAATTTGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 763
DB      661 GATCAATTTGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
OY      764 CTCCTCTACCCAGAGCTTACGCTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 823
DB      721 CTCCTCTACCCAGAGCTTACGCTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 780
OY      824 AGCTAGTGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 883
DB      781 AGCTAGTGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 840
OY      884 TTTTAAATGTC 895
DB      841 TTTTAAATGTC 852

RESULT 4
AX092294      870 bp      DNA      linear      PAT 21-MAR-2001
LOCUS      AX092294
DEFINITION      Sequence 25 from Patent WO0116318.
ACCESSION      AX092294
VERSION      AX092294.1 GI:13444461
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
              Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS      Eaton,D.L., Filvaroff,E., Gerltsen,M.E., Goddard,A.,
              Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Matanabe,C.K. and
              Wood,W.I.
TITLE      Secreted and transmembrane polypeptides and nucleic acids encoding
JOURNAL      Patent: WO 0116318-A 25 08-MAR-2001;
FEATURES
source      Location/Qualifiers
              1. 870
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT      251 a 237 c 176 g 206 t
ORIGIN
Query Match      95.2%; Score 852; DB 6; Length 870;
Best Local Similarity 100.0%; Pred. No. 6.6e-251;
Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      44 CTCGCCCTCAATGGGAACGCTGGCTGGACTAAAGCATAGACACAGCGCTGATATC 103
DB      1 CTCGCCCTCAATGGGAACGCTGGCTGGACTAAAGCATAGACACAGCGCTGATATC 60
OY      104 CTGACCTGATCATCCCAAGGATCAGAGCCTCCAGCAGGAGAACTTCATTAATATCT 163
DB      61 CTGACCTGATCATCCCAAGGATCAGAGCCTCCAGCAGGAGAACTTCATTAATATCT 120
OY      164 TCAACCAACTTACAGCTGACCGACGATGGATGATGAATGATTAATCTCTCTCTCTCT 223

```

Db 121 TCAAGCACTTACAGCTGACACCGACAGTGGATGAAGTTCTAATCTCTCCCTCC 180  
 QY 224 TGTGGCTGACATGATGCTGATGTCATGGTCTCTAGACGCTGAATCCAGGGGTCCCA 283  
 Db 181 TGTGGCTGACATGATGCTGATGTCATGGTCTCTAGACGCTGAATCCAGGGGTCCCA 240  
 QY 284 GAGGCCACAGGAGCAGGACGAGGCTTCTAGAGAGTGGCTCCAGAGGCGGCGCAAGAT 343  
 Db 241 GAGGCCACAGGAGCAGGACGAGGCTTCTAGAGAGTGGCTCCAGAGGCGGCGCAAGAT 300  
 QY 344 GTAGTGTCAAAAGATGTTGCTCTGTAGAGCCCGAGAAATAATTCATGACAGTGTCTGGC 403  
 Db 301 GTAGTGTCAAAAGATGTTGCTCTGTAGAGCCCGAGAAATAATTCATGACAGTGTCTGGC 360  
 QY 404 TGCCAAAGAGAGAGTGGCTGCTGTGATCATTTCAAGGCAATGTGAAGAAAACAAGACAC 463  
 Db 361 TGCCAAAGAGAGAGTGGCTGCTGTGATCATTTCAAGGCAATGTGAAGAAAACAAGACAC 420  
 QY 464 AAAGGACACAGAGAAAGCAAGACAGTTCAGAGGCTGCGACAAATTTCTCAAAACAT 523  
 Db 421 AAAGGACACAGAGAAAGCAAGACAGTTCAGAGGCTGCGACAAATTTCTCAAAACAT 480  
 QY 524 GTAGCTAAGAGAGTGGCTGCTGTGATCATTTCAAGGCAATGTGAAGAAAACAAGACAC 583  
 Db 481 GTAGCTAAGAGAGTGGCTGCTGTGATCATTTCAAGGCAATGTGAAGAAAACAAGACAC 540  
 QY 584 AACATTCTCAGCAGAGAGAGAGTGAAGACACCTACAGACACTCTTCTCCACACTC 643  
 Db 541 AACATTCTCAGCAGAGAGAGAGTGAAGACACCTACAGACACTCTTCTCCACACTC 600  
 QY 644 ACTCTCCACTGTACCCACCCCTAATCATTCAGAGTCTCTCAAAAAGCATGTTTTCAA 703  
 Db 601 ACTCTCCACTGTACCCACCCCTAATCATTCAGAGTCTCTCAAAAAGCATGTTTTCAA 660  
 QY 704 GATCATTTTGTGTTGCTCTGTAGTGTCTCTCTGCGAGAGTCTAGGCTGAGCC 763  
 Db 661 GATCATTTTGTGTTGCTCTGTAGTGTCTCTCTGCGAGAGTCTAGGCTGAGCC 720  
 QY 764 CTCGCCCTTACCCAGGCTTAACTTAATTAACCTGAAGATTCAGAGAACTGTAGCTTCT 823  
 Db 721 CTCGCCCTTACCCAGGCTTAACTTAATTAACCTGAAGATTCAGAGAACTGTAGCTTCT 780  
 QY 824 AGTAGTGTATTTAATCTTAATGCATATGAGAAATAGCAAAAGAGTCAATTAATA 883  
 Db 781 AGTAGTGTATTTAATCTTAATGCATATGAGAAATAGCAAAAGAGTCAATTAATA 840  
 QY 884 TTTTAAATGTC 895  
 Db 841 TTTTAAATGTC 852

RESULT 5  
 AX376072 870 bp DNA linear PAT 01-MAR-2002  
 LOCUS Sequence 139 from Patent WO0168848.  
 AX376072  
 VERSION AX376072.1 GI:19170428  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1  
 AUTHORS Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P.J.,  
 Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, M.I. and  
 Zhang, Z.  
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
 the same  
 JOURNAL Patent: WO 0168848-A 139 20-SEP-2001;  
 Genentech, Inc. (US)  
 FEATURES  
 source location/Qualifiers  
 1..870  
 /organism="Homo sapiens"

BASE COUNT 251 a 237 c 176 g 206 t  
 ORIGIN  
 Query Match 95.2%; Score 852; DB 6; Length 870;  
 Best Local Similarity 100.0%; Pred. No. 6; 6e-251;  
 Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"

QY 44 CTCGCCCTCAAAATGGGAACGCTGGCGCTAAGACATAGACACAGGCTGATATC 103  
 Db 1 CTCGCCCTCAAAATGGGAACGCTGGCGCTAAGACATAGACACAGGCTGATATC 60  
 QY 104 CTGACCTGAGTCATCCCGAGGATCAGAGGCTCCAGAGGAACTTCAATTAATCT 163  
 Db 61 CTGACCTGAGTCATCCCGAGGATCAGAGGCTCCAGAGGAACTTCAATTAATCT 120  
 QY 164 TCAAGCACTTACAGCTGACACCGACAGTGGATGAAGTTCTAATCTCTCCCTCC 223  
 Db 121 TCAAGCACTTACAGCTGACACCGACAGTGGATGAAGTTCTAATCTCTCCCTCC 180  
 QY 224 TGTGGCTGACATGATGCTGATGTCATGGTCTCTAGACGCTGAATCCAGGGGTCCCA 283  
 Db 181 TGTGGCTGACATGATGCTGATGTCATGGTCTCTAGACGCTGAATCCAGGGGTCCCA 240  
 QY 284 GAGGCCACAGGAGCAGGACGAGGCTTCTAGAGAGTGGCTCCAGAGGCGGCGCAAGAT 343  
 Db 241 GAGGCCACAGGAGCAGGACGAGGCTTCTAGAGAGTGGCTCCAGAGGCGGCGCAAGAT 300  
 QY 344 GTAGTGTCAAAAGATGTTGCTCTGTAGAGCCCGAGAAATAATTCATGACAGTGTCTGGC 403  
 Db 301 GTAGTGTCAAAAGATGTTGCTCTGTAGAGCCCGAGAAATAATTCATGACAGTGTCTGGC 360  
 QY 404 TGCCAAAGAGAGAGTGGCTGCTGTGATCATTTCAAGGCAATGTGAAGAAAACAAGACAC 463  
 Db 361 TGCCAAAGAGAGAGTGGCTGCTGTGATCATTTCAAGGCAATGTGAAGAAAACAAGACAC 420  
 QY 464 AAAGGACACAGAGAAAGCAAGACAGTTCAGAGGCTGCGACAAATTTCTCAAAACAT 523  
 Db 421 AAAGGACACAGAGAAAGCAAGACAGTTCAGAGGCTGCGACAAATTTCTCAAAACAT 480  
 QY 524 GTAGCTAAGAGAGTGGCTGCTGTGATCATTTCAAGGCAATGTGAAGAAAACAAGACAC 583  
 Db 481 GTAGCTAAGAGAGTGGCTGCTGTGATCATTTCAAGGCAATGTGAAGAAAACAAGACAC 540  
 QY 584 AACATTCTCAGCAGAGAGAGTGAAGACACCTACAGACACTCTTCTCCACACTC 643  
 Db 541 AACATTCTCAGCAGAGAGAGTGAAGACACCTACAGACACTCTTCTCCACACTC 600  
 QY 644 ACTCTCCACTGTACCCACCCCTAATCATTCAGAGTCTCTCAAAAAGCATGTTTTCAA 703  
 Db 601 ACTCTCCACTGTACCCACCCCTAATCATTCAGAGTCTCTCAAAAAGCATGTTTTCAA 660  
 QY 704 GATCATTTTGTGTTGCTCTGTAGTGTCTCTCTGCGAGAGTCTAGGCTGAGCC 763  
 Db 661 GATCATTTTGTGTTGCTCTGTAGTGTCTCTCTGCGAGAGTCTAGGCTGAGCC 720  
 QY 764 CTCGCCCTTACCCAGGCTTAACTTAATTAACCTGAAGATTCAGAGAACTGTAGCTTCT 823  
 Db 721 CTCGCCCTTACCCAGGCTTAACTTAATTAACCTGAAGATTCAGAGAACTGTAGCTTCT 780  
 QY 824 AGTAGTGTATTTAATCTTAATGCATATGAGAAATAGCAAAAGAGTCAATTAATA 883  
 Db 781 AGTAGTGTATTTAATCTTAATGCATATGAGAAATAGCAAAAGAGTCAATTAATA 840  
 QY 884 TTTTAAATGTC 895  
 Db 841 TTTTAAATGTC 852

RESULT 6  
 AX403277 870 bp DNA linear PAT 14-JUN-2002  
 LOCUS AX403277

```

DEFINITION Sequence 164 from Patent WO0073454.
ACCESSION AX403277
VERSION AX403277.1 GI:21436848
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Ashkenazi, A.J., Baker, K.P., Bolstein, D., Deanoyers, L., Eaton, D.,
          Ferrar, N., Gerber, H., Gertsen, M., Godard, A., Godowski, P.,
          Grimaldi, C.J., Gurney, A.L., Kijavlin, I., Napier, M.A., Pan, J.,
          Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K.,
          Williams, P., Wood, W.I. and Zhang, Z.
          Secreted and transmembrane polypeptides and nucleic acids encoding
          the same
          Patent: WO 0073454-A 164 07-DEC-2000;
JOURNAL
FEATURES
    source      location/Qualifiers
                1..870
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
BASE COUNT    251 a      237 c      176 g      206 t
ORIGIN
Query Match      95.2%; Score 852; DB 6; Length 870;
Best Local Similarity 100.0%; Pred. No. 6.6e-251;
Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 44 CTCGCCCTCAAAATGGGAACGCTGGCCCTGGAGCTAAAGCATAGACACAGGCTGAGTATC 103
DB 1 CTCGCCCTCAAAATGGGAACGCTGGCCCTGGAGCTAAAGCATAGACACAGGCTGAGTATC 60
OY 104 CTGACCTGATGATCCCGAGGAGTACAGAGACCTCCAGACGGAGACCTTCATTATATTT 163
DB 61 CTGACCTGATGATCCCGAGGAGTACAGAGACCTCCAGAGGAGACCTTCATTATATTTCT 120
OY 164 TCAGCAACTTACAGCTGCACCGACGAGTTGCGATGAAATTTCTTCTTCTCTCTCC 223
DB 121 TCAGCAACTTACAGCTGCACCGACGAGTTGCGATGAAATTTCTTCTTCTCTCTCC 180
OY 224 TGTTCCTGCCATATGCTGATGTCATGTCCTTCTAGCAGCTGAAATCCAGGGGTCGCCA 283
DB 181 TGTTCCTGCCATATGCTGATGTCATGTCCTTCTAGCAGCTGAAATCCAGGGGTCGCCA 240
OY 284 GAGGCCACAGGAGACGAGGCCAGGCTTCTAGAGATGGCTCCAGAGGCGGCCAAGAT 343
DB 241 GAGGCCACAGGAGACGAGGCCAGGCTTCTAGAGATGGCTCCAGAGGCGGCCAAGAT 300
OY 344 GTGAGTGCAGAAATGGTTGTTCTGAGAGCCCGAGAGAAATTCATGACGTGTGGGC 403
DB 301 GTGAGTGCAGAAATGGTTGTTCTGAGAGCCCGAGAGAAATTCATGACGTGTGGGC 360
OY 404 TGCCCAAGAGAGAGTGGCCCTGTGATCATTTCAAGGGCAATGTGAAGAAACAGACACC 463
DB 361 TGCCCAAGAGAGAGTGGCCCTGTGATCATTTCAAGGGCAATGTGAAGAAACAGACACC 420
OY 464 AAAGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 523
DB 421 AAAGCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
OY 524 GTGAGCTAAGAGAGTTTGTCTGTGCTTGTGTAGAGAGCTGAGAGGCCACTTCCAAATTA 583
DB 481 GTGAGCTAAGAGAGTTTGTCTGTGCTTGTGTAGAGAGCTGAGAGGCCACTTCCAAATTA 540
OY 584 AACATTCTCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 643
DB 541 AACATTCTCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
OY 644 ACTCTCCAGCTGATACCAACCTTAATCATTTCCAGTGTCTCAAAAAGAGATTTTTTCAA 703
DB 601 ACTCTCCAGCTGATACCAACCTTAATCATTTCCAGTGTCTCAAAAAGAGATTTTTTCAA 660

```

```

OY 704 GATCATTTTGTGTTGTTGCTCTCTCTAGTGTCTTCTTCTCTGAGTCTTACCTGTGGCC 763
DB 661 GATCATTTTGTGTTGTTGCTCTCTCTAGTGTCTTCTTCTCTGAGTCTTACCTGTGGCC 720
OY 764 CTCGCCCTTACCAAGGCTTATGCTTATACCTGAAAGATTCAGAAATGTAGTCTCT 823
DB 721 CTCGCCCTTACCAAGGCTTATGCTTATACCTGAAAGATTCAGAAATGTAGTCTCTCT 780
OY 824 ACCTAGTGTCAATTAACTTAAATGCAATCAGAGAAAGTAGAACAAGATCAATTAATA 883
DB 781 ACCTAGTGTCAATTAACTTAAATGCAATCAGAGAAAGTAGAACAAGATCAATTAATA 840
OY 884 TTTTAAATGTC 895
DB 841 TTTTAAATGTC 852

RESULT 7
AX675218      870 bp      DNA      linear      PAT 27-MAR-2003
LOCUS         AX675218
DEFINITION   Sequence 1 from Patent WO02070706.
ACCESSION    AX675218
VERSION      AX675218.1 GI:2933434
KEYWORDS
SOURCE
ORGANISM     Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS      French, D., Grimaldi, J.C., Hillan, R.J., Pisabarro, M.T.,
            Schmidt, K.N., Smith, V., Tumas, D., Vandlen, R.L., Watanabe, C.K.,
            Williams, P.M. and Wood, W.I.
            Interleukin-8 homologous polypeptides and therapeutic uses thereof
            Patent: WO 02070706-A 1 12-SEP-2002;
JOURNAL
FEATURES
    source      location/Qualifiers
                1..870
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
BASE COUNT    251 a      237 c      176 g      206 t
ORIGIN
Query Match      95.2%; Score 852; DB 6; Length 870;
Best Local Similarity 100.0%; Pred. No. 6.6e-251;
Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 44 CTCGCCCTCAAAATGGGAACGCTGGCCCTGGAGCTAAAGCATAGACACAGGCTGAGTATC 103
DB 1 CTCGCCCTCAAAATGGGAACGCTGGCCCTGGAGCTAAAGCATAGACACAGGCTGAGTATC 60
OY 104 CTGACCTGATGATCCCGAGGAGTACAGAGACCTCCAGACGGAGACCTTCATTATATTTCT 163
DB 61 CTGACCTGATGATCCCGAGGAGTACAGAGACCTCCAGAGGAGACCTTCATTATATTTCT 120
OY 164 TCAGCAACTTACAGCTGCACCGACGAGTTGCGATGAAATTTCTTCTTCTCTCTCTCC 223
DB 121 TCAGCAACTTACAGCTGCACCGACGAGTTGCGATGAAATTTCTTCTTCTCTCTCTCC 180
OY 224 TGTTCCTGCCATATGCTGATGTCATGTCCTTCTAGCAGCTGAAATCCAGGGGTCGCCA 283
DB 181 TGTTCCTGCCATATGCTGATGTCATGTCCTTCTAGCAGCTGAAATCCAGGGGTCGCCA 240
OY 284 GAGGCCACAGGAGACGAGGCCAGGCTTCTAGAGATGGCTCCAGAGGCGGCCAAGAT 343
DB 241 GAGGCCACAGGAGACGAGGCCAGGCTTCTAGAGATGGCTCCAGAGGCGGCCAAGAT 300
OY 344 GTGAGTGCAGAAATGGTTGTTCTGAGAGCCCGAGAGAAATTCATGACGTGTGGGC 403
DB 301 GTGAGTGCAGAAATGGTTGTTCTGAGAGCCCGAGAGAAATTCATGACGTGTGGGC 360
OY 404 TGCCCAAGAGAGAGTGGCCCTGTGATCATTTCAAGGGCAATGTGAAGAAACAGACACC 463

```

```

Db      |||||
361  TGCCAAAGAGAGGCCCCGTGTGATCTTCAAGGGCAATGTGAAGAAACAGACACC 420
QY      |||||
464  AAAGGACACACAGAAAGCCAAACAGCATTCAGAGCCCTGCAGACAAATTTCTCAACAAAT 523
Db      |||||
421  AAAGGACACACAGAAAGCCAAACAGCATTCAGAGCCCTGCAGACAAATTTCTCAACAAAT 480
QY      |||||
524  GTGACCTAAGAGCTTTGCTGCTGTGTAGAGCTCTGAGCGGCCACTCTCCAAATTA 583
Db      |||||
481  GTGAGCTAAGAGCTTTGCTGCTGTGTAGAGCTCTGAGCGGCCACTCTCCAAATTA 540
QY      |||||
584  AACATTCACGCAAGAGAGAGAGAGACACTTACAGACACTTTTCTCCACCTC 643
Db      |||||
541  AACATTCACGCAAGAGAGAGAGAGACACTTACAGACACTTTTCTCCACCTC 600
QY      |||||
644  ACTGCCACATGTACCCACCCCTTAATCATTCACAGTGTCTCAAAAAGCATGTTTTCAA 703
Db      |||||
601  ACTGCCACATGTACCCACCCCTTAATCATTCACAGTGTCTCTCAAAAAGCATGTTTTCAA 660
QY      |||||
704  GATCATTTGTTGTTGCTGCTCTCTAGTGTCTTCTCTCTGTCAGTCTTACCTGTGCC 763
Db      |||||
661  GATCATTTGTTGTTGCTGCTCTCTAGTGTCTTCTCTCTGTCAGTCTTACCTGTGCC 720
QY      |||||
764  CTCCCTTACCCAGGCTTACCTTAATTAATCTGAAAGATTCAGAGAAATCTACCTTCT 823
Db      |||||
721  CTCCCTTACCCAGGCTTACCTTAATTAATCTGAAAGATTCAGAGAAATCTACCTTCT 780
QY      |||||
824  AGCTAGTGTCTTAACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 883
Db      |||||
781  AGCTAGTGTCTTAACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 840
QY      |||||
884  TTTTAAATGTC 895
Db      |||||
841  TTTTAAATGTC 852

```

```

RESULT 8
AR272401          533 bp   DNA      linear   PAT 10-Apr-2003
LOCUS             Sequence 113 from patent US 6504010.
DEFINITION        AR272401
ACCESSION         AR272401.1 GI:29704286
VERSION           AR272401.1 GI:29704286
KEYWORDS
SOURCE            Unknown.
ORGANISM          Unclassified.

```

```

REFERENCE 1 (bases 1 to 533)
AUTHORS  Wang,T., Bangur,C.S., Lodes,M.J., Fanger,G.R., Vedyick,T.S.,
          Carter,D., Retter,M.W., Mannion,J. and Fan,L.
          Compositions and methods for the therapy and diagnosis of lung
          cancer
          Patent: US 6504010-A 113 07-JAN-2003;
          Location/Qualifiers
            source          1..533
            /organism="unknown"

```

```

BASE COUNT      152 a      154 c      113 g      114 t
ORIGIN

```

```

Query Match      58.7%; Score 525.8; DB 6; Length 533;
Best Local Similarity 99.6%; Pred. No. 2..2e-150;
Matches 527; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      |||||
179  CTGCACGACAGTGGATGAAGTCTAATCTTCCCTCCCTCCCTGTTGCTGCCACTAA 238
Db      |||||
1  CTGCACGACAGTGGATGAAGTCTAATCTTCCCTCCCTCCCTGTTGCTGCCACTAA 60
QY      |||||
239  TCGTATGTCAATGCTCTCTAGACGCTGAATCCAGGGGTGCGCAGAGCCACAGGGACC 298
Db      |||||
61  TCGTATGTCAATGCTCTCTAGACGCTGAATCCAGGGGTGCGCAGAGCCACAGGGACC 120
QY      |||||
299  GAGGCCAGGCTTCTAGAGATGGCTCCAGAAAGCGGCCAAGAATGTGATGCAAGATT 358
Db      |||||
121  GAGGCCAGGCTTCTAGAGATGGCTCCAGAAAGCGGCCAAGAATGTGATGCAAGATT 180

```

```

QY      |||||
359  GGTCTCTGAGAGCCCCGAGAAATAATTCATGACAGTGTCTGGGCTGCCAAGAAGCAGT 418
Db      |||||
181  GGTCTCTGAGAGCCCCGAGAAATAATTCATGACAGTGTCTGGGCTGCCAAGAAGCAGT 240
QY      |||||
419  GCGCCCTGATCATTTCAAGGGCAATGTGAAGAAACAGACACCAAGGACACAGAA 478
Db      |||||
241  GCGCCCTGATCATTTCAAGGGCAATGTGAAGAAACAGACACCAAGGACACAGAA 300
QY      |||||
479  AGCCAAACAGCATTCAGAGCCTGCCAGCAATTTCTCAAAACATGTCTAGCTAAGAGCT 538
Db      |||||
301  AGCCAAACAGCATTCAGAGCCTGCCAGCAATTTCTCAAAACATGTCTAGCTAAGAGCT 360
QY      |||||
539  TTGCTGCGCTTTTGTAGAGAGTCTGAGCGCCACTTCTCCAAATTAACATTTTCAGCAA 598
Db      |||||
361  TTGCTGCGCTTTTGTAGAGAGTCTGAGCGCCACTTCTCCAAATTAACATTTTCAGCAA 420
QY      |||||
599  GAAAGCAGTGAAGCAGACCTACAGACACTCTTCTTCTCCACCTACTCTCCACGTAC 658
Db      |||||
421  GAAAGCAGTGAAGCAGACCTACAGACACTCTTCTTCTCCACCTACTCTCCACGTAC 480
QY      |||||
659  CCACCCCTTAATCATTCACAGTGTCTTCAAAAAGCATGTTTCAAGATC 707
Db      |||||
481  CCACCCCTTAATCATTCACAGTGTCTTCAAAAAGCATGTTTCAAGATC 529

```

```

RESULT 9
AR275982          533 bp   DNA      linear   PAT 10-Apr-2003
LOCUS             Sequence 113 from patent US 6509448.
DEFINITION        AR275982
ACCESSION         AR275982.1 GI:29709627
VERSION           AR275982.1 GI:29709627
KEYWORDS
SOURCE            Unknown.
ORGANISM          Unclassified.

```

```

REFERENCE 1 (bases 1 to 533)
AUTHORS  Wang,T., Bangur,C.S., Lodes,M.J., Fanger,G.R., Vedyick,T.S.,
          Carter,D., Retter,M.W., Mannion,J., Fan,L. and Wang,A.
          Compositions and methods for the therapy and diagnosis of lung
          cancer
          Patent: US 6509448-A 113 21-JAN-2003;
          Location/Qualifiers
            source          1..533
            /organism="unknown"

```

```

BASE COUNT      152 a      154 c      113 g      114 t
ORIGIN

```

```

Query Match      58.7%; Score 525.8; DB 6; Length 533;
Best Local Similarity 99.6%; Pred. No. 2..2e-150;
Matches 527; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      |||||
179  CTGCACGACAGTGGATGAAGTCTAATCTTCCCTCCCTCCCTGTTGCTGCCACTAA 238
Db      |||||
1  CTGCACGACAGTGGATGAAGTCTAATCTTCCCTCCCTCCCTGTTGCTGCCACTAA 60
QY      |||||
239  TCGTATGTCAATGCTCTCTAGACGCTGAATCCAGGGGTGCGCAGAGCCACAGGGACC 298
Db      |||||
61  TCGTATGTCAATGCTCTCTAGACGCTGAATCCAGGGGTGCGCAGAGCCACAGGGACC 120
QY      |||||
299  GAGGCCAGGCTTCTAGAGATGGCTCCAGAAAGCGGCCAAGAATGTGATGCAAGATT 358
Db      |||||
121  GAGGCCAGGCTTCTAGAGATGGCTCCAGAAAGCGGCCAAGAATGTGATGCAAGATT 180
QY      |||||
359  GGTCTCTGAGAGCCCCGAGAAATAATTCATGACAGTGTCTGGGCTGCCAAGAAGCAGT 418
Db      |||||
181  GGTCTCTGAGAGCCCCGAGAAATAATTCATGACAGTGTCTGGGCTGCCAAGAAGCAGT 240
QY      |||||
419  GCGCCCTGATCATTTCAAGGGCAATGTGAAGAAACAGACACCAAGGACACAGAA 478
Db      |||||
241  GCGCCCTGATCATTTCAAGGGCAATGTGAAGAAACAGACACCAAGGACACAGAA 300
QY      |||||
479  AGCCAAACAGCATTCAGAGCCTGCCAGCAATTTCTCAAAACATGTCTAGCTAAGAGCT 538

```



|||||  
Db AGCCAAACAGATCCAGAGCCTCCAGCAATTTCTAACAATGTCAAGCTAAGAGCT 360  
OY TTGCTCTGCTTTTGTAGAGAGCTCTGAGGCGCCACTCTTCAATTAAGATTCTGAGCCAA 598  
Db TTGCTCTGCTTTTGTAGAGAGCTCTGAGGCGCCACTCTTCAATTAAGATTCTGAGCCAA 420  
OY GAAGACAGTGAAGACACCTTACCAGACTCTTCTCCACCTGACCTGCTCCACTGTAC 658  
Db GAAGACAGTGAAGACACCTTACCAGACTCTTCTCCACCTGACCTGCTCCACTGTAC 480  
OY CCACCCCTAAATCATTCAGTGTCTCAAAAAGCATGTTTTCAGATC 707  
Db CCACCCCTAAATCATTCAGTGTCTCAAAAAGCATGTTTTCAGATC 529

RESULT 10  
AX062486 533 bp DNA linear PAT 24-JAN-2001  
LOCUS Sequence 113 from Patent W00100828.  
DEFINITION AX062486  
ACCESSION AX062486.1 GI:12540361  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S.,  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
TITLE Carter, D., Retter, M.W. and Mannion, J.  
JOURNAL Compositions and methods for the therapy and diagnosis of lung  
CORIXA CORPORATION (US)  
FEATURES Location/Qualifiers  
source 1..533  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 152 a 154 c 113 g 114 t  
ORIGIN

Query Match 58.7%; Score 525.8; DB 6; Length 533;  
Best Local Similarity 99.6%; Pred. No. 2.2e-150;  
Matches 527; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 179 CTGCACGACAGTTCGATGAAGATTCTAATCTCTCCCTCTGTTGTCGACATA 238  
Db 1 CTGCACGACAGTTCGATGAAGATTCTAATCTCTCCCTCTGTTGTCGACATA 60  
OY 239 TGTGATGTCCATGGTCTCTAGACAGCTGAATCCAGGGGTGCGCAGAGGCCACAGGAGC 298  
Db 61 TGTGATGTCCATGGTCTCTAGACAGCTGAATCCAGGGGTGCGCAGAGGCCACAGGAGC 120  
OY 299 GAGGCGAGGCTTCTAGAGAGTGGCTCCAGGAAGGGGGCCAGAAATGTGAGTCCAAAGATT 358  
Db 121 GAGGCGAGGCTTCTAGAGAGTGGCTCCAGGAAGGGGGCCAGAAATGTGAGTCCAAAGATT 180  
OY 359 GGTTCCTGAGAGCCCGAGAGAAATTCATGACAGTGTCTGGGTGCGCAAGAAGACAT 418  
Db 181 GGTTCCTGAGAGCCCGAGAGAAATTCATGACAGTGTCTGGGTGCGCAAGAAGACAT 240  
OY 419 GCCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAAACAAGACCAAGAGCCACAGAA 478  
Db 241 GCCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAAACAAGACCAAGAGCCACAGAA 300  
OY 479 AGCCAAACAGATTCGAGAGCTTCCAGCAATTTCTCAACATGTACAGTAAAGCT 538  
Db 301 AGCCAAACAGATTCGAGAGCTTCCAGCAATTTCTCAACATGTACAGTAAAGCT 360  
OY 539 TTGCTCTGCTTTTGTAGAGAGCTCTGAGGCGCCACTCTTCAATTAAGATTCTGAGCCAA 598  
Db 361 TTGCTCTGCTTTTGTAGAGAGCTCTGAGGCGCCACTCTTCAATTAAGATTCTGAGCCAA 420

OY 599 GAAGACAGTGAAGACACCTTACCAGACTCTTCTCCACCTGACCTGCTCCACTGTAC 658  
Db 421 GAAGACAGTGAAGACACCTTACCAGACTCTTCTCCACCTGACCTGCTCCACTGTAC 480  
OY 659 CCACCCCTAAATCATTCAGTGTCTCAAAAAGCATGTTTTCAGATC 707  
Db 481 CCACCCCTAAATCATTCAGTGTCTCAAAAAGCATGTTTTCAGATC 529

RESULT 11  
AX367403 533 bp DNA linear PAT 16-FEB-2002  
LOCUS Sequence 113 from Patent W00204514.  
DEFINITION AX367403  
ACCESSION AX367403.1 GI:18855507  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Wang, T., Malanbe, Y., Henderson, R.A., Johnson, J.C., Retter, M.W.,  
AUTHORS Marnerakis, M., Carter, D., Fanger, G.R., Vedvick, T.S., Bangur, C.S.,  
McNabb, A., Fanger, N., Switzer, A., McNeill, P.D. and Clapper, J.D.  
1  
TITLE Compositions and methods for the therapy and diagnosis of lung  
cancer  
JOURNAL Patent: WO 0204514-A 113 17-JAN-2002;  
CORIXA CORPORATION (US)  
FEATURES Location/Qualifiers  
source 1..533  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 152 a 154 c 113 g 114 t  
ORIGIN

Query Match 58.7%; Score 525.8; DB 6; Length 533;  
Best Local Similarity 99.6%; Pred. No. 2.2e-150;  
Matches 527; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 179 CTGCACGACAGTTCGATGAAGATTCTAATCTCTCCCTCTGTTGTCGACATA 238  
Db 1 CTGCACGACAGTTCGATGAAGATTCTAATCTCTCCCTCTGTTGTCGACATA 60  
OY 239 TGTGATGTCCATGGTCTCTAGACAGCTGAATCCAGGGGTGCGCAGAGGCCACAGGAGC 298  
Db 61 TGTGATGTCCATGGTCTCTAGACAGCTGAATCCAGGGGTGCGCAGAGGCCACAGGAGC 120  
OY 299 GAGGCGAGGCTTCTAGAGAGTGGCTCCAGGAAGGGGGCCAGAAATGTGAGTCCAAAGATT 358  
Db 121 GAGGCGAGGCTTCTAGAGAGTGGCTCCAGGAAGGGGGCCAGAAATGTGAGTCCAAAGATT 180  
OY 359 GGTTCCTGAGAGCCCGAGAGAAATTCATGACAGTGTCTGGGTGCGCAAGAAGACAT 418  
Db 181 GGTTCCTGAGAGCCCGAGAGAAATTCATGACAGTGTCTGGGTGCGCAAGAAGACAT 240  
OY 419 GCCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAAACAAGACCAAGAGCCACAGAA 478  
Db 241 GCCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAAACAAGACCAAGAGCCACAGAA 300  
OY 479 AGCCAAACAGATTCGAGAGCTTCCAGCAATTTCTCAACATGTACAGTAAAGCT 538  
Db 301 AGCCAAACAGATTCGAGAGCTTCCAGCAATTTCTCAACATGTACAGTAAAGCT 360  
OY 539 TTGCTCTGCTTTTGTAGAGAGCTCTGAGGCGCCACTCTTCAATTAAGATTCTGAGCCAA 598  
Db 361 TTGCTCTGCTTTTGTAGAGAGCTCTGAGGCGCCACTCTTCAATTAAGATTCTGAGCCAA 420  
OY 599 GAAGACAGTGAAGACACCTTACCAGACTCTTCTCCACCTGACCTGCTCCACTGTAC 658  
Db 421 GAAGACAGTGAAGACACCTTACCAGACTCTTCTCCACCTGACCTGCTCCACTGTAC 480

QY 659 CCACCCCTAAATCATTCAGTGTCTCTCAAAAAAGCATGTTTTCAGATC 707  
DB 481 CCACCCCTAAATCATTCAGTGTCTCTCAAAAAAGCATGTTTTCAGATC 529

RESULT 12  
BD107982 481 bp DNA linear PAT 18-SEP-2002  
LOCUS EST and encoded human protein.  
DEFINITION BD107982  
ACCESSION BD107982.1 GI:23202800  
VERSION JP 2002010789-A/59.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens (human)  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 481)  
AUTHORS Edwards,J.B.D.M., Jobert,S. and Giordano,J.E..  
TITLE EST and encoded human protein  
JOURNAL Patent: JP 2002010789-A 59 15-JAN-2002;  
GENSET CORP

COMMENT OS Homo sapiens (human)  
PN JP 2002010789-A/59  
PD 15-JAN-2002  
PF 07-AUG-2000 JP 2000280989  
PR 05-AUG-1999 US 60/147499  
PI JEAN BAPTISTE DOMAS MILNE EDWARDS,SEVELIN JOBERT,JEAN EVE PI  
GIORDANO  
PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,PC  
C12N1/21,  
PC C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00,PC  
C12N5/00  
CC Von Heljng matrix  
CC score 8.3000019073486  
CC seq LILPLMLMSVSS/SL  
FH key Location/Qualifiers  
FT CDS 144..479  
FT sig\_peptide 144..209.  
Location/Qualifiers

FEATURES  
source 1..481  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 139 a 128 c 121 g 93 t

ORIGIN

Query Match 53.7%; Score 481; DB 6; Length 481;  
Best Local Similarity 100.0%; Pred. No. 1.4e-136;  
Matches 481; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 AAATGGGAACGGCGCTGGGACTAAAGCATATACACACAGGCTGATCTGACCTGA 112  
DB 1 AAATGGGAACGGCGCTGGGACTAAAGCATATACACACAGGCTGATCTGACCTGA 60  
QY 113 GTCATCCCGAGGATAGAGAGCTCCAGACAGGACCTTCATTAATCTTCAACCAAC 172  
DB 61 GTCATCCCGAGGATAGAGAGCTCCAGACAGGACCTTCATTAATCTTCAACCAAC 120  
QY 173 TTACAGCTCCACGACAGTGTGGGATGAAGTTCTAATCTTCCCTCTCTGTTGCTGC 232  
DB 121 TTACAGCTCCACGACAGTGTGGGATGAAGTTCTAATCTTCCCTCTCTGTTGCTGC 180  
QY 233 CACTATGTGTGATGTGCATGTCTCTAGAGAGCTGATCAATCAGGGGTGCGCAGAGGCCACA 292  
DB 181 CACTATGTGTGATGTGCATGTCTCTAGAGAGCTGATCAATCAGGGGTGCGCAGAGGCCACA 240  
QY 293 GGGACCGAGAGCGCTTCTAGAGAGTGGCTCCAGAGAGGCGCCAGAATGTGAGTGA 352  
DB 241 GGGACCGAGAGCGCTTCTAGAGAGTGGCTCCAGAGAGGCGCCAGAATGTGAGTGA 300  
QY 353 AAGATTGTCTCTGAGAGCGCCGAGAGAAATTCATGACAGTGTCTGCGCTGCCAAGA 412  
DB 301 AAGATTGTCTCTGAGAGCGCCGAGAGAAATTCATGACAGTGTCTGCGCTGCCAAGA 360

QY 413 AGCAGTCCCTCTGTGATCATTTTCAAGGCAATGTGAAGAAAAAGACACCAAGGACCC 472  
DB 361 AGCAGTCCCTCTGTGATCATTTTCAAGGCAATGTGAAGAAAAAGACACCAAGGACCC 420  
QY 473 ACAGAAAGCCAAACATTCAGAGCTGCGCCAGCAATTTCTCAACATTCAGCTAA 532  
DB 421 ACAGAAAGCCAAACATTCAGAGCTGCGCCAGCAATTTCTCAACATTCAGCTAA 480  
QY 533 G 533  
DB 481 G 481

RESULT 13  
AX182041 626 bp DNA linear PAT 06-AUG-2001  
LOCUS Sequence  
DEFINITION AX182041  
ACCESSION AX182041  
VERSION AX182041.1 GI:15133314  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1  
AUTHORS Lillie,J., Palermo,A., Wang,Y., Steinmann,K. and Elias,J.  
TITLE Identification, assessment, prevention, and therapy of breast  
JOURNAL Cancer  
Patent: WO 0146697-A 51 28-JUN-2001;  
Millennium Predictive Medicine, Inc. (US)  
Location/Qualifiers

FEATURES  
source 1..626  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 172 a 170 c 149 g 133 t 2 others

ORIGIN

Query Match 53.1%; Score 475; DB 6; Length 626;  
Best Local Similarity 97.1%; Pred. No. 1e-134;  
Matches 494; Conservative 0; Mismatches 12; Indels 3; Gaps 1;

QY 57 GGGACGCTGCGCTGGGACTAAAGCATATACACACAGGCTGATCTGACCTGACTA 116  
DB 35 GGGACGCTGCGCTGGGACTAAAGCATATACACACAGGCTGATCTGACCTGACTA 94  
QY 117 TCCCGAGGATCAGAGGCTCCAGCAGGAGACCTTCATTAATCTTCAACCAACTTAC 176  
DB 95 TCCCGAGGATCAGAGGCTCCAGCAGGAGACCTTCATTAATCTTCAACCAACTTAC 154  
QY 177 AGCTGACGACAGTGGGATGAAGTTCTAATCTTCCCTCTCTGTTGCTGCACT 236  
DB 155 AGCTGACGACAGTGGGATGAAGTTCTAATCTTCCCTCTCTGTTGCTGCACT 214  
QY 237 AATGCTGATGTCATGTGCTTACAGAGCTGATCAAGGAGTGGCGCAGAGGCCACAGGA 296  
DB 215 AATGCTGATGTCATGTGCTTACAGAGCTGATCAAGGAGTGGCGCAGAGGCCACAGGA 274  
QY 297 CCGAGGCGAGGCTTCTAGAGATGCTCCAGAGAGGCGCCAGAATGTGATGCAAGA 356  
DB 275 CCGAGGCGAGGCTTCTAGAGATGCTCCAGAGAGGCGCCAGAATGTGATGCAAGA 334  
QY 357 TTGGTTCCGAGAGCGCCGAGAGAAATTCATGACAGTGTGGGCTGCCAAGAGCA 416  
DB 335 TTGGTTCCGAGAGCGCCGAGAGAAATTCATGACAGTGTGGGCTGCCAAGAGCA 394  
QY 417 GTGCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAAAGACCAAGGACACACAG 476  
DB 395 GTGCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAAAGACCAAGGACACACAG 454  
QY 477 AAAGCCAAACAGCATTCAGAGCTGCGCAGCAATTTCTCAACATTCAGCTAAGAG 536

Db	455	AAACCCAAACAGACATTCACAGAGCCTGCACGACATTTCTCAAAACAGTACGCTTAAAGA	514
QY	537	CTTTGCTC---TGCCTTTGTAGAGCTCT	562
Db	515	GCTTTTGCTCTTGGCTTTGTATGAACTACT	543
RESULT 14			
LOCUS	BD082607	511 bp	DNA
DEFINITION	20 human secreted proteins.		linear
ACCESSION	BD082607		
VERSION	BD082607.1	GI:22628217	
KEYWORDS	JP 2001521383-A/17.		
SOURCE	unidentified		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 511)		
AUTHORS	Rosen,C.A., Ruben,S.M., Yu,G.L., Ni,J. and Feng,P.		
TITLE	20 human secreted proteins		
JOURNAL	Patent: JP 2001521383-A 17 06-NOV-2001;		
COMMENT	HUMAN GENOME SCIENCES INC		
	PN JP 2001521383-A/17		
	PD 06-NOV-2001		
	PF 07-APR-1998 JP 1998543005		
	PR 08-APR-1997 US 60/042728, 08-APR-1997 US 60/042754 PR		
	PR 08-APR-1997 US 60/042825, 08-APR-1997 US 60/042727 PR		
	08-APR-1997 US 60/042726, 30-MAY-1997 US 60/048184 PR		
	30-MAY-1997 US 60/048068, 30-MAY-1997 US 60/048070 PI		
	A ROSEN, STEVEN M RUBEN, GUO LIANG YU, JIAN NI, PING FENG PC		CHAIG
	G01N33/68, A61K48/00, C12N15/12, C12N1/21, C12N5/10, C12Q1/48, PC		
	A61K31/70,		
	PC C07K14/47, C12N15/62, G01N33/53, C12N15/11, C12Q1/68, C07K19/00, PC		
	G01N33/60,		
	PC A61K38/17		
	CC Strandedness: Double;		
	CC Topology: Linear;		
FEATURES	Key	Location/Qualifiers.	
source	1..511		
	/organism="unidentified"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:32644"		
BASE COUNT	138 a 138 c 125 g 104 t	6 others	
ORIGIN			
Query Match	49.7%; Score 445.2; DB 6; Length 511;		
Best Local Similarity	97.9%; Pred. No. 1.6e-125;		
Matches	466; Conservative 4; Mismatches 4; Indels 2; Gaps 2;		
QY	1	CTAATCTGTACGTAACAGCAAGACAGCGTCACCTACCTGTTCGCGCTCAATGGGA	60
Db	38	CTAATCTGTACGTAACAGCAAGACAGCGTCACCTACCTGTTCGCGCTCAATGGGA	97
QY	61	ACGCTGCGCTGGAGCTAAAGCATAGACCACGAGCTGATCTCTGACCTGAGTCATCC	120
Db	98	ACGCTGCGCTGGAGCTAAAGCATAGACCACGAGCTGATCTCTGACCTGAGTCATCC	157
QY	121	CAGGATCAGAGAGCCTCCAGCAGGAGAACCTTCATATATCTTCAAGCACTTACAGCT	180
Db	158	CAGGATCAGAGAGCCTCCAGCAGGAGAACCTTCATATATCTTCAAGCACTTACAGCT	217
QY	181	GCACCGACAGTTCGAGTGAAGTTCATATCTTCCCTCCGTCGTCGTCGCTGACCTAATG	240
Db	218	GCACCGACAGTTCGAGTGAAGTTCATATCTTCCCTCCGTCGTCGTCGCTGACCTAATG	277
QY	241	CTGATGTCATAGTCTCTTACGACGCTGATCCAGGGGTGCGCAGAGGCCACAGGAGCGCA	300
Db	278	CTGATGTCATAGTCTCTTACGACGCTGATCCAGGGGTGCGCAGAGGCCACAGGAGCGCA	337
QY	301	GGCCAGGCTTTCTAGAGATGGCTCCAGCAGAGCGCCCAAGATGTGAGTGCAGAAAGTTGG	360
Db	338	GGCCAGGCTTTCTAGAGATGGCTCCAGCAGAGCGCCCAAGATGTGAGTGCAGAAAGTTGG	397

OY	361	TTCTGTGAGACCCCGAGAAATAATTCAGACGTCTCTGGGTGCGCAAGAAGACAGTGC	420
Db	398	TTCTGTGAGAC-CCCGAGAAATAATTCAGACGTCTCTGGGTGCGCAAGAARCAATGC	456
OY	421	CCCGTATGATTCATTCAGGCAATGTGAAGAAACAAAGACACCAAGGACACACAG	476
Db	457	CCNGTGATTCATTCAGGAGGC-ATGTGAAGAAACAAAGACCAAGGACACACAG	511
RESULT 15			
AC011497			
LOCUS	AC011497	168586 bp	DNA linear PRI 14-JUL-2002
DEFINITION	Homo sapiens chromosome 19 clone CTB-50E14, complete sequence.		
ACCESSION	AC011497		
VERSION	AC011497.6	GI:8844110	
KEYWORDS	HTG.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 168586)		
TITLE	DOE Joint Genome Institute and Stanford Human Genome Center.		
JOURNAL	Unpublished		
AUTHORS	2 (bases 1 to 168586)		
TITLE	DOE Joint Genome Institute.		
REFERENCE	Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA		
AUTHORS	3 (bases 1 to 168586)		
TITLE	DOE Joint Genome Institute and Stanford Human Genome Center.		
JOURNAL	Submitted (30-JUN-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA		
REFERENCE	4 (bases 1 to 168586)		
AUTHORS	DOE Joint Genome Institute and Stanford Human Genome Center.		
TITLE	Direct Submission		
JOURNAL	Submitted (14-JUL-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA		
COMMENT	On Jun 30, 2000 this sequence version replaced gi:7711512. Draft Sequence Produced by DOE Joint Genome Institute www.jgi.doe.gov		
FEATURES	Finishing completed at Stanford Human Genome Center www.sngc.stanford.edu		
source	Quality: Phrap Quality >=40 100% of Sequence; Estimated Total Number of Errors is 0. Location/Qualifiers		
	1. 168586		
	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:9606"		
	/chromosome="19"		
	/clone="CTB-50E14"		
BASE COUNT	44482 a 43600 c 40989 g 39515 t		
ORIGIN			
Query Match	49.0%;	Score 438.4;	DB 9;
Best Local Similarity	99.8%;	Pred. No. 4.0e-123;	Length 168586;
Matches 439;	Conservative 0;	Mismatches 1;	Indels 0;
			Gaps 0;
OY	456	AGACACCAAGGACACAGAAAGCCAAACAGCATTCACAGAGCCTGCAGCAATTTCT	515
Db	70477	AGGACACCAAGGACACAGAAAGCCAAACAGCATTCACAGAGCCTGCAGCAATTTCT	70536
OY	516	CAACCAATGTGAGTAAGAGCTTTGCTGTGCTTTGTAGAGCTCTGAGCGCCACTCT	575
Db	70537	CAACCAATGTGAGTAAGAGCTTTGCTGTGCTTTGTAGAGCTCTGAGCGCCACTCT	70536
OY	576	TCCAATTAAACATTTCTAGCCAAAGACAGTGAAGACACCTTACCAAGACACTCTTCTCT	635
Db	70597	TCCAATTAAACATTTCTAGCCAAAGACAGTGAAGACACCTTACCAAGACACTCTTCTCT	70556

OY	636	CCACCCGACATGTCGCCAGCTGACCCAGCCCTAAATGATTCAGAGTGCTCCAAAAGCATG	695
Db	70557	CCACCGCAGCTTCCGCCAGCTGACCCAGCCCTAAATGATTCAGAGTGCTCCAAAAGCATG	70716
OY	696	TTTTTCAGATGCAATTTTGTTGTTGTCCTCTAGTGCTTCTCTGTCAGTCTTAG	755
Db	70717	TTTTTCAGATGCAATTTTGTTGTTGTCCTCTAGTGCTTCTCTGTCAGTCTTAG	70776
OY	756	CCGTGCGCCATCCCGCTTACCAGGCTTAAGGCTTAATACCTGAAAGATTCACAGAAAGCT	815
Db	70777	CCGTGCGCCATCCCGCTTACCAGGCTTAAGGCTTAATACCTGAAAGATTCACAGAAAGCT	70836
OY	816	AGCTTCCTAGCTAGTGATTTTAACTTAATGCAATGCAAGAAAGTAGCAAAACAGAGTC	875
Db	70837	AGCTTCCTAGCTAGTGATTTTAACTTAATGCAATGCAAGAAAGTAGCAAAACAGAGTC	70896
OY	876	AAATAATATTTTAAATGTC 895	
Db	70897	AAATAATATTTTAAATGTC 70916	

Search completed: October 9, 2003, 19:48:23  
Job time : 3449.74 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2003, 13:21:47 ; Search time 1316.03 Seconds  
(without alignments)  
10028.129 Million cell updates/sec

Title: US-09-700-770-6

Perfect score: 543  
Sequence: 1 ccggcgctggagggcgagg.....gttaagagcaaaaaaaaaa 543

Scoring table: IDENTITY-NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estom:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_fod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	475	87.5	490	12	BM977626 UI-CF-EN1
2	474	87.3	496	12	B1818715 603037535
3	462.4	85.2	1059	13	B0067622 AGENCOURT
4	461	84.9	1083	12	BM921624 AGENCOURT

5	457.6	84.3	550	10	AM974727	AM974727 EST386817
6	457	84.2	473	12	BM920793	BM920793 AGENCOURT
7	457	84.2	473	12	BM920794	BM920794 AGENCOURT
8	453.4	83.5	880	12	B1489765	B1489765 603032283
9	453	83.4	875	12	B1822360	B1822360 603037920
10	451	83.1	496	12	B1818795	B1818795 603041303
11	448.8	82.7	491	12	B1819014	B1819014 603033130
12	444	81.8	885	12	B1824102	B1824102 603039244
13	441	81.2	472	12	BM977779	BM977779 UI-CF-EN1
14	439.2	80.9	680	12	B1821791	B1821791 603035866
15	439	80.8	439	9	A1685860	A1685860 tt90f09.x
16	438	78.8	437	14	CB049699	CB049699 NISC-g112
17	425	78.3	425	9	A1187341	A1187341 qe26d06.x
18	425	78.3	961	12	B1819045	B1819045 603033186
19	424	78.1	424	9	A1333740	A1333740 qp98f05.x
20	420.8	77.5	424	9	A1744099	A1744099 wc36c10.x
21	416.4	76.7	526	9	AA742697	AA742697 nc30g04.s
22	413	76.1	413	9	A1745557	A1745557 wc34e01.x
23	412.8	76.0	416	10	BE221778	BE221778 7062e02.x
24	409.4	75.4	420	12	BM982112	BM982112 UI-CF-EN1
25	400.4	73.7	662	12	BM982925	BM982925 UI-CF-EN1
26	400.4	73.7	711	12	BM982925	BM982925 UI-CF-EN1
27	400.4	73.7	718	14	CA313307	CA313307 UI-CF-ENO
28	400.4	73.7	731	12	BM980649	BM980649 UI-CF-EN1
29	391.2	72.0	1004	12	B1769722	B1769722 603055021
30	387	71.3	476	12	B1818534	B1818534 603033053
31	386.6	71.2	896	12	B1824919	B1824919 603032441
32	384.6	70.8	878	12	B1823159	B1823159 603039406
33	383.4	70.6	407	12	B1820788	B1820788 603034390
34	378	68.6	378	9	A1684641	A1684641 wa84n08.x
35	377.8	69.6	416	12	B1490604	B1490604 603032283
36	368	67.8	1000	12	B1908998	B1908998 603070132
37	339.8	62.6	343	9	AA649864	AA649864 ns54a03.s
38	338	62.2	435	14	CB049698	CB049698 NISC-g112
39	335.2	61.7	887	12	B1818788	B1818788 603037535
40	335.2	61.7	320	13	BE679439	BE679439 UI-CF-D01
41	306.6	57.6	335	9	AA902200	AA902200 ok69a06.s
42	293.4	54.0	380	14	N95182	N95182 zb52d10.s1
43	285.4	52.6	323	10	BE707758	BE707758 QV3-H7054
44	280	51.6	389	14	W72786	W72786 z661a04.s1
45	277.8	51.2	427	14	W76414	W76414 z661a04.r1

## ALIGNMENTS

RESULT 1  
LOCUS BM977626 490 bp mRNA linear EST 21-FEB-2003  
DEFINITION UI-CF-EN1-ae1-o-13-0-UI.s1 UI-CF-EN1 Homo sapiens CDNA clone  
UI-CF-EN1-ae1-o-13-0-UI 3', mRNA sequence.  
BM977626 GI:195966235

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
Genome Res. 6 (9), 791-806 (1996)  
97044477  
8889548

COMMENT  
Contact: McCray, PB  
McCray Lab  
University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171  
Email: paul-mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa

CDNA library preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com) or from Open Biosystems  
 (www.openbiosystems.com).  
 The following repetitive elements were found in this cDNA  
 sequence: 459-484, >gc\_rich#low\_complexity  
 Seq primer: M13 FORWARD  
 PolYA=Yes.

# FEATURES

Location/Qualifiers

1..490

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="UI-CF-EN1-aef-o-13-0-ui"

/tissue\_type="Primary Lung Cystic Fibrosis Epithelial  
 Cells"

/dev\_stage="Adult"

/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone\_lib="UI-CF-EN1"

/note="Organ: Lung; Vector: pRT73-Pac (Pharmacia) with a  
 modified polylinker; Site 1: EcoR I; Site 2: Not I;  
 UI-CF-EN1 is a normalized cDNA library containing the  
 following tissue(s): Primary Lung Cystic Fibrosis  
 Epithelial Cells. The library was constructed according to  
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
 1996. First strand cDNA synthesis was primed with an  
 oligo-dT primer containing a Not I site. Double stranded  
 cDNA was ligated to an EcoR I adaptor, digested with Not  
 I, and cloned directionally into pRT73-Pac vector. The  
 oligonucleotide used to prime the synthesis of  
 first-strand cDNA contains a library tag sequence that is  
 located between the Not I site and the (dr)18 tail. The  
 sequence tag for this library is CTCCTCAGGT.  
 TAG\_LIB=UI-CF-EN1  
 TAG\_TISSUE=Human Lung Epithelial Cell lines untreated LPS  
 6hr to LPS 24h  
 TAG\_SEQ=CTGCTCAGGT"

BASE COUNT 73 a 154 c 175 g 88 t

ORIGIN

Query Match 87.5%; Score 475; DB 12; Length 490;  
 Best Local Similarity 100.0%; Pred. No. 8.2e-81;  
 Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

69 CCGCGGCCCCGAGACCCCGCCAGTGAAGCTCCGCTGCGGCTCTGCGGCC 128  
 |||||||  
 482 CCGCGGCCCCGAGACCCCGCCAGTGAAGCTCCGCTGCGGCTCTGCGGCC 423  
 |||||||  
 129 CTGTCGCGAGCCCGCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 188  
 |||||||  
 422 CTGTCGCGAGCCCGCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 363  
 |||||||  
 189 GTGCTGCGCTGAGTCTGCGGCGAGAGCCGGGGCCGCTGCGCAACCCCTCGGC 248  
 |||||||  
 362 GTGCTGCGCTGAGTCTGCGGCGAGAGCCGGGGCCGCTGCGCAACCCCTCGGC 303  
 |||||||  
 249 ACCCTCAACCCGCTGAAGCTCTGCTGAGCAGCTGGGCAATCCCTGTAACCACTCA 308  
 |||||||  
 302 ACCCTCAACCCGCTGAAGCTCTGCTGAGCAGCTGGGCAATCCCTGTAACCACTCA 243  
 |||||||  
 309 GAGGCTCCCAAGAGTGTGGGCTGAGCGGGGCTGAGCGGCTGGGGGCTGTAAGGCC 368  
 |||||||  
 242 GAGGCTCCCAAGAGTGTGGGCTGAGCGGGGCTGAGCGGCTGGGGGCTGTAAGGCC 183  
 |||||||  
 369 CTGAAGGCTCTGCTGGGGGCTGAGCAGTGTGGGCTGAGCGGCTGGGGGCTGTAAGGCC 428  
 |||||||  
 182 CTGAAGGCTCTGCTGGGGGCTGAGCAGTGTGGGCTGAGCGGCTGGGGGCTGTAAGGCC 123  
 |||||||  
 429 CCGTGAAGAGAAAGCTGCGCCACCGCGAGGGCTGAAAACCCGCGCGGGAGAGACCGT 488  
 |||||||  
 122 CCGTGAAGAGAAAGCTGCGCCACCGCGAGGGCTGAAAACCCGCGCGGGAGAGACCGT 63

QY 489 CCATCCCTTCCCGCGCCCTCTCAATTAACGTTGTTAGAGCAAAAAA 543  
 |||||||  
 DB 62 CCATCCCTTCCCGCGCCCTCTCAATTAACGTTGTTAGAGCAAAAAA 8

RESULT 2  
 B1818715  
 LOCUS  
 DEFINITION  
 mRNA sequence.  
 ACCESSION  
 B1818715  
 VERSION  
 B1818715.1 GI:15930265  
 KEYWORDS  
 EST.  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 NIH-MGC http://mgc.ncl.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished  
 Contact: Robert Strausberg, Ph.D.  
 Email: c9apbs-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 CDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ILNL at:  
 http://image.llnl.gov  
 Plate: ILNL1445 row: e column: 09

FEATURES

source

Location/Qualifiers

1..496

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5178608"

/lab\_host="DH10B"

/clone\_lib="NIH-MGC\_115"

/note="Organ: Pooled brain, lung, testis; Vector:  
 pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA  
 source anonymous pool of 6 male brains, age range 23-27; 1  
 male lung, age 27; and 1 male testis, age 69. Library is  
 oligo-dT primed and directionally cloned (EcoRV site is  
 destroyed upon cloning). Average insert size 1.8 kb,  
 insert size range 1-3 kb. Library is normalized and  
 enriched for full-length clones and was constructed by C.  
 Gruber (Invitrogen). Research Genetics tracking code  
 021. Note: this is a NIH-MGC Library."

BASE COUNT 93 a 176 c 153 g 74 t

ORIGIN

Query Match 87.3%; Score 474; DB 12; Length 496;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-80;  
 Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

70 CCGGCGCCCGAGAGCCCGCGCATGAAGCTCGCCCTCTGCGGCTCTGCGGCC 129  
 |||||||  
 1 CCGGCGCCCGAGAGCCCGCGCATGAAGCTCGCCCTCTGCGGCTCTGCGGCC 60  
 |||||||  
 130 TGTCTGAGGCTCCGCTCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 189  
 |||||||  
 61 TGTCTGAGGCTCCGCTCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 120  
 |||||||  
 190 TCGCTGCGCTGAGTCTGCGGCGAGAGCCGGGCGGAGACCTGCGCAACCCCTCGCA 249  
 |||||||  
 121 TCGCTGCGCTGAGTCTGCGGCGAGAGCCGGGCGGAGACCTGCGCAACCCCTCGCA 180  
 |||||||  
 250 CCGTCAACCCGCTGAAGCTCTGCTGAGCAGCTGGGCAATCCCGTGAACCACTCATAG 309  
 |||||||  
 181 CCGTCAACCCGCTGAAGCTCTGCTGAGCAGCTGGGCAATCCCGTGAACCACTCATAG 240  
 |||||||

QY 310 AGGCTCCCAAGATGTGTGCTAGTGGTCTCCCAAGCCGTGGGGCCGTGAAGGCC 369  
 DB 241 AGGCTCCCAAGATGTGTGCTAGTGGTCTCCCAAGCCGTGGGGCCGTGAAGGCC 300  
 OY 370 TGAAGGCCCTGCTGGGGCCCTGACAGTGTGCTGAGCCGAGACTGTGACATCTAC 429  
 DB 301 TGAAGGCCCTGCTGGGGCCCTGACAGTGTGCTGAGCCGAGACTGTGACATCTAC 360  
 OY 430 CTGAGACAAGAGCTGCTGCCACCCGAGGAGCTGAAGACCCCGCGGGAGAGACCTC 489  
 DB 361 CTGAGACAAGAGCTGCTGCCACCCGAGGAGCTGAAGACCCCGCGGGAGAGACCTC 420  
 OY 490 CATCCCTTCCCGCGGGCCCTCTCATTAACGTGGTTAAGACAAAAA 543  
 DB 421 CATCCCTTCCCGCGGGCCCTCTCATTAACGTGGTTAAGACAAAAA 474

RESULT 3  
 B0067622 1059 bp mRNA linear EST 02-APR-2002  
 LOCUS AGENCOURT\_6759083 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5755192  
 DEFINITION 5', mRNA sequence.  
 ACCESSION B0067622  
 VERSION B0067622.1 GI:19896668  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1059)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.llnl.gov  
 Plate: L1AM12793 row: m column: 17  
 High quality sequence stop: 343.  
 Location/Qualifiers  
 1..1059  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5755192"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH\_MGC\_115"  
 /note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH-MGC Library."  
 BASE COUNT 199 a 339 c 304 g 217 t  
 ORIGIN

Query Match 85.2%; Score 462.4; DB 13; Length 1059;  
 Best Local Similarity 99.8%; Pred. No. 1.8e-78;  
 Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 71 GCGGCGCCCGAGCGCCCGCCGAGAGCTGCGCGCCCTCTCGGGCTGCGGCCCT 130  
 DB 1 GCGGCGCCCGAGCGCCCGCCGAGAGCTGCGCGCCCTCTCGGGCTGCGGCCCT 60

OY 131 GTCTGACAGCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGT 190  
 DB 61 GTCTGACAGCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGT 120  
 OY 191 CGCTGCGCTGAGTGGCGGGGAGAGCGGGGCGGGAGCCCTGTGGCAACCCCTCGGAC 250  
 DB 121 CGCTGCGCTGAGTGGCGGGGAGAGCGGGGCGGGAGCCCTGTGGCAACCCCTCGGAC 180  
 OY 251 CCTGACCCGCTGAAGCTCTGCTGAGAGAGCTGGGCATCCCGTGAACCACTCATAGA 310  
 DB 181 CCTGACCCGCTGAAGCTCTGCTGAGAGAGCTGGGCATCCCGTGAACCACTCATAGA 240  
 OY 311 GGGCTCCAGAAAGTGTGCTGAGCTGGTCCCAAGCCGTGGGGCGGTGAAGGCCCT 370  
 DB 241 GGGCTCCAGAAAGTGTGCTGAGCTGGTCCCAAGCCGTGGGGCGGTGAAGGCCCT 300  
 OY 371 GAAGGCCCTGCTGGGGCCCTGACAGTGTGGCTGAGCCGAGACTGAGCATCTACAC 430  
 DB 301 GAAGGCCCTGCTGGGGCCCTGACAGTGTGGCTGAGCCGAGACTGAGCATCTACAC 360  
 OY 431 TGAGGACAAGAGCGTGGCCACCCGAGAGGCTGAAACCCCGCGGGGAGAGACCTCC 490  
 DB 361 TGAGGACAAGAGCGTGGCCACCCGAGAGGCTGAAACCCCGCGGGGAGAGACCTCC 420  
 OY 491 ATCCCTTCCCGCGGGCCCTCTCATTAACGTGGTTAAGACAA 534  
 DB 421 ATCCCTTCCCGCGGGCCCTCTCATTAACGTGGTTAAGACGA 464

RESULT 4  
 B0921624 1083 bp mRNA linear EST 12-MAR-2002  
 LOCUS B0921624  
 DEFINITION 5', mRNA sequence.  
 ACCESSION B0921624  
 VERSION B0921624.1 GI:19372003  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1083)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.llnl.gov  
 Plate: L1AM12788 row: h column: 07  
 High quality sequence stop: 486.  
 Location/Qualifiers  
 1..1083  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5753142"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH\_MGC\_115"  
 /note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C.









```
QY 319 AGAAGTGTGCTGCTGAGTGGGTCCCGAGCGCTGGGGCCCTGAAGCCCTGAAGCCCC 378
Db 240 AGAAGTGTGCTGCTGAGTGGGTCCCGAGCGCTGGGGCCCTGAAGCCCTGAAGCCCC 299
QY 379 TGGTGGGGCCCTGACAGTGTGGCTGAGCCAGACTGAGCATCTACACCGAGGACA 438
Db 300 TGGTGGGGCCCTGACAGTGTGGCTGAGCCAGACTGAGCATCTACACCGAGGACA 359
QY 439 AGACGCTGCCACCCCGAGGGCTGAAAAACCCCGCGGGAGAGACCTCCATCCCTT 498
Db 360 AGACGCTGCCACCCCGAGGGCTGAAAAACCCCGCGGGAGAGACCTCCATCCCTT 419
QY 499 CCCCCGCCCCCTCTCATTAAGCTGTTAAGACCAAAAAAAA 543
Db 420 CCCCCGCCCCCTCTCATTAAGCTGTTAAGACCAAAAAAAA 464

RESULT 10
LOCUS B1819795 496 bp mRNA linear EST 04-OCT-2001
DEFINITION 603041303F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5182081 5',
mRNA sequence.
ACCESSION B1819795
VERSION B1819795.1 GI:15931345
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/
AUTHORS 1 (bases 1 to 496)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1454 row: f column: 02
High quality sequence start: 6
High quality sequence stop: 496.
Location/Qualifiers
1.496
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5182081"
/lab_host="DH10B"
/clone_11b="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH-MGC Library."

BASE COUNT 96 a 171 c 156 g 73 t

Query Match 83.1%; Score 451; DB 12; Length 496;
Best Local Similarity 99.6%; Pred. No. 3e-76;
Matches 473; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
```

```
QY 69 CCGCGGGCCCCGAGCCCCCGGCGCAGAGCTGCGGCCCTCTGAGGGCTCTCCGAGGCC 128
Db 1 CCGCGGGCCCCGAGCCCCCGGCGCAGAGCTGCGGCC-CCTCTGAGGGCTCTGCGAGGCC 59
```

```
QY 129 CTGTCTGAGCTCCGCTGCTGCTTCTTAAGTGGGCTCGGCCAAGCTGTGGCCAGCCT 188
Db 60 CTGTCTGAGCTCCGCTGCTGCTTCTTAAGTGGGCTCGGCCAAGCTGTGGCCAGCCT 119
QY 189 GTTCGTGCGCTGAGATCGGCGGAGAGCCGGGGCCGGGACCAACCTGGCCACTCGGC 248
Db 120 GTTCGTGCGCTGAGATCGGCGGAGAGCCGGGGCCGGGACCAACCTGGCCACTCGGC 179
QY 249 ACCCTAACCCGGTGAAGCTCGTGAAGAGCTGGGATCCCGCTGAACCAACCTCATTA 308
Db 180 ACCCTAACCCGGTGAAGCTCGTGAAGAGCTGGGATCCCGCTGAACCAACCTCATTA 239
QY 309 GAGGGCTCCCAAGAGTGTGTGCTGAGTGGGTCCCGAGCGCTGGGGCCCTGAAGGCC 368
Db 240 GAGGGCTCCCAAGAGTGTGTGCTGAGTGGGTCCCGAGCGCTGGGGCCCTGAAGGCC 299
QY 369 CTGAAGGCCCTGCTGGGGCCCTGACAGTGTGGCTGAGCCGAGACTGAGCATCTACA 428
Db 300 CTGAAGGCCCTGCTGGGGCCCTGACAGTGTGGCTGAGCCGAGACTGAGCATCTACA 359
QY 429 CCGAGAGACAAGAGCTGGCCCAACCCCGAGGGCTGAAAAACCCCGCGGGAGAGACCT 488
Db 360 CCGAGAGACAAGAGCTGG-CACCCGAGGGCTGAAAAACCCCGCGGGAGAGACCT 418
QY 489 CCATCCCTTCCCGCCCGCCCTCTCATTAAGCTGTTAAGACCAAAAAAAA 543
Db 419 CCATCCCTTCCCGCCCGCCCTCTCATTAAGCTGTTAAGACCAAAAAAAA 473

RESULT 11
LOCUS B1819014 491 bp mRNA linear EST 04-OCT-2001
DEFINITION 603033130F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5174526 5',
mRNA sequence.
ACCESSION B1819014
VERSION B1819014.1 GI:15930564
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/
AUTHORS 1 (bases 1 to 491)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1434 row: k column: 07
High quality sequence stop: 470.
Location/Qualifiers
1.491
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5174526"
/lab_host="DH10B"
/clone_11b="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
```

Gruber (Invitrogen). Research Genetics tracking code  
 021. Note: this is a NIH\_MGC Library."  
 BASE COUNT 90 a 172 c 155 g 74 t  
 ORIGIN

Query Match 82.7%; Score 448.8; DB 12; Length 491;  
 Best Local Similarity 98.3%; Pred. No. 8e-76;  
 Matches 464; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

72 CGCGCCCCGAGCCCGCCGATGAGAGCTGCGGCCCTCTGGGGCTGCGTGGCCGCG 131  
 1 CGCGCCCGAGCCCGCCGATGAGAGCTGCGGCCCTCTGGGGCTGCGTGGCCGCG 59  
 132 TCCCTGAGCTGCGTGGCTGCTTCTTCTAGTGGCTGCGCCAGCCTGTGGCCGCGCTGC 191  
 60 TCCCTGAGCTGCGTGGCTGCTTCTTCTAGTGGCTGCGCCAGCCTGTGGCCGCGCTGC 119  
 192 GCTGGCGTGGCTGCGGCCGCGGAGCCGCGGCCGCGGAGCCCTGTGGCCAGCCCTGTGGCACC 251  
 120 GCTGGCGTGGCTGCGGCCGCGGAGCCGCGGCCGCGGAGCCCTGTGGCCAGCCCTGTGGCACC 179  
 252 CTCACACCGCTGAGCTGCTGCTGAGCAGACCTGCGGCATCCCGGTGACACCACTCATAGAG 311  
 180 CTCACACCGCTGAGCTGCTGCTGAGCAGACCTGCGGCATCCCGGTGACACCACTCATAGAG 239  
 312 GCTGCCGAGAGTGTGTGGCTGAGTGGTCCCAAGCCGCTGGGGCCGCTGAAGCCCTG 371  
 240 GCTGCCGAGAGTGTGTGGCTGAGTGGTCCCAAGCCGCTGGGGCCGCTGAAGCCCTG 299  
 372 AAGCCCTGCTGGGGCCCTGTGACAGTGTGGCTGAGCGAGACCTGAGACCTCATACACT 431  
 300 AAGCCCTGCTGGGGCCCTGTGACAGTGTGGCTGAGCGAGACCTGAGACCTCATACACT 359  
 432 GAGGACAGAGCTGCTGCCACCGCGAGGGCTGAAAAACCCCGCGGGGAGAGACCTGCA 491  
 360 GAGGACAGAGCTGCTGCCACCGCGAGGGCTGAAAAACCCCGCGGGGAGAGACCTGCA 419  
 492 TCCCTTCCCGCGGCCCTGTCAATAAAGCTGTGTTAAAGCAAAAAA 543  
 420 TCCCTTCCCGCGGCCCTGTCAATAAAGCTGTGTTAAAGCAAAAAA 471

RESULT 12 885 bp mRNA linear EST 04-OCT-2001  
 B1824102  
 LOCUS 603039244p1 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5180195 5',  
 DEFINITION mRNA sequence.  
 ACCESSION B1824102  
 VERSION B1824102.1 GI:15935652  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 NIH-MGC http://mhc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished  
 Contact: Robert Strausberg, Ph.D.  
 Email: rgs@bbs-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: L14M1449 row: 9 column: 12  
 High quality sequence stop: 469.  
 Location/Qualifiers

FEATURES  
 SOURCE 1..885  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"

/db\_xref="taxon:9606"  
 /clone="IMAGE:5180195"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH\_MGC\_115"  
 /note="Organ: pooled brain, lung, testis; Vector:  
 pCMV-Sport6; Site: 1; NotI; Site 2: EcoRV (destroyed); RNA  
 source anonymous pool of 6 male brains, age range 23-27; 1  
 male lung, age 27; and 1 male testis, age 69. Library is  
 oligo-dT primed and directionally cloned (EcoRV site is  
 destroyed upon cloning). Average insert size 1.8 kb,  
 insert size range 1-3 kb. Library is normalized and  
 enriched for full-length clones and was constructed by C.  
 Gruber (Invitrogen). Research Genetics tracking code  
 021. Note: this is a NIH\_MGC Library."  
 BASE COUNT 215 a 328 c 266 g 76 t  
 ORIGIN

Query Match 81.8%; Score 444; DB 12; Length 885;  
 Best Local Similarity 98.5%; Pred. No. 5.9e-75;  
 Matches 469; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

70 CGCGCCCCGAGCCCGCCGATGAGAGCTGCGGCCCTCTGGGGCTGCGTGGCCGCG 129  
 1 CGCGCCCGAGCCCGCCGATGAGAGCTGCGGCCCTCTGGGGCTGCGTGGCCGCG 60  
 130 TGTCTGAGCTGCGTGGCTGCTTCTTCTTATGAGGGCTGGCCCAACCTGTGGCCGCGCTG 189  
 61 TGTCTGAGCTGCGTGGCTGCTTCTTCTTATGAGGGCTGGCCCAACCTGTGGCCGCGCTG 120  
 190 TCGCTGC-GCTGAGTC-GGCGGGGAGGCGCGGGCCGCGGAGCCCTGTGGCCCAACCCCTGCG 247  
 121 TCGCTGAGCTGCGTGGCTGCTTCTTCTTATGAGGGCTGGCCCAACCTGTGGCCGCGCTG 180  
 248 CAGCCTCAACCGCTGTAAGCTGCTGCTGAGAGCTGCGGCATCCCGGTGACACCACTCAT 307  
 181 CAGCCTCAACCGCTGTAAGCTGCTGCTGAGAGCTGCGGCATCCCGGTGACACCACTCAT 240  
 308 AGAGGGCTGCCAGAGTGTGTGCTGAGTGGTCCCAAGCCGCTGGGGCCGCGTAAGGC 367  
 241 AGAGGGCTGCCAGAGTGTGTGCTGAGTGGTCCCAAGCCGCTGGGGCCGCGTAAGGC 300  
 368 CTTGAAGCCCTGCTGGGGCCCTGTGACAGTGTGTGGCTGAGCCGAGACTGAGCATCTAC 427  
 301 CTTGAAGCCCTGCTGGGGCCCTGTGACAGTGTGTGGCTGAGCCGAGACTGAGCATCTAC 360  
 428 ACTGAGGAGAGAGAGCTGCGCCACCGCGAGGGCTGAAAAACCCCGCGGGGAGAGACCG 487  
 361 ACTGAGGAGAGAGAGCTGCGCCACCGCGAGGGCTGAAAAACCCCGCGGGGAGAGACCG 420  
 488 TCCATCCCTTCCCGCGGCCCTGTCAATAAAGCTGTGTTAAAGCAAAAAA 543  
 421 TCCATCCCTTCCCGCGGCCCTGTCAATAAAGCTGTGTTAAAGCAAAAAA 476

RESULT 13 472 bp mRNA linear EST 21-FEB-2003  
 B977779/c  
 LOCUS B977779  
 DEFINITION UI-CF-EN1-aef-n-17-0-UI-s1 UI-CF-EN1 Homo sapiens cDNA clone  
 B977779  
 ACCESSION B977779.1 GI:15956542  
 VERSION B977779.1  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 472)  
 AUTHORS Bonaldo,M.F., Dennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 PUBMED 8889548

## COMMENT

Contact: McCray, PB  
 McCray Lab  
 University of Iowa  
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
 Tel: 319 356 4866  
 Fax: 319 356 7171  
 Email: paul.mccray@uiowa.edu  
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

## FEATURES

Location/Qualifiers  
 1. 472

BASE COUNT 80 a 148 c 158 g 86 t  
 ORIGIN  
 Query Match 81.2%; Score 441; DB 12; Length 472;  
 Best Local Similarity 97.8%; Pred. No. 2.5e-74;  
 Matches 447; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 87 CGCGCATGAGAGCTGCGCCCTCTGCGGCGCTGCGGCCCTGCTGACAGCTCCGT 146  
 464 CGCGCATGAGAGCTGCGCCCTCTGCGGCGCTGCGGCCCTGCTGACAGCTCCGT 405  
 147 GCTGCTTCTAGTGGGCTCGGCCAAGCTGTGGCCCAAGCTGTGCGTGGAGTGC 206  
 404 GCTGCTTCTAGTGGGCTCGGCCAAGCTGTGGCCCAAGCTGTGCGTGGAGTGC 345  
 207 GCGGGGAGGCGGGGCGGAGCCCTGGCCAAACCCCTGGGACCTCAACCCGCTGAAG 266  
 344 GCGGGGAGGCGGGGCGGAGCCCTGGCCAAACCCCTGGGACCTCAACCCGCTGAAG 285  
 267 CTCCTGAGAGAGCTGGGATCCCGGTGAACCAACCTATGAGAGGCTCCAGAGAGT 326  
 284 CTCCTGAGAGAGCTGGGATCCCGGTGAACCAACCTATGAGAGGCTCCAGAGAGT 225  
 327 GTGGCTGAGCTGGGATCCCGAGGCGCTGGGGCCGCTGAAGGCGCTTGTGGAG 386  
 224 GTGGCTGAGCTGGGATCCCGAGGCGCTGGGGCCGCTGAAGGCGCTTGTGGAG 165  
 387 GCCCTGACAGTGTGGCTGAGCGGAGACTGGAGCATCTACACCTGAGAGCAAGAGCTG 446

Db

164 GCGCTGACAGTGTGGCTGAGCGGAGACTGGAGCATTTAAACCTGAGAGCAAGAGCTG 105

QY

447 CCACACCCGAGAGGCTGAAACCCCGCGGGGAGGAGACCGTCATCCCTCCCGGCG 506

Db

104 CCACACCCGAGAGGCTGAAACCCCGCGGGGAGGAGACCGTCATCCCTCCCGGCG 45

QY

507 CCTCTCAATAACGTGGTTAAGACAAACAAAAA 543

Db

44 CCTTCAATAACGTGGTTAAGGCAAAAAA 8

## RESULT 14

BI821791 680 bp mRNA linear EST 04-OCT-2001  
 LOCUS 603035866F1 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5176672 5',  
 DEFINITION mRNA sequence.

## ACCESSION

BI821791 GI:15933341

## VERSION

BI821791.1 GI:15933341

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## REFERENCE

1 (bases 1 to 680)

## AUTHORS

NIH-MGC http://mgc.ncl.nih.gov/.

## TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

## JOURNAL

Unpublished

## COMMENT

Contact: Robert Strusberg, Ph.D.

## FEATURES

Location/Qualifiers

## source

1. 680

## FEATURES

Location/Qualifiers

## source

1. 680

## FEATURES

Location/Qualifiers

## source

1. 680

## FEATURES

Location/Qualifiers

## source

1. 680

## FEATURES

Location/Qualifiers

## source

1. 680

## FEATURES

Location/Qualifiers

## source

1. 680

## FEATURES

Location/Qualifiers

## source

1. 680

## FEATURES

Location/Qualifiers

## source

1. 680

## FEATURES

Location/Qualifiers

```

Db      121 TCCTGGCTGGAGTGGCGGCGGAGCCGGGGCCCGGACCCCTGGCCCTCGGC 180
QY      249 ACCCTCAACCCGGTGAAGTCTCTGCTAGCAGCCCTGGGGCATCCCGTGAACCACTCAT 308
Db      181 ACCCTCAACCCGGTGAAGTCTCTGCTAGCAGCCCTGGGGCATCCCGTGAACCACTCAT 240
QY      309 GAGGGCTCCAGAAAGTGTGTGCTGAGCTGGTCCCGAGCCGCTGGGGCCGTGAAGGCC 368
Db      241 GAGGGCTCCAGAAAGTGTGTGCTGAGCTGGTCCCGAGCCGCTGGGGCCGTGAAGGCC 300
QY      369 CTGAAGCCCTCTGTGGGGCCCTGACAGTGTGTGGCTGAGCCGAGACTGAGCATCTACA 428
Db      301 CTGAAGCCCTCTGTGGGGCCCTGACAGTGTGTGGCTGAGCCGAGACTGAGCATCTACA 360
QY      429 CTGAGGACAAGACGCTGCGCCACCCGCGAGGGCTGAACCCCGCGGGGAGAGCCGT 488
Db      361 CTGAGGACAAGACGCTGCGCCACCCGCGAGGGCTGAACCCCGCGGGGAGAGCCGT 420
QY      489 CCATCCCTCTTCCCGCGCCCTCTCAA-TAAGCTGGTTAAGACCAAAAAAAAA 543
Db      421 CCATCCCTCTTCCCGCGCCCTCTCAAAGTAAAGCTGGTTAAGACCAAGAAAGA 476

```

RESULT 15  
 A1685860/c 439 bp mRNA linear EST 27-MAY-1999  
 LOCUS tt90f09.x1 NCI\_CGAP\_Pr28 Homo sapiens cDNA clone IMAGE:2248841 3',  
 DEFINITION mRNA sequence.

ACCESSION A1685860  
 VERSION A1685860.1 GI:4897154  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 439)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 JOURNAL Tumor Gene Index  
 COMMENT Unpublished  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL at:  
 www.bio.lnl.gov/dbp/image/image.html  
 Seq primer: -400P from Gibco.

FEATURES  
 source  
 1. 439  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2248841"  
 /sex="male"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI\_CGAP\_Pr28"  
 /note="Organ: Prostate; Vector: pT73D-Pac (Pharmacia)  
 with a modified polylinker; Plasmid DNA from the  
 normalized library NCI\_CGAP\_Pr22 was prepared, and ss  
 circles were made in vitro. Following HAP purification,  
 this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (clones  
 985608-986759, 1101192-1101959, and 1217928-1220615).  
 Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT  
 ORIGIN

71 a 140 c 155 g 73 t

Query Match 80.8%; Score 439; DB 9; Length 439;  
 Best Local Similarity 100.0%; Pred. No. 66-74;  
 Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      103 CCGCCCTCTGGGGCTCTGCGTGGCCCTGTCTGACAGCTCCGCTGCTTTCTAGTGG 162
Db      439 CCGCCCTCTGGGGCTCTGCGTGGCCCTGTCTGACAGCTCCGCTGCTTTCTAGTGG 380
QY      163 GCTCGCCCAAGCCTGTGGGCCCAACCTGTGCTCCGCTGGAAGTGGCGGGAGCCGGGG 222
Db      379 GCTCGCCCAAGCCTGTGGGCCCAACCTGTGCTCCGCTGGAAGTGGCGGGAGCCGGGG 320
QY      223 CCGGAGCCCTGGGCAACCCCTCGGACCCCTCAACCCGCTGAAGTCTCTGCTAGCAGCC 282
Db      319 CCGGAGCCCTGGGCAACCCCTCGGACCCCTCAACCCGCTGAAGTCTCTGCTAGCAGCC 260
QY      283 TGGGCATCCCGTGAACCACTCATAGAGGCTCCAGAAAGTGTGTGCTGAGCTGGTGC 342
Db      259 TGGGCATCCCGTGAACCACTCATAGAGGCTCCAGAAAGTGTGTGCTGAGCTGGTGC 200
QY      343 CCGAGGCGGTGGGGGCGGTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTGACAGTGTGG 402
Db      199 CCGAGGCGGTGGGGGCGGTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTGACAGTGTGG 140
QY      403 GCTGAGCCGAGACTGGAGCATCTACACTGAGGACAAAGAGCTGCCACCCGAGAGGCT 462
Db      139 GCTGAGCCGAGACTGGAGCATCTACACTGAGGACAAAGAGCTGCCACCCGAGAGGCT 80
QY      463 GAAACCCCGCGCGGGGAGAGACCGTCCATCCCTTCCCGCGCCCTCTCAATAAAGCT 522
Db      79 GAAACCCCGCGCGGGGAGAGACCGTCCATCCCTTCCCGCGCCCTCTCAATAAAGCT 20
QY      523 GGTTAAGACCAAAAAAAAA 541
Db      19 GGTTAAGACCAAAAAAAAA 1

```

Search completed: October 9, 2003, 23:30:33  
 Job time : 1321.03 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2003, 13:25:26 ; Search time 35.3894 Seconds  
(without alignments)  
6772.395 Million cell updates/sec

Title: US-09-700-770-6

Perfect score: 543  
Sequence: 1 ccggcgctggagggcgag9.....gttaagagcaaaaaaaaaa 543

Scoring table: IDENTITY\_NUC  
Gap 10.0, Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Issued Patents, NA: \*
- 2: /cgn2\_6/ptodata/2/1na/5A.COMB.seq: \*
- 3: /cgn2\_6/ptodata/2/1na/5B.COMB.seq: \*
- 4: /cgn2\_6/ptodata/2/1na/6A.COMB.seq: \*
- 5: /cgn2\_6/ptodata/2/1na/6B.COMB.seq: \*
- 6: /cgn2\_6/ptodata/2/1na/Backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	529	97.4	570 4	US-09-966-243-407
2	56.4	10.4	263 2	US-08-964-725-2
3	56.4	10.4	507 2	US-08-964-725-4
4	56.4	10.4	519 2	US-08-964-725-5
5	49.8	9.2	2497 4	US-09-620-312D-47
6	48	8.8	4403765 3	US-09-103-840A-2
7	48	8.8	4411529 3	US-09-103-840A-1
8	46.6	8.6	2274 4	US-09-252-991A-3660
9	46.6	8.6	3297 4	US-09-252-991A-3615
10	46.2	8.5	432 4	US-09-252-991A-13281
11	46.2	8.5	1425 4	US-09-252-991A-12820
12	46.2	8.5	1428 4	US-09-252-991A-12677
13	46.2	8.5	1611 4	US-09-252-991A-13122
14	45.6	8.4	6453 1	US-08-306-691B-14
15	45.6	8.4	6453 3	US-09-356-952-8
16	45.4	8.4	2721 6	US-07-945-283-1
17	45.4	8.4	8438 1	US-09-252-991A-2920
18	44.4	8.2	996 4	US-09-105-537-21
19	44.4	8.2	1209 3	US-09-252-991A-3041
20	44.4	8.2	1284 4	US-09-105-537-3
21	44.4	8.2	13613 3	US-09-105-537-3
22	44.4	8.2	38506 3	US-09-320-878-19
23	44.4	8.2	38506 4	US-09-141-908-1
24	44.4	8.2	38506 4	US-09-657-440-19
25	44.2	8.1	636 4	US-09-252-991A-467
26	44.2	8.1	1278 4	US-09-252-991A-442
27	44.2	8.1	1473 4	US-09-252-991A-420

C 28	44	8.1	930	4	US-09-252-991A-1173	Sequence 1173, App
C 29	44	8.1	6453	3	US-09-209-668-10	Sequence 10, App1
C 30	44	8.1	6858	4	US-09-252-991A-1219	Sequence 1219, App
C 31	43.6	8.0	432	1	US-08-642-255-48	Sequence 48, App1
C 32	43.6	8.0	756	1	US-08-642-255-50	Sequence 50, App1
C 33	43.2	8.0	1740	4	US-09-252-991A-554	Sequence 554, App
C 34	43.2	8.0	2100	4	US-09-252-991A-502	Sequence 502, App
C 35	42.8	7.9	1641	4	US-09-252-991A-2396	Sequence 2396, App
C 36	42.8	7.9	13842	3	US-09-105-537-30	Sequence 30, App1
C 37	42.8	7.9	36778	3	US-09-105-537-5	Sequence 5, App1
C 38	42.8	7.9	77536	4	US-09-410-551B-1	Sequence 1, App1
C 39	42.6	7.8	951	4	US-09-252-991A-13389	Sequence 13389, App
C 40	42.6	7.8	2543	3	US-08-555-663-11	Sequence 11, App1
C 41	42.6	7.8	2543	3	US-09-073-663-11	Sequence 11, App1
C 42	42.4	7.8	1818	4	US-09-252-991A-2891	Sequence 2891, App
C 43	42.2	7.8	1050	4	US-09-252-991A-791	Sequence 791, App
C 44	42.2	7.8	1116	4	US-09-252-991A-8238	Sequence 8238, App
C 45	42.2	7.8				

# ALIGNMENTS

RESULT 1  
US-09-966-243-407  
; Sequence 407, Application US/09966243  
; Patent No. 6478825  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, David  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gottlieb, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tamas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2/30PIC13  
; CURRENT APPLICATION NUMBER: US/09/996,243  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/075945  
; PRIOR FILING DATE: 1998-02-25  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28







;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 97.4%; Score 529; DB 4; Length 570;  
Best Local Similarity 100.0%; Pred. No. 3,6e-104;  
Matches 529; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 15 GCGAGGACGGGGTAAAGAGCTGTGAGCCCTGCGGGGACGGGAGTTCCCGGGC 74
DB 1 GCGAGGACGGGGTAAAGAGCTGTGAGCCCTGCGGGGACGGGAGTTCCCGGGC 60
QY 75 GCGCGAGACCCCGGCGCATGAGCTCGCCGCTCTGAGGCTGTGCTGAGCTGCTC 134
DB 61 GCGCGAGACCCCGGCGCATGAGCTCGCCGCTCTGAGGCTGTGCTGAGCTGCTC 120
QY 135 TGACGCTCCGCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 194
DB 121 TGACGCTCCGCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 180
QY 195 GCGGTGAGCTGCGGGGCGGAGCGCGGGGCGGGGACCTGCGCAACCCCTCGGACCTGC 254
DB 181 GCGGTGAGCTGCGGGGCGGAGCGCGGGGCGGGGACCTGCGCAACCCCTCGGACCTGC 240
QY 255 AACCGCTGAAGCTCTGCTGAGCAGCTGGGACCTGCGCAACCCCTCGGACCTGC 314
DB 241 AACCGCTGAAGCTCTGCTGAGCAGCTGGGACCTGCGCAACCCCTCGGACCTGC 300
QY 315 TCACGAAAGTGTGTGCTGAGCTGGGTCCCGAGGCGGTGGGGCGGTGAAGGCGCTGAG 374
DB 301 TCACGAAAGTGTGTGCTGAGCTGGGTCCCGAGGCGGTGGGGCGGTGAAGGCGCTGAG 360
QY 375 GCGCGTGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 434
DB 361 GCGCGTGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
QY 435 GACAGAGCGTCCCGACCGCGGAGGCGTGAAGGCGGCGGCGGCGGCGGCGGCGGCGG 494
DB 421 GACAGAGCGTCCCGACCGCGGAGGCGTGAAGGCGGCGGCGGCGGCGGCGGCGGCGG 480
QY 495 CCTTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 543
DB 481 CCTTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 529

```

RESULT 2  
; Sequence 2, Application US/08964725  
; Patent No. 5939265

;; GENERAL INFORMATION:  
;; APPLICANT: COHEN, Maurice  
;; APPLICANT: FRIEDMAN, Paula N.  
;; APPLICANT: GORDON, Julian  
;; APPLICANT: HODGES, Steven C.  
;; APPLICANT: KRATOCHVIL, Jon D.  
;; APPLICANT: KRATOCHVIL, Lisa  
;; APPLICANT: ROBERTS-RAPP, Lisa  
;; APPLICANT: RUSSELL, John C.  
;; APPLICANT: STROUPE, Steven D.  
;; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
;; NUMBER OF SEQUENCES: 19  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Abbott Laboratories  
;; STREET: 100 Abbott Park Road  
;; CITY: Abbott Park  
;; STATE: IL  
;; COUNTRY: USA  
;; ZIP: 60064-3500  
;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FASTSEQ for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/964,725  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Becker, Cheryl L.  
;; REGISTRATION NUMBER: 35,441  
;; REFERENCE/DOCKET NUMBER: 5997.US.P1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 847/935-1729  
;; TELEFAX: 847/938-2623  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 263 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; US-08-964-725-2

Query Match 10.4%; Score 56.4; DB 2; Length 263;  
Best Local Similarity 60.4%; Pred. No. 0.00086;  
Matches 93; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

```

QY 229 CCTGAGCAACCCCTCGGACCCCTCAACCCGCTGAGCTCTGCTGAGCAGCTGGGCA 288
DB 60 CTTGTGAGCAACCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 119
QY 288 TCACGAAAGTGTGTGCTGAGCTGGGTCCCGAGGCGGTGGGGCGGTGAAGGCGCTGAG 348
DB 120 TTTCTGTGAGCAACCTTGTGAGGCGGTGAAGGAGTGTGTAATGAGCTGGGACGAGAG 179
QY 349 CCGTGGGGCGGTGAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 382
DB 180 CTTGTGAGCTGTGAAGAACTGTGAGGCGCT 213

```

RESULT 3  
; Sequence 4, Application US/08964725  
; Patent No. 5939265

;; GENERAL INFORMATION:  
;; APPLICANT: COHEN, Maurice  
;; APPLICANT: FRIEDMAN, Paula N.  
;; APPLICANT: GORDON, Julian  
;; APPLICANT: HODGES, Steven C.  
;; APPLICANT: KRATOCHVIL, Jon D.  
;; APPLICANT: KRATOCHVIL, Lisa  
;; APPLICANT: ROBERTS-RAPP, Lisa  
;; APPLICANT: RUSSELL, John C.  
;; APPLICANT: STROUPE, Steven D.  
;; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
;; NUMBER OF SEQUENCES: 19  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Abbott Laboratories  
;; STREET: 100 Abbott Park Road  
;; CITY: Abbott Park  
;; STATE: IL  
;; COUNTRY: USA  
;; ZIP: 60064-3500  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FASTSEQ for Windows Version 2.0

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,725
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 5997.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 507 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-964-725-4

```

```

Query Match          10.4%; Score 56.4; DB 2; Length 507;
Best Local Similarity 60.4%; Pred. No. 0.00093;
Matches 93; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

```

```

QY 229 CCTGGCCCAACCCCTGGGACCCCTCAACCCGCTGAAGCTCTCTGAGCAGCCTGGGCA 288
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 195 CTCGGACACATCTCTCCCTTATGATCATTAAGCTTCTTGAAAACTGTGGGCA 254
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 289 TCCCGCGAACACCTCATAGAGGGCTCCCAAGAGTGTGTGCTGAGCTGGTCCCGAG 348
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 255 TTCTGTGTGAGCACCTGTGTGAGGGGCTGAAGAGTGTGTAAATGAGCTGGACCAAGG 314
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 349 CCGTGGGGGCGCTGAAGGCCCTGAAGGCCCTGCT 382
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 315 CTCTGAAGCTGTGAAGAAACTGCTGGAGGCGCT 348
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

RESULT 4
US-08-964-725-5
Sequence 5, Application US/08964725
Patent No. 5939265
GENERAL INFORMATION:
APPLICANT: COHEN, Maurice
APPLICANT: FRIEDMAN, Paula N.
APPLICANT: GORDON, Julian
APPLICANT: HODGES, Steven C.
APPLICANT: KLAS, Michael R.
APPLICANT: KRATOCHVIL, Jon D.
APPLICANT: ROBERTS-RAPP, Lisa
APPLICANT: RUSSELL, John C.
APPLICANT: STROUPE, Steven D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,725
FILING DATE:
CLASSIFICATION: 435

```

```

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 5997.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-964-725-5

```

```

Query Match          10.4%; Score 56.4; DB 2; Length 519;
Best Local Similarity 60.4%; Pred. No. 0.00093;
Matches 93; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

```

```

QY 229 CCTGGCCCAACCCCTGGGACCCCTCAACCCGCTGAAGCTCTCTGAGCAGCCTGGGCA 288
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 208 CTCGGACACATCTCTCCCTTATGATCATTAAGCTTCTTGAAAACTGTGGGCA 267
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 289 TCCCGCGAACACCTCATAGAGGGCTCCCAAGAGTGTGTGCTGAGCTGGTCCCGAG 348
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 268 TTCTGTGTGAGCACCTGTGTGAGGGGCTGAAGAGTGTGTAAATGAGCTGGGACCAAGG 327
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 349 CCGTGGGGGCGCTGAAGGCCCTGAAGGCCCTGCT 382
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 328 CTCTGAAGCTGTGAAGAAACTGCTGGAGGCGCT 361
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

RESULT 5
US-09-620-312D-47
Sequence 47, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aildong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yungqun
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhilwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radote T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 47
LENGTH: 2497
TYPE: DNA
ORGANISM: Homo sapiens

```

FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (107)..(1756)  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(2497)  
; OTHER INFORMATION: n - a,t,c or g  
US-09-620-312D-47

Query Match 9.2%; Score 49.8; DB 4; Length 2497;  
Best Local Similarity 50.9%; Pred. No. 0.028;  
Matches 144; Conservative 0; Mismatches 137; Indels 2; Gaps 1;

OY 113 GGGGCTGCGTGGCCCTGCTCTGAGCTCGCTGCTGCTCTTCTTAGTGGCTCG--GCC 170  
DB 1118 GGGGCTGAGCGAGCCCTGGGAGCAAGTCCCTGCGCCCTCTGTTGGGAGATGGGTGCC 1177  
OY 171 AAGGCTGTGGGCGGAGCCGTGTGCTGAGTGTGGGGGGGAGAGCCGGGGCCGGAGCC 230  
DB 1178 GCGTGTGGGCGCCCGGGGGGGGCTGGGTGGGGGGGCGCTGCGCCATGGGTGGCGG 1237  
OY 231 CTGGCCAAACCCCTCGGACCCCTCAACCCGCTGAAGCTCTGTTGAGCAGCCTGGGCAATC 290  
DB 1238 CTGGGCTCCATGTGTGGGCTCATGACCTAGCGGGGGGCGCCCAATTCCTGACACG 1297  
OY 291 CCCGTGAACACCTCATAGAGAGGCTCCGAGAGTGTGTGCTGAGCTGGTCCCGCCAGCC 350  
DB 1298 ACGATGCGGCGCCCTGATCCCGCCCTTCGCGAGGCTTGGCCCAAGCTAACACAGCTGTG 1357  
OY 351 GTGGGGGCGCGTGAAGGCCCTGAGAGCCCTGCTGGGGGCGCCGA 393  
DB 1358 GATGCGGAGCGGAGGCGCTTACCGCTTACCTGGAAGCAATGA 1400

## RESULT 6

US-09-103-840A-2

; Sequence 2, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103.840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 4403765  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; FEATURE:  
; OTHER INFORMATION: CDC 1551  
; OTHER INFORMATION: "n" bases at various positions throughout the sequence  
; OTHER INFORMATION: represent a, t, c or g  
US-09-103-840A-2

Query Match 8.8%; Score 48; DB 3; Length 4403765;  
Best Local Similarity 45.3%; Pred. No. 0.17;  
Matches 212; Conservative 0; Mismatches 255; Indels 1; Gaps 1;

OY 67 CCGCGGCGGCGCGCGCGCGCGCATGAAGCTGCGGCGCTCTGCGGCTCTGCGTGG 126  
DB 1637512 CCGATCGGGGCGGGGCGCGCGCACCTCGTCCGCGGCGCGCGCATGAAGGTTCCCGCC 1637571  
OY 127 CCGTGTCTGAGCTCCGCTGCTCTTCTTAGTGGGCTCGGCAAGCTG-TGGCCAG 185  
DB 1637572 AGGCACCGGACACACGCGTACCGCGGAGCCCGCGGGGCGCGCGCGCGCGCGCG 1637631  
OY 186 CCGTGTGCTGCGCTGAGTGTGGCGGCGGAGGCGCGGCGCGCGCGCGCGCGCGCGCTC 245

DB 1637632 CCGGTTCCGCGAGCCCGGACAGTCCGGCTTGGCCCGCGGCGCGCGCGCGCGCGCC 1637691  
OY 246 GGCACCTTCACACCCGCTGAAGTCTCTGCTGAGCAGCAGCTGGGAGTCCCGGTACACACTC 305  
DB 1637692 AGCAGGCTGTGCGTA 1637751  
OY 306 ATAGAGGCTCCACAGAGTGTGTGCTGAGTGTGGTGTCCAGAGCGGTGGGGCGCTGAG 365  
DB 1637752 CCGCGGCGTA 1637811  
OY 366 GCGCTGAAGCGCTGCTGGGGGCGCTGACAGTGTGCTGAGCGGAGACTGAGCATCT 425  
DB 1637812 AACCGGCGTA 1637871  
OY 426 ACACCTGAGGACAGCAGTGTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTA 485  
DB 1637872 CCGTGTGCGTA 1637931  
OY 486 GCGTCATCCCTTCCCGTA 1637979  
DB 1637932 GCGCATCATCGATACAGCGGCGGAGCCAGCAAGCGCTGTGGTGGCGCA

## RESULT 7

US-09-103-840A-1

; Sequence 1, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103.840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4411529  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; OTHER INFORMATION: H37Rv  
US-09-103-840A-1

Query Match 8.8%; Score 48; DB 3; Length 4411529;  
Best Local Similarity 45.3%; Pred. No. 0.17;  
Matches 212; Conservative 0; Mismatches 255; Indels 1; Gaps 1;

OY 67 CCGCGGCGGCGCGCGCGCGCGCATGAAGCTGCGGCGCTCTGCGGCGCTCTGCGTGG 126  
DB 1637829 CCGATCGGGGCGGGGCGCGCGCACCTCGTCCGCGGCGCGCGCGCGCATGAAGGTTCCCGCC 1637888  
OY 127 CCGTGTCTGAGCTCCGCTGCTGCTTCTTAGTGGGCTCGGCAAGCTG-TGGCCAG 185  
DB 1637889 AGGCACCGGACACACGCGTACCGCGGAGCCCGCGGGGCGCGCGCGCGCGCGCGCG 1637948  
OY 186 CCGTGTGCTGCGCTGAGTGTGGCGGAGGCGCGGCGCGGAGCCCTGCGCAACCCCTC 245  
DB 1637949 CCGGTTCCGCGAGCCCGGACAGTCCGCGTGTGCGGCGGCGCGCGCGCGCGCGCGCG 1637408  
OY 246 GGCACCTTCACACCCGCTGAAGTCTCTGCTGAGCAGCAGCTGGGAGTCCCGGTGAACCACTC 305  
DB 1634009 AGCAGGCTGTGCGTA 1634068  
OY 306 ATAGAGGCTCCACAGAGTGTGTGCTGAGTGTGGTGTCCAGAGCGGTGGGGCGCTGAG 365  
DB 1634069 CCGCGGCGTA 1634128  
OY 366 GCGCTGAAGCGCTGCGGGGCGCTGACAGTGTGCTGAGCGGAGACTGAGCATCT 425

Db 1634119 AACCCGGGGGCCCCGGCGGCCGCGCACTTGGCGGGGGCGGCCCGACCCCGCGGCCCA 16341188

QY 426 ACACCTGAGCAGACAGCGTGGTCCCAACCCGGAGGGCGTAAACCCCGCGGGGGAGAC 485

Db 1634189 CCGTTGGCCCCACAGATTCGCCCGCCCCCGCGGCTTGGCGGGGGGTCTCCAGCC 1634248

QY 486 CGTCATCCCTCTTCCCCGGCGCCCTCTCATTAACGTGGTTAAGACA 533

Db 1634249 GCCCATTCACCGATTCACAGGGCGACCCACGCAACGCTCTGGGTGGGGCGCA 1634296

## RESULT 8

```

US-09-252-991A-3660
? Sequence 3660, Application US/09252991A
? Patent No. 6551795
? GENERAL INFORMATION:
? APPLICANT: Marc J. Rubenfield et al.
? TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
? TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
? FILE REFERENCE: 107196.136
? CURRENT APPLICATION NUMBER: US/09/252,991A
? CURRENT FILING DATE: 1999-02-18
? PRIOR APPLICATION NUMBER: US 60/074,788
? PRIOR FILING DATE: 1998-02-18
? PRIOR APPLICATION NUMBER: US 60/094,190
? PRIOR FILING DATE: 1998-07-27
? NUMBER OF SEQ ID NOS: 33142
? SEQ ID NO 3660
? LENGTH: 2274
? TYPE: DNA
? ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3660

```

	Query Match Best Local Similarity	8.6%; 51.2%;	Score 46.6; Pred. 0.13;	DB 4;	Length 2274;
Matches	109;	Conservative	0;	Mismatches 104;	Indels 0;
					Gaps 0;
QY	180	GCCACGCTGTGCGTGGAGTGGCGGCGGAGCGCGGGGCGGAGCCCTGGAC	239		
Db	112	GTCTGTGTTTCCGGCGAGCGCTGGCGCCCGAGATCGCAGTACCCGCCACATAC	171		
QY	240	CCCCGCGCACCCATACCCCGCTGAAGTCTGCTGAGACGCTGGCATCCCCGTGAC	299		
Db	172	TACCGGCTGCCCGCGAGCCGCTGAGTAGAGCGGTGAACCACTAAGCGCGGACCGGCG	231		
QY	300	CACCTCATAGAGGCTCCCAAGATGTGTGCTAGATGGTGTCCCAAGCGCTGGGGGCC	359		
Db	232	GTGCTGTATCGCCTTCACGCCGGAACACAGCCGCGGGGCGCCACAGCGCCTGAGAGCC	291		
QY	360	GTGAAGGCCCTGAAGAGCCCTGCTGGGGGCCCTG	392		
Db	292	GAGTACACCCCTGGAGGAAGCGCTGGCGGCTTG	324		

## RESULT 9

```

US-09-252-991A13615
; Sequence 3615, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 3615
; LENGTH: 3297
; TYPE: DNA

```

ORGANISM: *Pseudomonas aeruginosa*  
US-09-252-991A-3615

[illegible]

RESULT 10  
HE-00-353

```

US-09-252-991A-13281/C
/ Sequence 13281, Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ TITLE OF INVENTION: AERGININOSA FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ CURRENT FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 13281
/ LENGTH: 432
/ TYPE: DNA
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13281

```

Query Match	8.5%;	Score 46.2;	DB 4;	Length 432;
Best Local Similarity	47.2%;			
Matches 141;	Conservative	0;	Mismatches 158;	Indels 0;
				Gaps 0;

QY	161	GGGCTGGGCCAAGCTGTGGCCAGCCTGTGGCTGCTGGAGTGGGCGGAGGCGG	220
Db	348	CGCGCGCGAATGGGGCTCTCCCTGTGGCCGCGCGCAACAAGTTCGGCGGCTTGGGCGG	285
QY	221	GGCGGGAGACCTGGGCCAACCCCGTGGGGAACCCCTCAACCCGCTGAAGCTCTGCTGACAG	280
Db	288	CCACGAGCGCGGTGGTATCTCTTCGGGGCGCCCTGAAAGAGCCCTGGCGGCTGAGTAA	229
QY	281	CCGTGGGATATCCCGGTGAACCACTCAATGAGAGGGTCCCAAGTGTGTGGCTGACTGGG	340
Db	228	GATCGGCAACGACTTGGCGCTGCTGTGGTTCGGGGCCACGCGCCGGCTTCGCGGAGTGAA	169
QY	341	TCCCCAGGCGCTGGGGGCGGTGAAGGCGCTGAAGGCGTGGTGGGGCCCTGACAGTGT	399
Db	168	GCTGGCGGCAACGAGCGGGGCACTTCATATATGCGCGGCAAGGTCAACCGACCACT	110

## RESULT 11

US-09-252-991A-12820

```

Sequence 12820, Application US/09252991A
Patient No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIORITY FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 12820
LENGTH: 1425
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12820

```

Query Match	8.5%;	Score 46.2;	DB 4;	Length 1425;
Best Local Similarity	47.2%;	Pred. NO. 0.15;		
Matches 141;	Conservative	0;	Mismatches 158;	Indels 0;
				Gaps 0;

[illegible]

RESULT 12  
 US-09-252-991A-12677  
 : Sequence 12677, Application US/09252991A  
 : Patent No. 6551795  
 : GENERAL INFORMATION:  
 : APPLICANT: Marc J. Rubenfield et al.  
 : TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 : TITLE OF INVENTION: AERGININOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 : FILE REFERENCE: 107396.136  
 : CURRENT APPLICATION NUMBER: US/09/252,991A  
 : CURRENT FILING DATE: 1999-02-18  
 : PRIOR APPLICATION NUMBER: US 60/074,788  
 : PRIOR FILING DATE: 1998-02-18  
 : PRIOR APPLICATION NUMBER: US 60/094,190  
 : PRIOR FILING DATE: 1998-07-27  
 : NUMBER OF SEQ. ID NOS: 33142  
 : SEQ ID NO 12677  
 : LENGTH: 1428  
 : TYPE: DNA  
 : ORGANISM: Pseudomonas aeruginosa  
 : US-09-252-991A-12677

Query Match	8.5%	Score 46.2;	DB 4;	Length 1428;
Best Local Similarity	47.2%;	Pred. No. 0.15;		
Matches 141;	Conservative 0;	Mismatches 158;	Indels 0;	Gaps 0;

QY	101	CGCGGCGCTCTGGAGGCTCTGCGTGGCCCTGTCTCTGCGACGTCGCTGCTTTTCTTAACT	160

Db	661	CGGGGTGGGACCGGGGCTACAGCGCGCGAAGGGGCTTCGCGACGCAATCGCGGGGAAAT	720
Oy	161	GGGCTGGCCAAAGCTGTGGGCCAGCCTGTGCTGCGTGGAGTGTGGCGCGGAGGCGCG	220
Db	721	CGCGCGCGGATCGGGGCTCGCTGTGTCGCGCGCGGAAACAAGTGTGCGCGGCTTGCGCGG	780
Oy	221	GGCGGGAGCCTGGGCCAACCCCTCGGCGACCCCTCAACCGGTGAAAGCTCTGTGTGAGCAG	280
Db	781	CCACGAGCCGTGTGTATCTCTCTCGCGCGCGCTGGAAAGCCTGGCGGCTGGCGCTGATGAA	840
Oy	281	CGTGGGCAATCCCGTGAAACCACTCATAGAGGGCTCCGAGAAGTGTGTGGCTGAGCTGGG	340
Db	841	GATGCGCAAGACTCTCGGCTGTCTGAGTTCGAGGCCAACGCGCGGCTTCGGCGAGGTGAA	900
Oy	341	TCCCGAAGGCGCTGGGGGCGGTGAAGGCCCTGAAGGCCCTGTGTGGGCGGCTGACAAGTGT	399
Db	901	GCTTCCGGCCACGAGCCCGGACGCTCATCTATGCTCCCGGCAAGGTCAACCCGACCCAGT	959

RESULT 13  
US-09-252-991A-13122/c  
; Sequence 13122, Application US/09252991A  
; Patent No. 6551795

```

: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
:
: TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
:
: FILE REFERENCE: 107196.136
:
: CURRENT APPLICATION NUMBER: US/09/252,991A
:
: CURRENT FILING DATE: 1999-02-18
:
: PRIOR APPLICATION NUMBER: US 60/074,788
:
: PRIOR FILING DATE: 1998-02-18
:
: PRIOR APPLICATION NUMBER: US 60/094,190
:
: PRIOR FILING DATE: 1998-07-27
:
: NUMBER OF SEQ ID NOS: 33142
:
: SEQ ID NO 13122
:
: LENGTH: 1611
:
: TYPE: DNA
:
: ORGANISM: Pseudomonas aeruginosa
:
: US-09-252-991A-13122

```

[illegible]

RESULT 14  
 US-08-306-691B-14  
 ; Sequence 14, Application US/08306691B  
 ; Patent No. 5734039  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Calabretta, Bruno  
 ; APPLICANT: Skorski, Tomasz



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2003, 12:42:26 ; Search time 2090.54 Seconds

(without alignments)  
10625.902 Million cell updates/sec

Title: US-09-700-770-6

Perfect score: 543

Sequence: 1 ccgagcgtgagagggcgaggg.....gttaagagcaaaaaaaaaa 543

Scoring table: IDENTITY\_NTC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmb1:\*  
1: gb\_da:\*  
2: gb\_hlg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sta:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_da:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sta:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_hlg\_hum:\*  
31: em\_hlg\_inv:\*  
32: em\_hlg\_other:\*  
33: em\_hlg\_mus:\*  
34: em\_hlg\_pln:\*  
35: em\_hlg\_rod:\*  
36: em\_hlg\_man:\*  
37: em\_hlg\_vtl:\*  
38: em\_sy:\*  
39: em\_higo\_hum:\*  
40: em\_higo\_mus:\*  
41: em\_higo\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	532.6	98.1	562	6 BD082141	BD082141 Reagents
2	529	97.4	569	6 AX201348	AX201348 Sequence
3	529	97.4	570	6 AR252648	AR252648 Sequence
4	529	97.4	570	6 AX403520	AX403520 Sequence
5	519	95.6	519	6 BD082142	BD082142 Reagents
6	471	86.7	471	9 HUMZB52D10	AF086152 Homo sapi
7	466	85.8	503	9 BC029176	BC029176 Homo sapi
8	457	84.3	461	9 AY040564	AY040564 Homo sapi
9	345.4	63.6	347	9 AF313458	AF313458 Homo sapi
10	293.4	54.0	380	6 AX334451	AX334451 Sequence
11	241.4	44.5	244	6 BD082138	BD082138 Reagents
12	241.4	44.5	130129	2 AC108083	AC108083 Homo sapi
13	241.4	44.5	166777	2 AC106813	AC106813 Homo sapi
14	241.4	44.5	168347	2 AC025336	AC025336 Homo sapi
15	241.4	44.5	190024	2 AC122714	AC122714 Homo sapi
16	230.4	42.4	127488	2 AC022095	AC022095 Homo sapi
17	225	41.4	225	6 BD082139	BD082139 Reagents
18	158	29.1	190	6 BD082137	BD082137 Reagents
19	118.8	21.9	525	10 AF313456	AF313456 Mus muscu
20	114	21.0	114	6 BD082140	BD082140 Reagents
21	101.6	18.7	630	10 AF313457	AF313457 Mus muscu
22	93.6	17.2	245659	2 AC098957	AC098957 Rattus no
23	93.6	17.2	283593	2 AC131433	AC131433 Rattus no
24	91	16.8	254981	10 AL606479	AL606479 Mouse DNA
25	89.6	16.5	130129	2 AC108083	AC108083 Homo sapi
26	60.4	11.1	291000	1 SC0939105	AL939105 Streptomy
27	60.2	11.1	292100	1 SC0939121	AL939121 Streptomy
28	58.2	10.7	869	11 PM2A12B	AL664671 Penicilliu
29	56.4	10.4	366	9 AF313455	AF313455 Homo sapi
30	56.4	10.4	508	6 AX376176	AX376176 Sequence
31	56.4	10.4	550	6 BC024232	BC024232 Homo sapi
32	56	10.3	208936	2 AC010821	AC010821 Homo sapi
33	55.8	10.3	166644	9 AC011352	AC011352 Homo sapi
34	55.4	10.2	310550	1 SC0939113	AL939113 Streptomy
35	53.4	9.8	125020	9 AF429315	AF429315 Homo sapi
36	53	9.8	306650	1 AP005221	AP005221 Corynebac
37	52.8	9.7	523	10 AF274959	AF274959 Mus muscu
38	52.8	9.7	589	10 AF274960	AF274960 Mus muscu
39	52.8	9.7	853	10 AF274961	AF274961 Mus muscu
40	52.8	9.7	147774	2 AC104867	AC104867 Mus muscu
41	52.8	9.7	237987	2 AC106616	AC106616 Rattus no
42	52.8	9.7	303550	1 SC0939131	AL939131 Streptomy
43	52.6	9.7	298300	1 AP005025	AP005025 Streptomy
44	52.4	9.7	52884	2 AC068018	AC068018 Homo sapi
45	52.4	9.7	166050	1 AL646085	AL646085 Ralstonia

# ALIGNMENTS

RESULT 1  
BD082141  
LOCUS  
DEFINITION  
Reagents and methods useful for detecting diseases of the lung.  
ACCESSION  
BD082141  
VERSION  
BD082141.1 GI:22627751  
KEYWORDS  
JP 2001522225-A/5.  
SOURCE  
Zea mays  
ORGANISM  
Zea mays

562 bp DNA linear PAT 27-AUG-2002

REFERENCE  
Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J.,  
Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Rapp,L.R.,

Pred. No. 15 is the number of results predicted by chance to have a

TITLE Russell, J.C. and Stroupe, S.D.  
 Reagents and methods useful for detecting diseases of the lung  
 JOURNAL Patent: JP 2001522225-A 5 13-NOV-2001.  
 COMMENT ABBOTT LABORATORIES  
 JP 2001522225-A/5  
 PD 13-NOV-2001  
 PR 30-JAN-1998 JP 1998533078  
 PR 31-JAN-1997 US 08/791710  
 PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA  
 PI N FRIEDMAN,  
 PI JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R PI  
 PI KLAS, JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D  
 PI STROPE  
 PI C12N15/63, C12N5/10, C12Q1/68, C07K14/47//C07K16/30, G01N33/574 CC  
 Strandedness: Single;  
 CC Topology: Linear;  
 PH Key Location/Qualifiers.

FEATURES  
 source Location/Qualifiers  
 1. 562  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:4577"

BASE COUNT 82 a 200 c 192 g 86 t 2 others

ORIGIN

Query Match 98.1%; Score 532.6; DB 6; Length 562;  
 Best Local Similarity 99.8%; Pred. No. 9.7e-76;  
 Matches 532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGGCGTGGAGGGGCGAGGACCGGGTATTAAGACCTCTGCGCTCCCGGGAGCGG 60  
 DB 30 CGGGGCGTGGAGGGGCGAGGACCGGGTATTAAGACCTCTGCGCTCCCGGGAGCGG 89  
 QY 61 CAGTTCCTCCCGGGCGCGCGAGCGCGCGCATGAAGCTGCGCTCCCGGGAGCGG 120  
 DB 90 CAGTTCCTCCCGGGCGCGCGAGCGCGCGCATGAAGCTGCGCTCCCGGGAGCGG 149  
 QY 121 GCGTGGCCCTGCTGCAAGCTGCTGCTGCTTCTTATGAGGGGCTGCGCAAGCTGAG 180  
 DB 150 GCGTGGCCCTGCTGCAAGCTGCTGCTGCTTCTTATGAGGGGCTGCGCAAGCTGAG 209  
 QY 181 CCGAGCCGTGCTGCTGCAAGCTGCTGCTGCTTCTTATGAGGGGCTGCGCAAGCTGAG 240  
 DB 210 CCGAGCCGTGCTGCTGCAAGCTGCTGCTGCTTCTTATGAGGGGCTGCGCAAGCTGAG 269  
 QY 241 CCGTGGGCAACCTCAACCGGCTGAAGCTCTGCTGAGGAGGCTGGGCAATCCCGCTGAAC 300  
 DB 270 CCGTGGGCAACCTCAACCGGCTGAAGCTCTGCTGAGGAGGCTGGGCAATCCCGCTGAAC 329  
 QY 301 ACCTCATAGAGGGGCTCCAGAAAGTGTGTGCTGAGCTGGTCCCGAGGCGCTGGGGCGG 360  
 DB 330 ACCTCATAGAGGGGCTCCAGAAAGTGTGTGCTGAGCTGGTCCCGAGGCGCTGGGGCGG 389  
 QY 361 TGAAGGCGCTTAAGGCGCTGCTGGGGGCGCTGAGACGTGTTGGCTGAGCCGAGAGCTGAG 420  
 DB 390 TGAAGGCGCTTAAGGCGCTGCTGGGGGCGCTGAGACGTGTTGGCTGAGCCGAGAGCTGAG 449  
 QY 421 CATCTACACCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480  
 DB 450 CATCTACACCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 509  
 QY 481 AGGACCGTCAATCCCTTCCCGGCGCGCTCTCAATAAAGCTGGTTAAGAGCA 533  
 DB 510 AGGACCGTCAATCCCTTCCCGGCGCGCTCTCAATAAAGCTGGTTAAGAGCA 562

RESULT 2  
 AX201348 569 bp DNA Linear PAT 30-AUG-2001  
 LOCUS AX201348  
 DEFINITION Sequence 27 from Patent WO0153486.  
 ACCESSION AX201348

VERSION AX201348.1 GI:15391167  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1  
 ASHKENAZI, A.J., GODDARD, A., GODEWSKI, P.J., GURNEY, A.L.,  
 HILLAN, K.J., MARSTERS, S.A., PAN, O., PILLI, R.M., ROY, M.A., SMITH, V.,  
 STONE, D.M., WATANABE, C.K. and WOOD, W.I.  
 Compositions and methods for the treatment of tumour  
 Patent: WO 0153486-A 27 26-JUL-2001;  
 Genentech, Inc. (US)

TITLE  
 JOURNAL  
 Genentech, Inc. (US)

FEATURES  
 source Location/Qualifiers  
 1. 569  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"

BASE COUNT 128 a 190 c 170 g 81 t

ORIGIN

Query Match 97.4%; Score 529; DB 6; Length 569;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-75;  
 Matches 529; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 GCGAGGACCGGGTATTAAGAGGCTGCGGCTGCGCGGGGAGCGGAGGCTTCCCGCGG 74  
 DB 1 GCGAGGACCGGGTATTAAGAGGCTGCGGCTGCGCGGGGAGCGGAGGCTTCCCGCGG 60  
 QY 75 GCGCGGAGCGCGCGCGCGCATGAAGCTGCGCGCGCGCTGCGGGGCTGCGGCGCTGCG 134  
 DB 61 GCGCGGAGCGCGCGCGCGCATGAAGCTGCGCGCGCGCTGCGGGGCTGCGGCGCTGCG 120  
 QY 135 TGCAAGCTCCCGTGTGCTTCTTATGAGGGGCTGCGCGCAAGCTGCGCGCGCTGCGCT 194  
 DB 121 TGCAAGCTCCCGTGTGCTTCTTATGAGGGGCTGCGCGCAAGCTGCGCGCGCTGCGCT 180  
 QY 195 GCGTGGAGTGGGCGGCGGAGGCGGCGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 254  
 DB 181 GCGTGGAGTGGGCGGCGGAGGCGGCGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 240  
 QY 255 AACCGCTGAAGCTCTGCTGAGGAGGCTGCGGCGGAGGCGGAGGCGGAGGCGGAGG 314  
 DB 241 AACCGCTGAAGCTCTGCTGAGGAGGCTGCGGCGGAGGCGGAGGCGGAGGCGGAGG 300  
 QY 315 TCCAGAAAGTGTGCTGAGGAGGCTGCGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAG 374  
 DB 301 TCCAGAAAGTGTGCTGAGGAGGCTGCGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAG 360  
 QY 375 GCGCTGCTGGGGGCGCTGAGAGGCTTGGCTGAGGCGGAGGCTGAGGAGGCTGAGGAGG 434  
 DB 361 GCGCTGCTGGGGGCGCTGAGAGGCTTGGCTGAGGCGGAGGCTGAGGAGGCTGAGGAGG 420  
 QY 435 GACAAAGCGTGGCGGCGGCGGAGGCGGAGGCGGAGGCGGCGGCGGAGGCGGAGGCGG 494  
 DB 421 GACAAAGCGTGGCGGCGGCGGAGGCGGAGGCGGAGGCGGCGGCGGAGGCGGAGGCGG 480  
 QY 495 CTTTCCCGCGCGCGCTCTCAATAAAGCTGGTTAAGAGCAAAAAA 543  
 DB 481 CTTTCCCGCGCGCGCTCTCAATAAAGCTGGTTAAGAGCAAAAAA 529

RESULT 3  
 AR252648 570 bp DNA Linear PAT 20-DEC-2002  
 LOCUS AR252648  
 DEFINITION Sequence 407 from patent US 6478825.  
 ACCESSION AR252648  
 VERSION AR252648.1 GI:27300556  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 570)



AUTHORS	Winterbottom, J. M., Shimp, L., Boyce, T. M. and Kres, D.
TITLE	Implant, method of making same and use of the implant for the treatment of bone defects
JOURNAL	Patent: US 6478825-A 407 12-NOV-2002;
FEATURES	Location/Qualifiers
source	1..570
BASE COUNT	129 a 190 c 170 g 81 t
ORIGIN	/organism="unknown"
Query Match	97.4%; Score 529; DB 6; Length 570;
Best Local Similarity	100.0%; Pred. No. 3.6e-75;
Matches	529; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	15 GCGAGGACCGGGATATAAGAACCTCTGAGGCTTGCCCGGGAGCGCGAGGTTCCTCCGCG 74
DB	1 GCGAGGACCGGGATATAAGAACCTCTGAGGCTTGCCCGGGAGCGCGAGGTTCCTCCGCG 60
QY	75 GCGCCGAGCCCGCGCGCATGAAAGCTGTGCGGCCCTCTGTGGGCTCTGTGCTGTGCTTCC 134
DB	61 GCGCCGAGCCCGCGCGCATGAAAGCTGTGCGGCCCTCTGTGGGCTCTGTGCGGCCCTGTCC 120
QY	135 TGCAGCTCCGCTGCTGCTTCTTCTTATGTTGGGCTCGGCGCAAGCCTTGAGGCGACGCTGTGGCT 194
DB	121 TGCAGCTCCGCTGCTGCTTCTTATGTTGGGCTCGGCGCAAGCCTTGAGGCGACGCTGTGGCT 180
QY	195 GCGCTGTGAGTCTGGCGGCGAGCGCGGGCGCGGAGCCTTGCGCAACCCCTTGCGACCCCTC 254
DB	181 GCGCTGTGAGTCTGGCGGCGAGCGCGGGCGCGGAGCCTTGCGCAACCCCTTGCGACCCCTC 240
QY	255 AACCCGCTGAAAGCTCTCTGCTGAGCAGCCTTGGGCATCCCTGTGAACCACTCATATGAGGGC 314
DB	241 AACCCGCTGAAAGCTCTCTGCTGAGCAGCCTTGGGCATCCCTGTGAACCACTCATATGAGGGC 300
QY	315 TCCGAGAAAGTGTGGGCTGAGCTGGGCTGCCAGGCGGTTGGGGGGCGCGTGAAGGGCCCTGAAG 374
DB	301 TCCGAGAAAGTGTGTGGCTGAGCTGGGCTGCCAGGCGGTTGGGGGGCGCGTGAAGGGCCCTGAAG 360
QY	375 GCCCTGTCTGGGGGGCCCTGACAGAGTGTGTTGGCTGAGCCGAGACTGGAGCATCTACACCTGAG 434
DB	361 GCCCTGTCTGGGGGGCCCTGACAGAGTGTGTTGGCTGAGCCGAGACTGGAGCATCTACACCTGAG 420
QY	435 GACAAAGACGCTGCCACCCGCGAGGGCTGAAAACCCCGCGCGGGGAGAGACCTTCATCC 494
DB	421 GACAAAGACGCTGCCACCCGCGAGGGCTGAAAACCCCGCGCGGGGAGAGACCTTCATCC 480
QY	495 CATTCCCCCGGGCCCTCTCAATTAACGTGGTTAGACCAAAAAA 543
DB	481 CATTCCCCCGGGCCCTCTCAATTAACGTGGTTAGACCAAAAAA 529
RESULT 4	
AX403520	570 bp DNA linear PAT 14-JUN-2002
LOCUS	AX403520
DEFINITION	Sequence 407 from Patent WO0073454.
ACCESSION	AX403520
VERSION	AX403520.1 GI:21437002
KEYWORDS	
SOURCE	
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
	1 Ashkenazi, A. J., Baker, K. P., Botstein, D., Desnoyers, L., Eaton, D., Ferrara, N., Gerber, H., Gertsen, M., Goddard, A., Godowski, P., Grimaldi, C. J., Gurney, A. L., Kijavita, I., Napier, M. A., Pan, J., Paoni, N. F., Roy, M., Stewart, T. A., Tumas, D., Watanabe, C. K., Williams, P., Wood, W. I. and Zhang, Z.
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL	Patent: WO 0073454-A 407 07-DEC-2000;
FEATURES	Genentech Inc. (US)
	Location/Qualifiers

Source	1. 570	/organism="Homo sapiens"
		/mol_type="genomic DNA"
		/db_xref="taxon:9606"
BASE COUNT	129 a 190 c 170 g 81 t	
ORIGIN		
Query Match	97.4% ; Score 529 ; DB 6 ; Length 570 ;	
Best Local Similarity	100.0% ; Pred. No. 3.6e-75 ;	
Matches 529 ;	Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;	
QY	15 GCGAGACCGGGTTTAAGAAAGCTCTGTCGCTTCCCGGAGACGCCAGTGTCCCGGCG 74	
Db	1 GCGAGGACCGGGTATTAAGAAAGCTCTGTCGCTTCCCGGAGACGCCAGTGTCCCGGCG 60	
OY	75 GCGCGGAGCGCCCGGCGCATGAAGCTGCGCGCCCTCTGCGGGGCTCTGCGGGCCCTGTC 134	
Db	61 GCGCGGAGCGCCCGGCGCATGAAGCTGCGCGCCCTCTGCGGGGCTCTGCGGGCCCTGTC 120	
QY	135 TGCAGCTCCGCTGCTGCTTCTTAGTGGGCTCGGACCAAGCCTGTGGCCAGCCTGTGCT 194	
Db	121 TGCAGCTCCGCTGCTGCTTCTTAGTGGGCTCGGACCAAGCCTGTGGCCAGCCTGTGCT 180	
QY	195 GCGCTGGAAGTCGCGGGGCGAGGCCCGGGGCGGGAACCTTGGCAACCCCTTGGCACCTTC 254	
Db	181 GCGCTGGAAGTCGCGGGGCGAGGCCCGGGGCGGGAACCTTGGCAACCCCTTGGCACCTTC 240	
QY	255 AACCCGCTGAAGCTCTGCTGAGCAGGCTGGGGCATCCCGCGTAACCAACCTCATAGAGGGC 314	
Db	241 AACCCGCTGAAGCTCTGCTGAGCAGGCTGGGGCATCCCGCGTAACCAACCTCATAGAGGGC 300	
QY	315 TCCCGAGAAGTGTGTGAGCTGAGCTGGGTCGCCAGGCGGTGGGGGCGCTGAAGGCGCTGAAG 374	
Db	301 TCCCGAGAAGTGTGTGAGCTGAGCTGGGTCGCCAGGCGGTGGGGGCGCTGAAGGCGCTGAAG 360	
QY	375 GCCCTGCTGGGGGCGCTGACAGTGTGTCGTGAGCCGAGACTGAGACATCTACACTGAG 434	
Db	361 GCCCTGCTGGGGGCGCTGACAGTGTGTCGTGAGCCGAGACTGAGACATCTACACTGAG 420	
QY	435 GACAAAGACGGTGGCCACCGCGGAGGGGTGAAACCCCGCGCGGGGAGAGACCGTCATCC 494	
Db	421 GACAAAGACGGTGGCCACCGCGGAGGGGTGAAACCCCGCGCGGGGAGAGACCGTCATCC 480	
QY	495 CCTTCCCGCGGCGCCCTCTCATATAACGTGTGTTAAGAGCAAAAAA 543	
Db	481 CCTTCCCGCGGCGCCCTCTCATATAACGTGTGTTAAGAGCAAAAAA 529	
RESULT 5		
BD082142	519 bp DNA linear PAT 27-AUG-2002	
LOCUS	BD082142	
DEFINITION	Reagents and methods useful for detecting diseases of the lung.	
ACCESSION	BD082142.1 GI:22627752	
VERSION	JP 2001522225-A/6.	
KEYWORDS	Zea mays	
SOURCE	Zea mays	
ORGANISM	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	
REFERENCE	1 (bases 1 to 519)	
AUTHORS	Medel,P.A.B., Cohen,M., Colplitts,T.L., Friedman,P.N., Gordon,J., Russell,J.C. and Stroepe,S.D.	
TITLE	Reagents and methods useful for detecting diseases of the lung	
JOURNAL	Patent: JP 2001522225-A 6 13-NOV-2001;	
COMMENT	ABSTRACT LABORATORIES	
	PN JP 2001522225-A/6	
	PD 13-NOV-2001	
	PF 30-JAN-1998 JP 1998533078	
	PR 31-JAN-1997 US 08/779170	
	PI PATRICIA A BILLING MEDEL,MAURICE COHEN,TRACEY L COLPLITTS,PAULA	

PI N FRIEDMAN,  
 PI JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R PI  
 KLAAS,  
 PI JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D  
 PI STROUPE  
 PC c12n15/63, c12n5/10, c12Q1/68, c07K14/47//c07K16/30, g01N33/574 CC  
 Strandedness: Single;  
 CC Topology: Linear;  
 FH Key Location/Qualifiers.

FEATURES  
 source  
 1..519  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:4577"

BASE COUNT  
 78 a 190 c 170 g 81 t

ORIGIN

Query Match  
 Best Local Similarity 100.0%; Pred. NO. 1.5e-73;  
 Matches 519; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

15 GCGAGACCGGGTATAGAAGCCCTGTGGCCCTTGGCCGGCAGCCGCAAGTTCCCGGCGC 74  
 1 GCGAGACCGGGTATAGAAGCCCTGTGGCCCTTGGCCGGCAGCCGCAAGTTCCCGGCGC 60  
 75 GCGCCGAGCCCGCGCCGCAAGCTCGCCGCTTCTGGGGCTCTGCGTGGCCCTGTCC 134  
 61 GCGCCGAGCCCGCGCCGCAAGCTCGCCGCTTCTGGGGCTCTGCGTGGCCCTGTCC 120  
 135 TGCACCTCCGGCTGCTTCTTCTAGTGGGCTGGCCAGCCGTCGAGCCGCAAGCTTCGCT 194  
 121 TGCACCTCCGGCTGCTTCTTCTAGTGGGCTGGCCAGCCGTCGAGCCGCAAGCTTCGCT 180  
 195 GCGCTGAGTGGCGCGCGAGGCGCGGGCCGGGACCTTGGCCACCCCTCGGCAACCTTC 254  
 181 GCGCTGAGTGGCGCGCGAGGCGCGGGCCGGGACCTTGGCCACCCCTCGGCAACCTTC 240  
 255 AACCCGCTGAAGCTCTCTGTAGCAGCTGGGCAATCCCGTGAAACCACTCATAGAGGC 314  
 241 AACCCGCTGAAGCTCTCTGTAGCAGCTGGGCAATCCCGTGAAACCACTCATAGAGGC 300  
 315 TCCCAAGAGTGTGGCTGAGCTGGGTCGCCGAGCGCGTGGGGGCGGTGAAGCCCTGAG 374  
 301 TCCCAAGAGTGTGGCTGAGCTGGGTCGCCGAGCGCGTGGGGGCGGTGAAGCCCTGAG 360  
 375 GCGCTGAGTGGGCGCGCTGACAGTGTGTTGGCTGAGCCGAGACTGAGCATCTACACTGAG 434  
 361 GCGCTGAGTGGGCGCGCTGACAGTGTGTTGGCTGAGCCGAGACTGAGCATCTACACTGAG 420  
 435 GACAAGAGCTGCCACCGCGAGAGGGCTGAAAAACCCCGCGGGGAGAGACCTGCAATCC 494  
 421 GACAAGAGCTGCCACCGCGAGAGGGCTGAAAAACCCCGCGGGGAGAGACCTGCAATCC 480  
 495 CTTTCCCGGCGCGCTCTCAATTAACGTGTTTAAGAGA 533  
 481 CTTTCCCGGCGCGCTCTCAATTAACGTGTTTAAGAGA 519

RESULT 6  
 HUM2B52D10  
 LOCUS HUM2B52D10 471 bp mRNA linear PRI 29-AUG-1998  
 DEFINITION Homo sapiens full length insert cDNA clone ZB52D10.  
 ACCESSION AF086152  
 VERSION AF086152.1 GI:3483497  
 KEYWORDS FTI\_CDNA.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 Mooser, J., Tan, F., Marra, M., Kucaba, T., Yandell, M., Martin, J.,  
 Marth, G., Bowles, L., Wylie, T., Bowers, Y., Stepien, M., Theising, B.,  
 Geisel, S., Allen, M., Underwood, K., Chappell, J., Person, B.,

GIBBONS, M., HARVEY, N., PAPE, D., CHAMBERLAIN, A., MORALES, R.,  
 SCHURK, R., RITTER, E., KOHN, S., SWALLER, T., BEHYMER, K., HILLER, L.,  
 WILSON, R. and WATERSTON, R.  
 Full Clone Sequencing of the Longest Available Member from Each  
 Unpublished  
 2 (bases 1 to 471)

JOURNAL  
 REFERENCE  
 AUTHORS  
 JOURNAL  
 Submitted (24-AUG-1998) Department of Genetics, Washington  
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 SUBMITTED BY:  
 Genome Sequencing Center  
 Department of Genetics  
 Washington University  
 St. Louis MO 63108, USA  
 http://genome.wustl.edu/gsc  
 mailto:est@wustl.wustl.edu

NOTICE: This sequence represents the full insert of this cDNA. No  
 attempt has been made to verify whether this corresponds to the  
 full-length of the original mRNA from which it was derived. We  
 have tried to obtain double-stranded, or double chemistry sequence  
 across the entire clone, but potentially, there are areas in the  
 sequence where this level of coverage was not achieved.  
 Nevertheless, we are confident of the accuracy of this sequence as  
 all regions of low quality, as defined by PHRAP (P. Green, in  
 preparation), were visually inspected and edited accordingly. The  
 consensus quality values for this sequence have been submitted  
 separately.

The location of this clone is unknown.

FEATURES  
 source  
 1..471  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:307219"  
 /clone\_11b="Soares\_fetal\_lung\_NbHu19W"

BASE COUNT  
 78 a 171 c 149 g 73 t

ORIGIN

Query Match  
 Best Local Similarity 100.0%; Pred. NO. 6.9e-66;  
 Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

72 GCGGCGCGGAGCGCGCGCCATGAAGCTCGCGGCGCTCGGGGCTGTGGTGGCCCTG 131  
 1 GCGGCGCGGAGCGCGCGCCATGAAGCTCGCGGCGCTCGGGGCTGTGGTGGCCCTG 60  
 132 TCTGACACTCCGCTGCTGCTTCTTCTAGTGGGCTCGGCAAGCTGTGGCCAGCTGTC 191  
 61 TCTGACACTCCGCTGCTGCTTCTTCTAGTGGGCTCGGCAAGCTGTGGCCAGCTGTC 120  
 192 GCTGCGCTGAGTGGGCGCGGAGGCGCGGGCCGGGACCTTGGCCAACTCCCTGGGACC 251  
 121 GCTGCGCTGAGTGGGCGCGGAGGCGCGGGCCGGGACCTTGGCCAACTCCCTGGGACC 180  
 252 CTCACCGCGTGAAGCTCTGCTGAGAGCTGGGAGCAATCCCGTGAACCACTCATAGAG 311  
 181 CTCACCGCGTGAAGCTCTGCTGAGAGCTGGGAGCAATCCCGTGAACCACTCATAGAG 240  
 312 GCGTCCGAGAAGTGTGGTGAAGCTGGTCCCAAGGCGCTGGGGGCGGTGAAGGCGCTG 371  
 241 GCGTCCGAGAAGTGTGGTGAAGCTGGTCCCAAGGCGCTGGGGGCGGTGAAGGCGCTG 300  
 372 AAGGCGCTGCGGGGCGCTTACAGTGTGTTGGCTGAGCCGAGACTGGAATCTACACT 431  
 301 AAGGCGCTGCGGGGCGCTTACAGTGTGTTGGCTGAGCCGAGACTGGAATCTACACT 360  
 432 GAGGCAAGAGCGTGGCCACCGCGAGAGGCTGAAAAACCCCGCGGGGAGAGACCTGCA 491  
 361 GAGGCAAGAGCGTGGCCACCGCGAGAGGCTGAAAAACCCCGCGGGGAGAGACCTGCA 420

```

OY      492  TCCCTTCCCGGCCCCCTCTCAATTAACGTGGTTAAGACCAAAAAAAAA 542
          |||||||
          421  TCCCTTCCCGGCCCCCTCTCAATTAACGTGGTTAAGACCAAAAAAAAA 471
          |||||||

RESULT 7
BC029176      503 bp  mRNA  linear  PRI 16-MAY-2002
LOCUS         Homo sapiens, secretoglobin, family 3A, member 1, clone MGC:34758
DEFINITION    IMAGE:5180304, mRNA, complete cds.
ACCESSION     BC029176
VERSION       BC029176.1  GI:20809672
KEYWORDS      MGC.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1  (bases 1 to 503)
AUTHORS       Strausberg, R.
JOURNAL       Direct Submision
Submitted (01-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amebcm.tmc.edu
Gumarate, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 50 Row: D Column: 24
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, Genomescan gene prediction.
location/Qualifiers
1.503
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="locusid:92304"
/db_xref="taxon:9606"
/clone="MGC:34758 IMAGE:5180304"
/tissue_type="Brain, Lung, Testis, adult, pooled whole"
/clone_id="NH_MGC_115"
/lab_host="DH10B"
/notes="Vector: PCMV-SPORT6"
16..330
/codon_start=1
/product="secretoglobin, family 3A, member 1"
/protein_id="AAH29176.1"
/db_xref="GI:20809673"
/translation="MKIALILGLCVALLSCSSAARFVGSAPVAPQPVAALESAAEAGA
GTIANPLGTINPLKLILSLISIGIPVNHILIEGSKCAVELGPQAVGAVAKALALGALTIV
FG"

BASE COUNT  116 a 167 c 147 g 73 t
ORIGIN
Query Match      85.8%; Score 466; DB 9; Length 503;
Best Local Similarity 100.0%; Pred. No. 4,3e-65;
Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      78  CCGAGCCCGCGGCATGAAGCTCCGCCCTCTGCGGCTCTGCGGCCCTGTCCTGC 137

```

```

DB      1  CCGAGCCCGCGGCATGAAGCTCCGCCCTCTGCGGCTCTGCGGCCCTGTCCTGC 60
          |||||||
OY      138  AGCTCCGCTCTGCTTCTTCTAGTGGGCTCGGCCAAGCCTTGAGCCAGCCTGTCGCTGC 197
          |||||||
DB      61  AGCTCCGCTCTGCTTCTTCTAGTGGGCTCGGCCAAGCCTTGAGCCAGCCTGTCGCTGC 120
          |||||||
OY      198  CTGAGAGTCGGCGGCGAGGCGCGGCGGAGCCCTGCGCAACCCCTCGGACCCCTCAAC 257
          |||||||
DB      121  CTGAGAGTCGGCGGCGGAGGCGCGGAGCCCTGCGCAACCCCTCGGACCCCTCAAC 180
          |||||||
OY      258  CCGCTGAAGCTCTGCTGACACAGCCTGCGCATCCCTGTAACCACTCATAGAGGCTCC 317
          |||||||
DB      181  CCGCTGAAGCTCTGCTGACACAGCCTGCGCATCCCTGTAACCACTCATAGAGGCTCC 240
          |||||||
OY      318  CAGAGTGTGGGTGAGTGGGTCGCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 377
          |||||||
DB      241  CAGAGTGTGGGTGAGTGGGTCGCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
          |||||||
OY      378  CTGCTGGGGGCGCTGACAGTGTGGTGGCTGAGCGGAGACTGAGCATCTACACCTGAGAGC 437
          |||||||
DB      301  CTGCTGGGGGCGCTGACAGTGTGGTGGCTGAGCGGAGACTGAGCATCTACACCTGAGAGC 360
          |||||||
OY      438  AAGACGCTGCCACCGCGGAGGGCTGAAGAACCCCGCGGCGGAGACCGTCCATCCCT 497
          |||||||
DB      361  AAGACGCTGCCACCGCGGAGGGCTGAAGAACCCCGCGGCGGAGACCGTCCATCCCT 420
          |||||||
OY      498  TCCCGCGGCCCTCTCAATTAACGTGGTTAAGACCAAAAAAAAA 543
          |||||||
DB      421  TCCCGCGGCCCTCTCAATTAACGTGGTTAAGACCAAAAAAAAA 466
          |||||||

RESULT 8
AY040564      461 bp  mRNA  linear  PRI 15-AUG-2001
LOCUS         Homo sapiens HIN-1 putative cytokine mRNA, complete cds.
DEFINITION    AY040564
ACCESSION     AY040564
VERSION       AY040564.1  GI:15079187
KEYWORDS
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1  (bases 1 to 461)
AUTHORS       Krop, I.E., Sgroi, D., Porter, D.A., Lunetta, K.L., LeVangie, R.,
Seth, P., Kaelin, C.M., Rhee, E., Bosenberg, M., Schitt, S.,
Marks, J.R., Pagon, Z., Belina, D., Razumovic, J. and Polyak, K.
HIN-1, a putative cytokine highly expressed in normal but not
cancerous mammary epithelial cells
Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9796-9801 (2001)
11481438
JOURNAL       MEDLINE
PUBMED        21396515
REFERENCE     2  (bases 1 to 461)
AUTHORS       Polyak, K., Krop, I. and Sgroi, D.
Direct Submission
Submitted (15-JUN-2001) Adult Oncology, Dana-Farber Cancer
Institute, 44 Binney St. D740C, Boston, MA 02115, USA
location/Qualifiers
1.461
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="5"
/map="5q35-tel"
22..336
/notes="High in normal -1 putative cytokine"
/codon_start=1
/product="HIN-1 putative cytokine"
/protein_id="AAK82942.1"
/db_xref="GI:15079188"
/translation="MKIALILGLCVALLSCSSARFVGSAPVAPQPVAALESAAEAGA
GTIANPLGTINPLKLILSLISIGIPVNHILIEGSKCAVELGPQAVGAVAKALALGALTIV
FG"

```



Matches 351: Conservative 0; Mismatches 23; Indels 8; Gaps 4;

QY 152 TTCTTAGTGGGCTGGCCAAAGCCTGTGGCCAGCTGTGCTGCTGCTGAGTGGGGC 211  
 |||||  
 Db 374 TTCTTAGTGGGCTGGCCAA----NCTGTGCCAGCCTNGMNTGGCTGGAGTGGGGC 319  
 |||||

QY 212 GGAGGCGGGGCGGGAGCCTGTGGCCAAACCCCTGTGGACCTTCAACCCGCTGAAGTCT 271  
 |||||  
 Db 318 GGA-GCGGGGCGGGAGCCTGTGGCCAAACCCCTGTGGACCTTCAACMC-NYGAAGTCT 261  
 |||||

QY 272 GCTGAGCAGCCTGCGGCAATCCCGTGAACCACTCATAGAGGGCTCCGAGAGTGTGGC 331  
 |||||  
 Db 260 GCTGAGCAGCCTGCGGCAATCCCGTGAACCACTCATAGAGGGCTCCGAGAGTGTGGC 201  
 |||||

QY 332 TGAGCTGGTCCCGAGGCGCTGGGGGCGCTGAAGCCCTGAAGCCCTGTGCGGGGCT 391  
 |||||  
 Db 200 TGAGCTGGTCCCGAGGCGCTGGGGG--CGTGAAGCCCTGAAGCCCTGTGCGGGGCT 143  
 |||||

QY 392 GACGCTTTTGGCTGAGACCCAGACTGAGACTTACACCTGAGACAGACAGCTGCGCAC 451  
 |||||  
 Db 142 GACGCTTTTGGCTGAGACCCAGACTGAGACTTACACCTGAGACAGACAGCTGCGCAC 83  
 |||||

QY 452 CCGGAGGCGTGAACCCCGCGGGGAGAGCAGTCAATCCCTGCCCGGCGCTC 511  
 |||||  
 Db 82 CCGGAGGCGTGAACCCCGCGGGGAGAGCAGTCAATCCCTGCCCGGCGCTC 23  
 |||||

QY 512 TCAATAACGTGTTAAGACA 533  
 |||||  
 Db 22 TCAATAACGTGTTAAGACA 1  
 |||||

RESULT 11  
 BD082138 244 bp DNA linear PAT 27-AUG-2002  
 LOCUS Reagents and methods useful for detecting diseases of the lung.  
 DEFINITION  
 ACCESSION BD082138  
 VERSION BD082138.1 GI:22627748  
 KEYWORDS JP 2001522225-A/2.  
 SOURCE  
 ORGANISM  
 Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 Clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 244)  
 Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J.,  
 Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Rapp,L.R.,  
 Russell,J.C. and Stroupe,S.D.  
 Reagents and methods useful for detecting diseases of the lung  
 Patent: JP 2001522225-A 2 13-NOV-2001;  
 ABBOTT LABORATORIES  
 PN JP 2001522225-A/2  
 PD 13-NOV-2001  
 PF 30-JAN-1998 JP 1998533078  
 PR 31-JAN-1997 US 08/791710  
 PI PATRICIA A BILLING MEDEL,MAURICE COHEN,TRACEY L COLPITTS,PAULA

PI N FRIEDMAN,  
 PI JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R PI  
 KLAS,  
 PI JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D  
 PI STRUPE  
 PC C12N15/63, C12N5/10, C12Q1/68, C07K14/47//C07K16/30, G01N33/574 CC  
 Strandness: Single;  
 CC Topology: Linear;  
 FH Key Location/Qualifiers.

FEATURES  
 SOURCE  
 1..244  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:4577"  
 25 a 97 c 82 g 39 t 1 others

BASE COUNT  
 ORIGIN

Query Match 44.5%; Score 241.4; DB 6; Length 244;  
 Best Local Similarity 99.2%; Pred. No. 3.8e-29;  
 Matches 242: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 GCGAGGACCGGGGTATAGAAAGCCTGTGCTTCCCGGGAGACCGCGAGTTCCTCCCGGC 74  
 |||||  
 Db 1 GCGAGGACCGGGGTATAGAAAGCCTGTGCTTCCCGGGAGACCGCGAGTTCCTCCCGGC 60  
 |||||

QY 75 GCCCGAGACCCCGCCGATGAGCTGAGCCGCTCTGGGGGCTGTGGCTGGCCCTGTC 134  
 |||||  
 Db 61 GCCCGAGACCCCGCCGATGAGCTGAGCCGCTCTGGGGGCTGTGGCTGGCCCTGTC 120  
 |||||

QY 135 TGCACTTCGCTGCTTCTTCTTAAGTGGCTGCGCAAGCCTGTGGCCAGCTGTGCT 194  
 |||||  
 Db 121 TGCACTTCGCTGCTTCTTCTTAAGTGGCTGCGCAAGCCTGTGGCCAGCTGTGCT 180  
 |||||

QY 195 GCGCTGAGTGGGGGGGAGCGGGGCGGGAGCCCGGCAACCCCTGTGGACCTC 254  
 |||||  
 Db 181 GCGCTGAGTGGGGGGGAGCGGGGCGGGAGCCCGGCAACCCCTGTGGACCTC 240  
 |||||

QY 255 AAC 258  
 |||||  
 Db 241 AAC 244  
 |||||

RESULT 12  
 AC108083 130129 bp DNA linear HTG 25-JAN-2002  
 LOCUS Homo sapiens chromosome 5 clone CTD-2013L15, WORKING DRAFT  
 DEFINITION  
 ACCESSION AC108083  
 VERSION AC108083.1 GI:18369929  
 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ACTIVEFIN.  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 130129)  
 DOE Joint Genome Institute.  
 Direct Submission  
 Submitted (25-JAN-2002) Production Sequencing Facility, DOE Joint  
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 -----Genome Center  
 Center: Joint Genome Institute  
 Center Code: JGI  
 Web site: http://www.jgi.doe.gov  
 -----  
 Project Information  
 Center Project Name: 632820  
 Center clone name: CTRB-H1\_2013L15  
 -----  
 Summary Statistics  
 Consensus quality: 124488 bases at least Q40  
 Consensus quality: 128031 bases at least Q30  
 Consensus quality: 128842 bases at least Q20  
 Estimated insert size: 135000; agarose-fp estimation  
 Estimated insert size: 129829; sum-of-ctdigs estimation  
 Quality coverage: 7.66 in Q20 bases; agarose-fp estimation  
 Quality coverage: 7.97 in Q20 bases; sum-of-ctdigs estimation.  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 4 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \* 1 4320: contig of 4320 bp in length  
 \* 4321 4420: gap of unknown length

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE	TITLE	AUTHORS
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	1 (bases 1 to 168347)	Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 5, clone RP11-451H23	Unpublished	
2 (bases 1 to 168347)		
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldoni,J., Barna,N., Bastien,V., Beda,F., Boguslavsky,L., Bouknight,B., Brown,A., Burnett,G., Campilongo,A., Castle,A., Choedel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Dearrellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domingo,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Glade,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kam,L., Karakas,A., Klein,J., LaCocque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lien,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,J.M., McEwan,P., McGurk,A., McKernan,K., MCPheeters,R., Meldrum,J., Meneses,L., Mihova,T., Mirkenan,C., Mlenka,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Olliver,T.M., Oliver,J., Peterson,K., Pierre,N., Pisanl,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy A., Santos,R., Schauer,S., Severy,P., Spencer,B., Strange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trifillio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,R., Wu,X., Wyman,D., Ye,W.J., Young,G., Zalnoun,J., Zimmer,A. and Zody,M.		
Whitehead Institute/MIT Center for Genome Research	Submitted (08-MAR-2000)	
Research, 320 Charles Street, Cambridge, MA 02141, USA	On Mar 25, 2000 this sequence version replaced gi:7210017.	
All repeats were identified using RepeatMasker:		
Smith, A.F.A. & Green, P. (1996-1997)		
http://ftp.genome.washington.edu/RM/RepeatMasker.html		
Genome Center		
Center: Whitehead Institute/ MIT Center for Genome Research		
Center code: MIBR		
Web site: http://www-seq.wi.mit.edu		
Contact: sequence_submissions@genome.wi.mit.edu		
Project information		
Center project name: L6686		
Center clone name: 451.H.23		
Summary Statistics		
Sequencing vector: M13; M77813; 100% of reads		
Chemistry: Dye-terminator Big Dye; 100% of reads		
Assembly program: Phrap; version 0.960731		
Consensus quality: 150422 bases at least Q40		
Consensus quality: 159524 bases at least Q30		
Consensus quality: 163013 bases at least Q20		
Insert size: 165247; sum-of-contigs		
Quality coverage: 3.6 in Q20 bases; sum-of-contigs		
NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.		
1 1389: contig of 1389 bp in length		
* 1390 1489: gap of 100 bp		
* 1490 3130: contig of 1641 bp in length		
* 3131 3230: gap of 100 bp		
* 3231 4942: contig of 1712 bp in length		
* 4943 5042: gap of 100 bp		
* 5043 6981: contig of 1939 bp in length		
* 6982 7081: gap of 100 bp		
* 7082 8708: contig of 1627 bp in length		
* 8709 8808: gap of 100 bp		
* 8809 10286: contig of 1478 bp in length		
* 10287 10386: gap of 100 bp		
* 10387 12212: contig of 1826 bp in length		

*	12213	12312: gap of 100 bp
*	12313	14658: contig of 2246 bp in length
*	14639	14758: gap of 100 bp
*	17941	17941: contig of 3183 bp in length
*	17942	18041: gap of 100 bp
*	18042	21297: contig of 3256 bp in length
*	21298	21397: gap of 100 bp
*	21398	24992: contig of 3395 bp in length
*	24993	25092: gap of 100 bp
*	25093	27768: contig of 2676 bp in length
*	27769	27868: gap of 100 bp
*	27869	31188: contig of 3320 bp in length
*	31189	31288: gap of 100 bp
*	31289	33714: contig of 2426 bp in length
*	33715	33814: gap of 100 bp
*	33815	37277: contig of 3463 bp in length
*	37278	37377: gap of 100 bp
*	37378	42302: contig of 4925 bp in length
*	42303	42402: gap of 100 bp
*	42403	47816: contig of 5414 bp in length
*	47817	47916: gap of 100 bp
*	47917	52586: contig of 4670 bp in length
*	52587	52686: gap of 100 bp
*	52687	55657: contig of 3881 bp in length
*	55658	56667: gap of 100 bp
*	56668	61557: contig of 4990 bp in length
*	61558	61657: gap of 100 bp
*	61658	66724: contig of 5067 bp in length
*	66725	66824: gap of 100 bp
*	66825	71568: contig of 4744 bp in length
*	71569	71668: gap of 100 bp
*	71669	76578: contig of 4910 bp in length
*	76579	76679: gap of 100 bp
*	76679	83312: contig of 6634 bp in length
*	83313	83412: gap of 100 bp
*	83413	90053: contig of 6641 bp in length
*	90054	90153: gap of 100 bp
*	90154	99426: contig of 9273 bp in length
*	99427	99526: gap of 100 bp
*	99527	108015: contig of 8489 bp in length
*	108016	108115: gap of 100 bp
*	108116	118144: contig of 10029 bp in length
*	118145	118244: gap of 100 bp
*	118245	130468: contig of 12224 bp in length
*	130469	130568: gap of 100 bp
*	130569	142239: contig of 11671 bp in length
*	142240	142339: gap of 100 bp
*	142340	157335: contig of 14796 bp in length
*	157136	157235: gap of 100 bp
*	157236	168347: contig of 11112 bp in length
* * *	157236	Location/Qualifiers
FEATURES		
source		
1..168347		
/organism="Homo sapiens"		
/mol_type="genomic DNA"		
/db_xref="taxon:9606"		
/chromosome="5"		
/map="5"		
/clone="RP11-451H23"		
/clone_id="RPC1-11 Human Male BAC"		
misc_feature	1..1389	/note="assembly_fragment"
misc_feature	1490..3130	/note="assembly_fragment"
misc_feature	3231..4942	/note="assembly_fragment"
misc_feature	5043..6981	/note="assembly_fragment"
misc_feature	7082..8708	/note="assembly_fragment"
misc_feature	8809..10286	/note="assembly_fragment"
misc_feature	10387..12212	/note="assembly_fragment"



Query Match	44.5%;	Score 241.4;	DB 2;	Length 168347;
Best Local Similarity	99.6%;	Pred. No. 1.1e-29;		
Matches 242; Conservative	0;	Mismatches 1;	Indels 0;	

RESULT 15  
AC122714/C

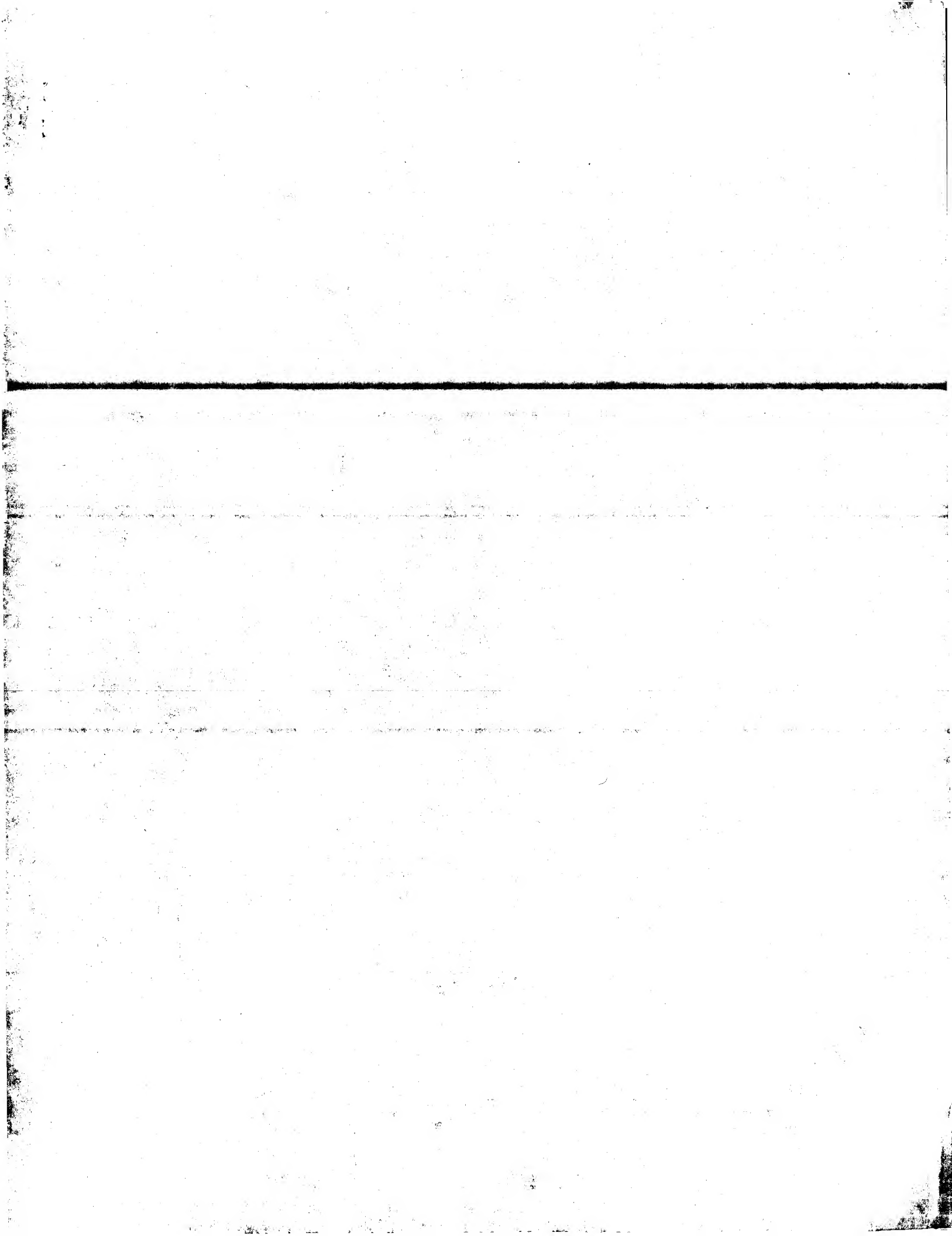
QY	142	CCCCGCTGCTTCTTCTAGTGGGCTGGCCCAAGCTGTGGCCAGCCTGACCTGCTGGCTGG	201
Db	80316	CACCTCTCTGTTTCTTCTAGTGGGCTCGGCCCAAGCTGTGGGCCAGCTGTCGCTGG	8025
QY	202	AGTCGGCGGGGAGAGCGCGGGGCGGGGAGCCCTGGCCAAACCCCTCGGACCCCTCAACCCCG	261
Db	80256	AGTCGGCGGGGAGAGCGCGGGGCGGGGAGCCCTGGCCAAACCCCTCGGACCCCTCAACCCCG	80197
QY	262	TGAAGTCGCGCTGAGCAGCGCTGGGGATCCCGTGAACCACTCATAGAGGGCTCCACA	321
Db	80196	TGAAGTCTCTGCTGAGACACAGCCTGGGCAATCCCGTGAACCACTCATAGAGGGCTCCACA	80137
QY	322	AGTGTGTGGCTGAGCTGGGCTCCCCAGAGCCGTGGGGGCGCTGAAGAGCCCTGAAGAGCCCTCG	381
Db	80136	AGTGTGTGGCTGAGCTGGGCTCCCCAGAGCCGTGGGGGCGCTGAAGAGCCCTGAAGAGCCCTCG	80077
QY	382	TGG 384	
Db	80076	TGG 80074	

RESULT 15  
AC122714/C



Job time : 2095.54 secs

---



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2003, 12:42:26 ; Search time 1212.75 Seconds  
(without alignments)  
10625.902 Million cell updates/sec

Title: US-09-700-770-4

Perfect score: 315  
Sequence: 1 taacactgactcagattt.....tggtattactactatgc 315

Scoring table: IDENTITY\_NUC  
Gapop 10-0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb\_da:\*  
2: gb\_hlg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_da:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vi:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rod:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	315	100.0	532	6	AX566036
C 2	315	100.0	705	6	AX566037
C 3	315	100.0	118068	9	AL356798
C 4	42.4	13.5	13413	1	AE014127
C 5	42	13.3	156149	2	BX296522
C 6	41.8	13.3	236285	2	AC106302
C 7	40.8	13.0	99576	5	BX005410
C 8	40.4	12.8	163777	2	AY193721
C 9	40.4	12.8	224940	2	AC025794
C 10	40	12.7	8737	1	AF435978
C 11	40	12.7	125020	9	AF429315
C 12	39.8	12.6	201794	9	CNS0180W
C 13	39.6	12.6	108873	14	AF318573
C 14	39.6	12.6	144727	2	AC102444
C 15	38.4	12.5	54700	3	CER1168A
C 16	38.4	12.5	110000	2	CER113B8_1
C 17	39.4	12.5	175281	2	CER113B8_2
C 18	39.4	12.5	175281	9	AC092859
C 19	39.4	12.5	197282	2	AC117659
C 20	39.4	12.5	247527	2	AC114406
C 21	39.2	12.4	11026	1	AE014120
C 22	38.2	12.4	179162	2	AC132076
C 23	39.2	12.4	236486	2	AC138166
C 24	39.2	12.4	118577	9	AC079997
C 25	39	12.4	150355	9	HSJ364H10
C 26	39	12.4	168043	2	AC011935
C 27	39	12.4	174578	9	AC013287
C 28	39	12.4	185437	9	AC012075
C 29	38.8	12.3	105400	9	AC125492
C 30	38.8	12.3	110000	2	PEFMA16P1_12
C 31	38.8	12.3	160402	2	AC136491
C 32	38.6	12.3	52236	2	AC139012
C 33	38.6	12.3	110000	2	PEFMA13P2_2
C 34	38.6	12.3	145612	2	BX470202
C 35	38.6	12.3	171481	5	AL840631
C 36	38.6	12.3	174311	2	BX324119
C 37	38.6	12.3	179144	2	AL954704
C 38	38.6	12.3	232070	2	BX000529
C 39	38.6	12.3	299850	1	AP004601
C 40	38.4	12.2	50234	2	AC144877
C 41	38.4	12.2	79230	9	AC113417
C 42	38.4	12.2	203259	9	AC013737
C 43	38.4	12.2	250823	3	AE014821
C 44	38.4	12.2	340552	3	PFA929354
C 45	38.2	12.1	124281	9	AL136101

# ALIGNMENTS

RESULT 1  
AX566036/c  
LOCUS AX566036  
DEFINITION Sequence 8 from Patent WO02077236.  
ACCESSION AX566036  
VERSION AX566036.1 GI:26001279  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
1  
Recipon, H., Sun, Y., Chen, S.Y., Liu, C. and Turner, L.R.  
Compositions and methods relating to lung specific genes and proteins

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: WO 02077236-A 8 03-OCT-2002;  
 Diadexus, Inc. (US)  
 Location/Qualifiers  
 FEATURES  
 SOURCE 1..532  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 BASE COUNT 161 a 93 c 100 g 178 t  
 ORIGIN

Query Match 100.0%; Score 315; DB 6; Length 532;  
 Best Local Similarity 100.0%; Pred. No. 1, le-60;  
 Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAACCTGACCTCAGATTTTAAAGAAATTAATTTGAGAAATAGACAATAGAAATGAGTT 60  
 DB 315 TAAACCTGACCTCAGATTTTAAAGAAATTAATTTGAGAAATAGACAATAGAAATGAGTT 256  
 QY 61 TCCGACCACTTAAAGATATATCTCTTAGAGATCTACAGCTCCCTTTAGGGGACATACAA 120  
 DB 255 TCCGACCACTTAAAGATATATCTCTTAGAGATCTACAGCTCCCTTTAGGGGACATACAA 196  
 QY 121 GTCAGTGTGTGTCCTTTGTGAGTCCACCTTATTTGACAGTATGACTACAAAT 180  
 DB 195 GTCAGTGTGTGTCCTTTGTGAGTCCACCTTATTTGACAGTATGACTACAAAT 136  
 QY 181 TTGAATAATGATGTGCACAAATAAATGAGTTTATGAAACATCAGTAGAAGAAATA 240  
 DB 135 TTGAATAATGATGTGCACAAATAAATGAGTTTATGAAACATCAGTAGAAGAAATA 76  
 QY 241 CAACATTCATCCCTTTACAGAGATCATTTACTTGCACTCAGATTAATTTGTCATGT 300  
 DB 75 CAACATTCATCCCTTTACAGAGATCATTTACTTGCACTCAGATTAATTTGTCATGT 16  
 QY 301 ATTATCTACTTATGC 315  
 DB 15 ATTATCTACTTATGC 1

RESULT 2  
 AX566037/c  
 LOCUS AX566037 705 bp DNA Linear PAT 29-NOV-2002  
 DEFINITION Sequence 9 from Patent WO02077236.  
 ACCESSION AX566037  
 VERSION AX566037.1 GI:26001280  
 KEYWORDS  
 SOURCE  
 ORGANISM Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
 AUTHORs Recipon, H., Sun, Y., Chen, S.Y., Liu, C. and Turner, L.R.  
 TITLE Compositions and methods relating to lung specific genes and  
 JOURNAL Patent: WO 02077236-A 9 03-OCT-2002;  
 Diadexus, Inc. (US)

FEATURES  
 source location/Qualifiers  
 1..705

BASE COUNT 225 a 123 c 128 g 227 t 2 others  
 ORIGIN

Query Match 100.0%; Score 315; DB 6; Length 705;  
 Best Local Similarity 100.0%; Pred. No. 1e-60;  
 Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAACCTGACCTCAGATTTTAAAGAAATTAATTTGAGAAATAGACAATAGAAATGAGTT 60  
 DB 384 TAAACCTGACCTCAGATTTTAAAGAAATTAATTTGAGAAATAGACAATAGAAATGAGTT 325  
 QY 61 TCTCACCACCTTAAAGTATATCTCTTAGAGATCTACAGCTCCCTTTAGGGGACATACAA 120

## FEATURES

Location/Qualifiers

DB 324 TCTCACCACCTTAAAGTATATCTCTTAGAGATCTACAGCTCCCTTTAGGGGACATACAA 265  
 QY 121 GTCAGTGTGTGTCCTTTGTGAGTCCACCTTATTTGACAGTATGACTACAAAT 180  
 DB 264 GTCAGTGTGTGTCCTTTGTGAGTCCACCTTATTTGACAGTATGACTACAAAT 205  
 QY 181 TTGAATAATGATGTGCACAAATAAATGAGTTTATGAAACATCAGTAGAAGAAATA 240  
 DB 204 TTGAATAATGATGTGCACAAATAAATGAGTTTATGAAACATCAGTAGAAGAAATA 145  
 QY 241 CAACATTCATCCCTTTACAGAGATCATTTACTTGCACTCAGATTAATTTGTCATGT 300  
 DB 144 CAACATTCATCCCTTTACAGAGATCATTTACTTGCACTCAGATTAATTTGTCATGT 85  
 QY 301 ATTATCTACTTATGC 315  
 DB 84 ATTATCTACTTATGC 70

## COMMENT

RESULT 3  
 AL356798/c  
 LOCUS AL356798 118068 bp DNA Linear PRI 26-SEP-2001  
 DEFINITION Human DNA sequence from clone RP11-467B11 on chromosome 9, complete  
 sequence.  
 ACCESSION AL356798  
 VERSION AL356798.18 GI:15795413  
 KEYWORDS HTG.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 118068)  
 Babbage, A.  
 Direct Submission  
 Submitted (26-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk  
 On Sep 27, 2001 this sequence version replaced gi:14455883.  
 During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.  
 This sequence was finished as follows unless otherwise noted: all  
 regions were either double-stranded or sequenced with an alternate  
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by at least  
 one plasmid subclone or more than one M13 subclone; and the  
 assembly was confirmed by restriction digest. The following  
 abbreviations are used to associate primary accession numbers given  
 in the feature table with their source databases: Em: EMBL, Sw: SWISSPROT, Tr: TREMBL, Wp: WORMPEP; Information on the WORMPEP  
 database can be found at  
 http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence  
 was generated from part of bacterial clone contigs of human  
 chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping  
 Group. Further information can be found at  
 http://www.sanger.ac.uk/HGP/Chr9  
 RP11-467B11 is from the library RPEC11.2 constructed by the group  
 of Pieter de Jong. For further details see  
 http://www.chori.org/daopac/home.htm  
 VECTOR: pBACe3.6  
 IMPORTANT: This sequence is not the entire insert of clone  
 RP11-467B11 it may be shorter because we sequence overlapping  
 sections only once, except for a short overlap.  
 The true right end of clone RP11-467B11 is at 118068 in this  
 sequence. The true left end of clone RP11-208F1 is at 29578 in this  
 sequence. The true right end of clone RP11-29B11 is at 2000 in this  
 sequence.

source 1..118068  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="9"  
/clone="Rp11-467B11"  
/clone\_1lb="RP11-11.2"  
/clone\_1lb="RP11-11.2"  
BASE COUNT 33053 a 23625 c 22510 g 38880 t  
ORIGIN

Query Match 100.0%; Score 315; DB 9; Length 118068;  
Best Local Similarity 100.0%; Pred. No. 3.9e-61;  
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAACACTGACACATTTTAAAGAAATACTTTTGAAGAATAGAACAAATGAAATACAGTT 60  
Db 96845 TAAACACTGACACATTTTAAAGAAATACTTTTGAAGAATAGAACAAATGAAATACAGTT 96786

QY 61 TCTCCACACATTAAGTATATCTCTTAGAGATCTACAGCCCTCTTGGGGACATACAAA 120  
Db 96785 TCTCCACACATTAAGTATATCTCTTAGAGATCTACAGCCCTCTTGGGGACATACAAA 96726

QY 121 GTCAGTGTGTCCTTGTGTAGTCCACCTTATATTCAGTATAGCTATGACTACAAAT 180  
Db 96725 GTCAGTGTGTCCTTGTGTAGTCCACCTTATATTCAGTATAGCTATGACTACAAAT 96666

QY 181 TTGAAAATGATTTGTCACAACTGAGCTTTATGGAACATCAGTAGAAGAAATA 240  
Db 96665 TTGAAAATGATTTGTCACAACTGAGCTTTATGGAACATCAGTAGAAGAAATA 96606

QY 241 CAACATTCATCCCTTTACAGAGATCATTTACTTGCACCTCAGGATTAATTTGTCATGT 300  
Db 96605 CAACATTCATCCCTTTACAGAGATCATTTACTTGCACCTCAGGATTAATTTGTCATGT 96546

QY 301 ATTATCTACTTATGCG 315  
Db 96545 ATTATCTACTTATGCG 96531

RESULT 4  
AE014127 13413 bp DNA linear BCT 28-JUN-2002  
LOCUS Buchnera aphidicola str. Sg (Schizaphis graminum) section 52 of 57  
DEFINITION of the complete genome.  
ACCESSION AE014127 AE013218  
VERSION AE014127.1 GI:21623437  
KEYWORDS Buchnera aphidicola str. Sg (Schizaphis graminum)  
ORGANISM Buchnera aphidicola str. Sg (Schizaphis graminum)  
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
Enterobacteriaceae; Buchnera.  
REFERENCE 1 (bases 1 to 13413)  
Tamas, I., Klasson, L., Canback, B., Naslund, A.K., Eriksson, A.S.,  
Wernegreen, J.J., Sandstrom, J.P., Moran, N.A. and Andersson, S.G.  
50 million years of genomic stasis in endosymbiotic bacteria  
Science 296 (5577), 2376-2379 (2002)  
JOURNAL MEDLINE 12084549  
PUBMED 12089438  
REFERENCE 2 (bases 1 to 13413)  
Klasson, L. and Andersson, S.G.E.  
Direct Submission  
TITLE Buchnera aphidicola str. Sg (Schizaphis graminum)  
AUTHORS Submitted (10-JUN-2002) Department of Molecular Evolution,  
Institution of Evolutionary Biology, Nordyagen 18C, Uppsala 75236,  
Sweden  
JOURNAL

FEATURES  
source Location/Qualifiers  
1..13413  
/organism="Buchnera aphidicola str. Sg (Schizaphis graminum)"  
/mol\_type="genomic DNA"  
/strain="Sg"  
/specific\_host="Schizaphis graminum"  
/db\_xref="taxon:198804"  
150..1164  
gene

gene  
CDS  
/gene="ansa"  
/note="Bugs524; this region contains an authentic frameshift"  
complement(1214..1792)  
/gene="yhgi1"  
/note="synonym: Bugs525"  
complement(1214..1792)  
/gene="yhgi1"  
/codon\_start=1  
/transl\_table=11  
/product="hypothetical 21.0 kD protein in bioh-gntt"  
/protein\_id="AA068067.1"  
/db\_xref="GI:21623438"  
/translation="MINISDKAQNHEPISLSKEPTIGTOIRVEIINFGTONACGVAYC  
TEDDYVNDHDKLNHNEFYVDRSIISFKNSRIDLIYVNSQLFKAPYAKONYSK  
NPAISLKERIENFINNINPDISMGGRXHLIOISNNNALIKFTGCGCNSMIGTTL  
KEIYKIKISFEPEIKYVDIDHILGNSFY"  
1925..2693  
/gene="bioh"  
/note="Bugs526; this region contains an authentic frameshift"  
complement(2745..3233)  
/gene="ssb"  
/note="synonym: Bugs527"  
complement(2745..3233)  
/gene="ssb"  
/codon\_start=1  
/transl\_table=11  
/product="single-strand binding protein"  
/protein\_id="AA068068.1"  
/db\_xref="GI:21623439"  
/translation="NASRGVNVYLIGHGODEPEVRYMENGNAVMMATISNMKDK  
NNGENKEKEMHRIYLFGLAEIAGEYLKGSQVYEGSLQTRKQDONGLEKTYTEV  
IYNGIGTQMGLGRNNSHNVTLNENNIVKTKRIKINNSPKRIKIDSEIDFDEI  
PP"  
4097..5494  
/gene="dnab"  
/note="synonym: Bugs528"  
4097..5494  
/gene="dnab"  
/codon\_start=1  
/transl\_table=11  
/product="replivative DNA helicase"  
/protein\_id="AA068069.1"  
/db\_xref="GI:21623440"  
/translation="WVPIYMAKNSVYLHOINRKPISIAEOSVIGIMDNBOM  
DSYSEHVADDPFSKPHRLIFQEQQLDLGHRIDITTSLSLQCKLESYGRSEYL  
AETSKTPESTANTIAIADITREAIYREMIIVANKIANGYDTQGRKSELDYAES  
VRIAKRRKKGSGPNIEOILDEYVTSLEKFLSPNDVGTGINTGYODLNKTSGLQ  
PSLLITIIARPSMGKTFPAMNLCENAMLYDKFVLIFSEMPGEQIMRMLASISVN  
QARIRPGONDEDSMSGCTINVLKKNYIDDSALPSEVRSRARRIYRNGLT  
LIMVDYLOIMRVPSLSDNRLTEIATSRILKALAKILOYPIALSOINSLDRSKR  
PMSNDRREGSLQEQDLDLMEFYIRDEIYHENSDFKVAEIIIGKONGPIGTCLTFN  
GMSRFDNTCGPYTD"  
5657..6619  
/gene="gsbB"  
/note="synonym: Bugs529"  
5657..6619  
/gene="gsbB"  
/codon\_start=1  
/transl\_table=11  
/product="glutathione synthetase"  
/protein\_id="AA068070.1"  
/db\_xref="GI:21623441"  
/translation="MRKKNLKIGIYMSITLINIKKSSPAILLEAQRORHEITYME  
MNDLYLRKQSYVATTSIEIQKNQNNYFETQKKDLSLWELAILMRKDPPEFTEIY  
AYIILERAEGVLYNKRPSLSDCKNEKFIISWSPFTDTDLTVTRLSIHNWKEKN  
DIILKPLDAMGKGIVYRIKKDDPNFVIEITLINYKKYCMQIOTYIPEYQFGKRILI  
VNGKPIPMGLTRIPKHGETRANLAVGEGVQVQALQKOWEIANIYLAIPILKKNGLIIVG  
LDVIGDKLIEINTVSPICIEIEEKNISITGLIDYIEDKIYK"  
6630..7043  
/gene="yqgF"  
/note="synonym: Bugs530"

CDS 6630..7043  
 /gene="yggf"  
 /codon\_start=1  
 /transl\_table=11  
 /product="hypothetical 15.2 kD protein in gshb-ansb"  
 /protein\_id="AA68071.1"  
 /db\_xref="GI:21623442"  
 /translation="MTVAFDRGLKNGVAVGNNILKKGALNKLAKNGSPDMNIR  
 NLKINOPKRLVGLPLNDIGTQDITKRAEKFAFLTKKFNIFVYLHDERLSTKAK  
 SLFEKNGEVYLRKEKIHSAVAVILLESWNQLY"  
 7075..7764  
 /gene="ygg5"  
 /note="synonym: BUSg531"  
 7075..7764  
 /gene="ygg5"  
 /codon\_start=1  
 /transl\_table=11  
 /product="hypothetical 25.8 kD protein in gshb-ansb"  
 /protein\_id="AA68072.1"  
 /db\_xref="GI:21623443"  
 /translation="MNNININIKIKKIQYFLKKNVPLKIKITIAVSKNOGIDKIK  
 LAISSGHEGENVYEGIDKIOKLNQNIWHFVIGVQSNKTKIAENPMQCID  
 RKRIATILKTRKESFPMNVLMQINISEVTKNGICINRKLAKTISIMENLNRG  
 IMMEVEVERKMTKQNDNYKNGNIFNELKKEYSIDTSLGTSFIENALFHSNMR  
 IGRFLFKQVR"  
 7793..8923  
 /gene="yggw"  
 /note="synonym: BUSg532"  
 7793..8923  
 /gene="yggw"  
 /codon\_start=1  
 /transl\_table=11  
 /product="hypothetical 42.6 kD protein in gshb-ansb"  
 /protein\_id="AA68073.1"  
 /db\_xref="GI:21623444"  
 /translation="WKLPIISLYIHFWCKKCCYDYSYVNSFPIPEKEYIDPHL  
 KLEKDLSEIKEREINISFISGTPSLKSSIKKMEIKRIINISWAEKTIAPN  
 TLEKRFENFKKSGINRSFISGVQFNEDLAKIERTYKRRBALIAVEIKKINEN  
 LDIMVGLPNOSLKYDLDOYAVKPNPHISWYOLTEPYYKRIKLNENNIET  
 MLVEGEFLKOSGYKKEISSAKLNECOMLNWNGEDTIGICSSHGKLTQING  
 IIRTKNNINDPMNGKYLKHKNPYLKDKRDEPVPNMFRLYKFLVKQFERNNINQ  
 NYIKKIKKALEGKLNKIDPWTITKGMFLNSLKLKIFLD"  
 complement(8930..9649)  
 /gene="yggH"  
 /note="synonym: BUSg533"  
 complement(8930..9649)  
 /gene="yggH"  
 /codon\_start=1  
 /transl\_table=11  
 /product="hypothetical 27.3 kD protein in ansb-muty"  
 /protein\_id="AA68074.1"  
 /db\_xref="GI:21623445"  
 /translation="MKNNITPOYNGCTPLKRRSRVCKRGRITKSQLAIERTWIS  
 IGDFKLEPLDFTSVKNSAPVILEIFGSGESLVKAANPNKRNFLGIEYKSGIS  
 CIRLAHSGINNKIITHDAIEVIDMILDTHTLSKVOIFPPDPNKRKRHRKRIODP  
 FLIKILKLNNDGILHIVTDSKEYNFILMLIONIDVYINLSKRMCFEHRKRYLVIN  
 FEKRAKLSGNKIFDLIFLKK"  
 9758..10801  
 /gene="muty"  
 /note="synonym: BUSg534"  
 9758..10801  
 /gene="muty"  
 /codon\_start=1  
 /transl\_table=11  
 /product="A/G-specific adenine glycosylase"  
 /protein\_id="AA68075.1"  
 /db\_xref="GI:21623446"  
 /translation="MTIYVSQILNMYHINGRKNLPMWKKDKTLVYVWISIMLOOTY  
 VKTAIFYKNIISRFPIQSLNOSKIDILCLNSGLGYRAKNRIKTYKIIKEEOE  
 KPTFGSLDLIKLIGRSTAGAILSLDFFPLGKRVKRIIMRYGIIIGYVTEKRI  
 EOKLWYLIELIPIHNGSGNOGINDIGALICPKPKKLCPLIOCAIYKKNMIRK  
 YPLKKKKIILEKSSWVYIKYONQWIEKNTKTKIMKNLFCFPNDTDTIKITLWMLK  
 MNINIDKKHKKIOSFYHKSHTLHITLIPILVINSFPRKPNQNSKKTGIWDLKNTHDIG

gene LRPVOKLIEIFK"  
 10827..11063  
 /gene="yggx"  
 /note="synonym: BUSg535"  
 10827..11063  
 /gene="yggx"  
 /codon\_start=1  
 /transl\_table=11  
 /product="hypothetical protein"  
 /protein\_id="AA68076.1"  
 /db\_xref="GI:21623447"  
 /translation="MNRIFCTFLQKSSGODPYPPKLGKRIYNQSLKAKMKRL  
 QQTKLINEELNMFQNDNRKRIEKYMKLFLFNNF"  
 11130..11900  
 /gene="muri"  
 /note="synonym: BUSg536"  
 11130..11900  
 /gene="muri"  
 /codon\_start=1  
 /transl\_table=11  
 /product="glutamate racemase"  
 /protein\_id="AA68077.1"

Query Match 13.5%; Score 42.4; DB 1; Length 13413;  
 Best Local Similarity 53.7%; Pred. No. 7.7;  
 Matches 88; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 147 CCACCTTATTCAGTAGTATGACTCAAAATTTGAAATAGATGTCACAGATPAA 206  
 DB 8792 CAATATTTATTAAGAAATATAAAGCAATAGAAAAGATACCTAAAAATVAA 8851  
 QY 207 CTGAGTTTATGAAACATCAGTAGAAGCAATPACACATCCATCCCTTACAGATC 266  
 DB 8852 ATGATTTTGGGATACACAAAAAGAAAAATGTTCTTAATTAATTAATTAAGATT 8911  
 QY 267 ATTACTTGACATCAGGATATTTGTCATGTCATTAATCTACT 310  
 DB 8912 TTTTAGATTAATAAATCTATTTTAAATTAATTAATTAAT 8955

RESULT 5  
 BX296522  
 LOCUS  
 DEFINITION Danio rerio clone DKEX-28611, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 2  
 ACCESSION BX296522  
 VERSION BX296522.3 GI:30962323  
 KEYWORDS HTG: HTGS-PHASE1; HTGS-DRAFT; HTGS-FULLTOP.  
 SOURCE Danio rerio (zebrafish)  
 ORGANISM Danio rerio  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 156149)  
 McIaren S.  
 Direct Submission  
 Submitted (28-MAY-2003) Wellcome Trust Sanger Institute, Hinxton,  
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
 On May 20, 2003 this sequence version replaced gi:29500947.  
 ----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: zfish-help@sanger.ac.uk  
 ----- Project Information  
 Center project name: ZK28611  
 ----- Summary Statistics  
 Assembly program: XGAP4; version 4.5  
 Chemistry: Dye-terminator; 100% of reads  
 Consensus quality: 155628 bases at least Q40  
 Consensus quality: 155755 bases at least Q30  
 Consensus quality: 155800 bases at least Q20

COMMENT  
 JOURNAL  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

Muzny, D., Mearse, M., Metker, M., Lee, S., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Albright, S., Amin, A., Anguiano, D., Anvalebecht, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Bartscheid, M., Benaim, F., Biswal, K., Blair, J., Blankenship, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Butch, P., Butrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Cesaar, H., Center, A., Chacko, J., Chaver, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., P. Souza, L., Davila, M. L., Davis, C., Day-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denison, S., Detramo, C., Ding, Y., Dihn, H., Diya, K., Drepper, H., Dugan-Kocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,

Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisti, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlik, P., Hayes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulys, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolliffe, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensunewa, L., Louisedge, H., Lozad, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindarte, M., Mahmud, M., Malloy, K., Mangum, A., Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E., Maminvey, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Milosavljevic, A., Miner, G., Ming, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, N., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaekemele, O., Okwuonu, G., Olarinpo, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Plankoch, C., Plapper, F., Polindexter, A., Popovic, D., Primus, E., Pu, L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rois, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shwartsbeyn, A., Sisson, I., Sitter, C. D., Smaj, D., Sneed, A., Sodergren, E., Song, X. Z., Sotelle, R., Sosa, J., Steidle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tinney, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villaana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willison, R., Wlezyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausen, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G. and Gibbs, R. A.

Direct Submission  
 2 (bases 1 to 236285)  
 Worley, K.C.

Direct Submission  
 Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 236285)  
 Rat Genome Sequencing Consortium.

Direct Submission  
 Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 On May 13, 2003 this sequence version replaced g1:23264471.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/atl1/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: hgsc-help@bcm.tmc.edu

----- Project Information  
 Center project name: GK0V  
 Center clone name: CH230-9983  
 ----- Summary Statistics

163777 bp





[illegible][illegible]





```
/product-"hypothetical protein pb03"
/protein_id-"AAK07924.1"
/db_xref-"GI:12802532"
/translation-"MGFNPVMLYFHPNCQTPSLKHLGILIKIYKISYLIRATFLVNV
HICPPKRRPRPGGPGPSPSLIVQRLAKK"
5943..9347
/feature="ORF 6"
/codon_start-1
/product-"single-stranded DNA-binding protein MD8P"
/protein_id-"AAK07925.1"
/db_xref-"GI:12802533"
/translation-"MAKTRAGQOYEDNIGSAPIGPGCIYVYKKEPPTYEASILG
KSPGIVSVAPLLEGLVEGPPIINVKAVHKIDITTVSVATVSHRIVMEINDC
ETPIFHGTLPQLCOETNDLFGFTHSPTSNTNMSLQDLGCTMDIEMLGVIT
EGFERLYGHGMIPLIGHVEEQISPOHAAKIPLYDEDLFSKIAIPDKRRHSYVS
OYLFNSLYAIAOAIKRVKDVAVIOMESOPFODHKMPKVVHKKDPSPSSSGPGL
SLIMDSVASLEAVSGLSFIDAPDMSALLDYTSMPIDVDCITTEDRLOALHAMLK
OSIHYNTOLFSTNSMLXLRIOKONPKTKGLNNTSYLDHGLSYSEANODEGQ
PVFOQVSNLHSGSTYTHHLVLAASMCPTLARCYYLQFCQHKSTQNSNTISNY
VGTAASSDMCNLCQGKRPVNCINTLEFLRDRPPIITSHRDPYITTSVGMNDLD
LGNFASFERKEDEGQVEVOQKYTWQLTLEKLGMGIKDTPPEKLVSDLPSE
IYFKDIDAHVDTEVLKFLNCVAKNNINFERITKSIHHVIOYCNVEAQPDPVFLQ
YKSLITLIDVCLPNCMAYEODNSMGMPTEMLKMHOTLMTNPKGCCPGVYGL
ALKYMSDPKDFEDFVDAIINGISPTQYRISAMLYVPTIKIKRITIFSNSG
SEAIOSGLKSGSKDNTLVTPYMKFELTHKIMPOYKMSLFWMHYFSTKQIPL
ITGVPDQDLVALANTYENSKLHSEIDVLDLIPDLITYAKIKLNNALIRAGQTOY
LITGKLPVTPVAVGEEYPAVLENEEPTGEQYLYLQNRTOAIQVATLKEDVQMG
KRLPLITVPMVINKYGLINGNGIFPCNGILGFMGVDRLIFENAPPKRSTNAYM
RKHYEMPIVDNLKIRRTVPPSPSEVENIRMDLLEEDKONONIPFDVYLAVKG
LGOACADLTADDLPYLGEBYIMSDILLRLOSISDAGVPCDEDSYSSLGELYTSEE
QLEFGLGEQTTSAFSEDFQASGLSTIAAKRKRLNCLMSDFL"
9352..11430
/feature="ORF 7"
/codon_start-1
/product-"transport protein"
/protein_id-"AAK07926.1"
/db_xref-"GI:12802534"
/translation-"MARELAAYSOVEFDSFTSLTFCDPRIHIDGAFQNRKKRLK
LIDALYSLVEONRESCISLELEHLINTYIMOKLETCLENTIEYDYAMLLS
DLCEFHKYVNLCEFYGDVPIISLINDIEFSPNSVFCISRNNALEHGETINF
LGTNRNISPILPDLYLPISGMNCLNETSILPNOGENEYTIMNSINCHVATPAPE
PROGLEENILMLNIPVODTKNOVLESDTRIQNSAIDQHNIFEVSOHILEIS
NLTNMSGHSNDQSPALCSQMATLLOHETRMASHKQVASHALATTPPIHFPDSRA
YPESLFCGFIYSINDNLQALKODCSTFLAKSNKTIMERNELVYLNILFDSH
TEGDIKDNTEISIKQARHTIGETSEQIFEAAPAKNNYLQKVTLEGKLTDCLET
OCKIKONTLTLLTGKMWYTKEAAILKNHEMIRKRFALPOMHNATYAIKELSSFEI
KSLVYOKLSOEHDSITLOFSLITGLPDEPPDPSPNILLANCLIAAAYVMPHK
MLISEYIMSPMERKMDIAENAFYNTIKTELSNVQCCWARTIRELYVSVLYNRWE
KRLNYSPTSLSPHNLSPKPTFKSGITTYETKVALIFIHNTGIMFKDLALYHN
LDLTSKKNYL"
11420..14044
/feature="ORF 8"
/codon_start-1
/product-"glycoprotein B"
/protein_id-"AAK07927.1"
/db_xref-"GI:12802535"
/translation-"MYKTLFPAIKVCSFNQTHSTTSPSISSTTSSTTSK
PSNTSTNSSLASPONTSTKSPSTDNOSTPTPIPTVDDTRASKNFYRYVCSASS
SEGLREFDLDTQCPTDKRKHVEGLLVYAKNIPVIFVRYRKJATSVTYRQSSO
AAVTNNDLISRAIPYNEISMDIRYHCFSAMATVINGILINTYIDRSESSVPLQVA
GILENNRYFSQPLIYABGMPGAIYRVATVNCVEVDVAGASVEYTFETALGPTI
EISPCNNHNSOCTGNSSTRDARKYIENHODVDERGHGPKDKRIRFLKDEBYTIS
KWAEDBERAIDCEVITKTPRPAIORTIHNSPFPVAVYASLTSQOETBELRGNEI
LACMNSTINETLEEVYKRNKSHIRGEEKYIKYNGGLYLMOAKMLSEHTNTTI
ERNKTKNSRKORSYDTKTEQAGKLSIAQVOYADHLRTSMNHLLEELATWCEQO
KDONLWYELSKINPVSMAAYIGKPAVAKAMDAPVSECINVDASVNIKRSMTD
DKRVCYSRLVTEFKFVNSYATFGQLGTNEELLNTHTVETCRPTADHFEKNNHY
FDYKVFVKTMDNNISITLDTPLNLTFIDNIDKVELYSEFERMAALADLETFMR
EYNYVOKLASIRELDNTIDLRDLVADSEMAADLDIGKVYNTSPGIVTYSGE
TYGGRVSEFTNPIGVTITLLLVVVFVIVSRRTNNNEAPIKMITYPNIDVASEQ
```

```
NTDLPGEIRKILLGMHQLQOSEHKGSEASHKRGLEFOLLGDLQLLRGRYLRP
TDDPSGNDTSEHORVY"
14184..17201
/feature="ORF 9"
/codon_start-1
/product-"DNA polymerase"
/protein_id-"AAK07928.1"
/db_xref-"GI:12802536"
/translation-"MEFENPYISKRTDRISCVDPPDKTKTNYCLTVKCRKTP
GVISITTDTPVLFHODKEYPIETSGDHRSWSALKPPAPIDPDKLFEFYVDIE
IYTPBRCDDIPLOFQTDIIPNGYVILKLGKTODGASVCVNOQVYVYVPOGVN
LSVIOQTLNGVKNQOTKEFSTIOEKKILKEKDELYVYVITTSAPETNOIGNLT
TSCGCCFVSNSASRPLIDKRSFEGVSSGNBPRIISQDSRDLDFDGLDQ
PHREBQMPYITMSFDIICISQCPKQKBDVLIQSLCITWVCSBPONILS
LQTDPIANTDVPEPSELDMPFAETFLLRDNIDVYGVNANDEFPYIDRAQVY
NPIRHFVTIVISGSEFEVNOYKEIPLSRSGEAGRARISYCVLDVYLDLKYFMIV
KNTVAKHCGMGTOKEDVYKEIPLSRSGEAGRARISYCVLDVYLDLKYFMIV
EISEIAKMAKIPARVYLDGQOIRVPSCLLEAKKEHFLPIPGAOKPGEYGATYIN
PIGEPNTPIIVDPASLYPSIIAANICYSIMODONTLHHRKDDYETPHLSTGP
IHFVOKHKLSLSTILTLMLAKRTIKRELANCDDPKTILDKQALIKYCNVY
GTGVASGLPCPIAEVTVLGRVTLERSKAVEITPERLSLDIVSYVPCDDPASF
RVYIGTDSLFTECRGYPMQSVLNEADKLTETTKALFDPPIKLEAKETFOCLIMLTK
KRYIGLISDSDKVMKGVDLIRKTAFCVOTTEKEIIDLPRPEVQAQYCLROMPA
KYVSDLPVGFPMKVIDLNNYSYAAATGAVESVLESEFSELSPEFEYTTPLPHLY
YKRINSRNEELQIHRIPIVPLFKGDRCKSDLADDPYVQONKPISEVIEFDKLI
HCVANTLQCLFGNSMAYELLNPNINITYST"
17297..18577
/feature="ORF 10; BORPB1; conserved in other
gamma-herpesviruses"
/codon_start-1
/product-"unknown"
/protein_id-"AAK07929.1"
/db_xref-"GI:12802537"
/translation-"MSTLVEFSIEGMVONICNGNIILMTNKDIPVQGYGLMYKV
FLPLSNQNLNNYISFGLVOSIFELEDYACQAMVOCFGRIPRLPTLPIHVEFN
MPLFVKTQNTINISLVSIAIEMKPPCPGIGYISTAPERTIPPOHSAHNHS
TPOGHLLTSGAOKICMKNKTYVMPFRBPNOFPKMHMAASRGDLQDQCYGMSYD
IKINMEVYNPNGLIKVSVNTLNKLYKTYTTRGNESTKAVAFITGTNTNPMVILEPTIS
CGRWNIYTDSEILKPVSNLTNKLKTYTTRGNESTKAVAFITGTNTNPMVILEPTIS
LPMTPLOVATIKNPTNMIITIKDLAIAMCVPYSTLEDRQPPASPSVYENPDLLTW
EEMNAVATGEMNIYSRCHLNKSENPSPMDPT"
complement(18848..19345)
/feature="ORF B04; short ORF of immediate early transcript 1"
Query Match 12.6%; Score 39.6; DB 14; Length 108873;
Best Local Similarity 50.4%; Pred. No. 22;
Matches 125; Conservative 0; Mismatches 119; Indels 4; Gaps 1;
CDS
32 TTGGCAATPAGAACAAATGATCAGTCTCCACCACTTAACTATGATCTTAAAGAT 91
|||||
49499 TTTCGATGTGAGCGGATATGTCAAAGATATTAATTAATATATATATATCCCAACAGCC 49558
92 CTACAGCCTCCCTTTAAGGGACATACAAAGTCAGTGTGCTTGTGAGTCCACC 151
|||
49559 TAACTATATGATATGATATGATATGCAAAAGTCCCAAGATGATTTTGGAGTGTCTCT 49618
152 TTAATCT---CAAGTAGGTATGACTACAAATTTGAAAATAGATGTCACACAAATAAC 207
|||
49619 TGATTTTGTATCAATATATCTCATGATGATAAATGGAAGTGTGATTTTGAACACAGACTG 49678
208 TGGAGTTTATGGAACATAGTGAAGGAATATCAACATCCATCCCTTACAGAGATCA 267
|||
49679 TTGTGTTTATGAAATTAATATGATATTAATGATATGATTTTCCAAATCGAATGTGATCC 49738
268 TTACTCTG 275
|||
49739 TTGTGATG 49746
RESULT 14
```

AC102444 144727 bp DNA linear HTG 16-MAR-2003  
 LOCUS Mus musculus clone RP24-196115, WORKING DRAFT SEQUENCE, 4 unordered  
 pieces.  
 AC102444  
 AC102444.3 GI:28975139  
 HTG: HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 144727)  
 Birren, B., Nusbaum, C. and Lande, E.  
 Mus musculus, clone RP24-196115  
 Unpublished  
 2 (bases 1 to 144727)  
 Birren, B., Linton, L., Nusbaum, C., Lande, E., All, A., Allen, N.,  
 Anderson, S., Bara, N., Bastien, V., Boguslavsky, L., Boukhgalter, B.,  
 Brown, A., Camarata, J., Campolano, A., Chang, J., Chazaro, B.,  
 Choepel, Y., Colangelo, M., Collins, S., Collamore, A., Cook, A.,  
 Cooke, P., Deatellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S.,  
 Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,  
 Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-pierre, N.,  
 Hago, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,  
 Jones, C., Kamet, A., Karatas, A., Kells, C., Lacroque, K.,  
 Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,  
 Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,  
 McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrum, J.,  
 Menus, L., Mihova, T., Mienna, V., Murphy, T., Naylor, J., Nguyen, C.,  
 Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D.,  
 Oliver, J., Peterson, K., Phukhang, P., Pierre, N., Pollara, V.,  
 Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,  
 Roman, J., Roselli, M., Roy, A., Santos, R., Schauer, S., Schuback, R.,  
 Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
 Strauss, N., Subramanian, A., Talamas, J., Testfaye, S., Theodore, J.,  
 Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H.,  
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G.,  
 Zahoun, J., Zemek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 144727)  
 Birren, B., Nusbaum, C., Lande, E., Abouelkell, A., Allen, N.,  
 Anderson, S., Arachchi, H. M., Bara, N., Bastien, V., Bloom, T.,  
 Boukhgalter, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,  
 Collamore, A., Cook, A., Cooke, P., Corum, B., Deatellano, K.,  
 Diaz, J. S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,  
 Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S.,  
 Graham, L., Grand-pierre, N., Hago, B., Heaford, A., Horton, L., Hulme, W.,  
 Iliev, I., Johnson, R., Jones, C., Kamet, A., Karatas, A., Kells, C.,  
 Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, A., Mabbitt, R., Maclean, C.,  
 Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,  
 Meldrum, J., Menus, L., Mihova, T., Mienna, V., Murphy, T., Naylor, J.,  
 Nguyen, C., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P.,  
 O'Neill, D., Oliver, J., Peterson, K., Phukhang, P., Pierre, N.,  
 Rachupia, A., Ramasamy, D., Raymond, C., Retta, R., Rise, C., Rogov, P.,  
 Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C.,  
 Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,  
 Talamas, J., Testfaye, S., Theodore, J., Topham, K., Travers, M.,  
 Vassiliev, H., Venkatarman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X.,  
 Wyman, D., Young, G., Zahoun, J., Zemek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (16-MAR-2003) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Mar 16, 2003 this sequence version replaced gi:2280929.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: http://www-seq.wi.mit.edu

Contact: sequence.submissions@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: L18811  
 Center clone name: 196-1-15  
 ----- Summary Statistics  
 Sequencing vector: Plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 143945 bases at least Q40  
 Consensus quality: 144256 bases at least Q30  
 Consensus quality: 144348 bases at least Q20  
 Insert size: 145000; agarose-fp  
 Insert size: 144427; sum-of-ctgigs  
 Quality coverage: 10.1 in Q20 bases; agarose-fp  
 Quality coverage: 10.2 in Q20 bases; sum-of-ctgigs  
 -----  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 4 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \*  
 \* 1 58558: contig of 58558 bp in length  
 \* 58559 58658: gap of 100 bp  
 \* 58659 93533: contig of 34875 bp in length  
 \* 93534 93634: gap of 100 bp  
 \* 93634 142651: contig of 49018 bp in length  
 \* 142652 142752: gap of 100 bp  
 \* 142752 144727: contig of 1976 bp in length.  
 \*  
 \* Location/Qualifiers  
 \* 1. 144727  
 \* /organism="Mus musculus"  
 \* /mol\_type="genomic DNA"  
 \* /db\_xref="taxon:10090"  
 \* /clone="RP24-196115"  
 \* /clone\_id="RPCI-24 Male Mouse BAC"  
 \* 1. 58558  
 \* /note="assembly-fragment  
 \* clone\_end:SP6  
 \* vector\_side:left"  
 \* 58659. 93533  
 \* /note="assembly-fragment"  
 \* 93634. 142651  
 \* /note="assembly-fragment"  
 \* 142752. 144727  
 \* /note="assembly-fragment  
 \* clone\_end:T7  
 \* vector\_side:right"  
 \* BASE COUNT 45046 a 27765 c 27878 g 43737 t 301 others  
 \* ORIGIN  
 \*  
 \* Query Match 12.6%; Score 39.6; DB 2; Length 144727;  
 \* Best Local Similarity 49.5%; Pred. No. 21;  
 \* Matches 102; Conservative 0; Mismatches 104; Indels 0; Gaps 0;  
 \*  
 \* 1 TAAACAGTGCAGTCTTAAGAAATTTGGAAATTAACAAATGAATCAATT 60  
 \* Db 139701 TAAACAGTGCAGTCTTAAGAAATTTGGAAATTTAACTAAATTTAAATTAATTAAT 139760  
 \* 61 TCTCCACCACTTAAATCTCTTGAAGATCTACAGCCCTCTTAAAGGACATCAAA 120  
 \* Db 139761 TTGAATATTAATAATTAATCTTAATATGTTTAACTATGCGCCGTAACCTTAATTAACAT 139820  
 \* 121 GTCAGTGTGCTGCTGCTTGTGAGTCCACCTTATTAATTCAGTAAGTATGACTACAAATT 180  
 \* Db 139821 TATTAAGCATGTTTATGATTATTAACACATTAACCTAATAAATGTTTCATATACAT 139880  
 \* 181 TTGAATAATAGTGTACACAAATAA 206  
 \* Db 139881 TTGGAATATGTTGTAAACAAACAAA 139906

RESULT 15  
CEY116A8A/c 54700 bp DNA linear INV 21-MAY-2003  
LOCUS  
DEFINITION Caenorhabditis elegans YAC Y116A8A, complete sequence.  
ACCESSION AL117205.298858  
VERSION AL117205.2 GI:6425237  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNML  
MEDLINE  
PUBMED  
REMARK  
REFERENCE  
AUTHORS  
TITLE  
JOURNML  
COMMENT

1  
none.  
Genome sequence of the nematode *C. elegans*: a platform for investigating biology. The *C. elegans* Sequencing Consortium Science 282 (5396), 2012-2018 (1998)

2  
The *C. elegans* Sequencing Consortium.  
McMurray, A.A.  
Submitted (31-DEC-1998) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 1SA, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jee@sanger.ac.uk or rwenematode.wustl.edu  
On Nov 15, 1999 this sequence version replaced GI:5832821.  
Coding sequences below are predicted from computer analysis, using predictions from GeneFinder (P. Green, U. Washington), and other available information.  
Current sequence finishing criteria for the *C. elegans* genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.  
For a graphical representation of this sequence and its analysis see: - <http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?name=Y116A8A>  
IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we arrange for a small overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.  
It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.  
The true left end of clone Y116A8 is at 1 in this sequence. The true left end of clone Y06A10 is at 54597 in this sequence. The start of this sequence (1..106) overlaps with the end of sequence AL132846.  
The end of this sequence (54397..54700) overlaps with the start of sequence AF099926.

Location/Qualifiers  
1..54700  
/organism="Caenorhabditis elegans"  
/mol\_type="genomic DNA"  
/strain="Bristol N2"  
/db\_xref="taxon:6239"  
/chromosome="IV"  
/clone="Y116A8A.1"  
/gene="Y116A8A.1"  
/join(1517..1562,1674..1768,3071..3330,3372..3516)  
/gene="Y116A8A.1"  
/join(1517..1562,1674..1768,3071..3330,3372..3516)  
/gene="Y116A8A.1"  
/standard\_name="Y116A8A.1"  
/codon\_start=1  
/product="Hypothetical protein Y116A8A.1"  
/protein\_id="CAB55161.1"  
/db\_xref="GI:5832824"  
/db\_xref="GOA:Q9U2M4"  
/db\_xref="SPTREMBL:Q9U2M4"  
/translation="MLHLTANSLGHRIDYSGYFLSFTFSINILKSCQITVEAVNP

VNPVASKLYLIAAQTACINIGALSGIÖNDKERWVIGKNKMEIHLANGTDSCTWLG  
AKCSSGCTWTDGNTVGTQGMFAFGEBNÖLSTPCLYIAWKIDFTLKRYPYGNGYID  
DTRCTTAMSYACGPGLRNN"  
complement(join(4463..4607,4651..4910,5667..5876))  
/gene="Y116A8A.3"  
complement(join(4463..4607,4651..4910,5667..5876))  
/gene="Y116A8A.3"  
/standard\_name="Y116A8A.3"  
/codon\_start=1  
/product="Hypothetical protein Y116A8A.3"  
/protein\_id="CAB55165.1"  
/db\_xref="GI:5832828"  
/db\_xref="GOA:Q9U2M0"  
/db\_xref="SPTREMBL:Q9U2M0"  
/translation="MKRLIOLIACFEFLIPPAVSFIRDPSSSSSEGGYGRKHGG  
HHSPTPDCVEGWAFHRRPGVWCYKVASLTYLIAQTACINIGALSGIÖNDKER  
WVIGKNKMEIHLANGTDSCTWLGAKCSSGCTWTDGNTVGTQGMFAFGEBNÖLSTP  
CLYIAWKIDFTLKRYPYGNGYIDTRCTTAMSYACGPGLRNN"  
complement(join(12804..13270,13318..13360))  
/gene="Y116A8A.2"  
complement(join(12804..13270,13318..13360))  
/gene="Y116A8A.2"  
complement(join(12804..13270,13318..13360))  
/gene="Y116A8A.2"  
/standard\_name="Y116A8A.2"  
/note="contains similarity to Pfam domain: PF00635 (MSP  
Major sperm protein domain), Score=64.0,  
E-value=1.1e-15, N=1"  
/codon\_start=1  
/product="Hypothetical protein Y116A8A.2"  
/protein\_id="CAB55164.1"  
/db\_xref="GI:5832827"  
/db\_xref="GOA:Q9U2M1"  
/db\_xref="SPTREMBL:Q9U2M1"  
/translation="MNNFLSLICLLFEDFLDFTSTNSDSLAPHPPIKRNITPEY  
OSVPGAVITPPAKRIIFNAPFDSMHYQVIVNLSDPTINIRITLMKRFSTYPC  
GIILKTQMFNITPAPFNITTEKTRITVKNLIPNNEDDEFREWFHGDGAVNO  
HHIYIQYNI"  
join(22305..22428,22472..22718,22764..22845,22914..23031,  
23074..23153,23203..23320,23373..23929)  
/gene="Y116A8A.4"  
join(22305..22428,22472..22718,22764..22845,22914..23031,  
23074..23153,23203..23320,23373..23929)  
/gene="Y116A8A.4"  
/standard\_name="Y116A8A.4"  
/note="CDNA EST YK377C3.3 comes from this gene  
CDNA EST YK232a10.5 comes from this gene  
CDNA EST YK232a10.3 comes from this gene"  
/codon\_start=1  
/product="Hypothetical protein Y116A8A.4"  
/protein\_id="CAB55162.1"  
/db\_xref="GI:5832825"  
/db\_xref="SPTREMBL:Q9U2M3"  
/translation="MKFOWIGVLFVIGVNCILISQKITVENEERLKSQNTFLP  
SINOTGKGFENDKTYTNSKSGWLLAGKNSTRYATAFPISEYHILISSVM  
TAEHRKWMNGKRPFDKNNCSGRHLDVDPVDVNDNLFWGKPKRADISEKAMFACDN  
ODLKAYPVILINKTSKRPANFVNCPLADFTSSKLDVHFGYSDYDLHHLIC  
KAVLDGGICTEYTYTEVYEGPLVNVSKATVIGIKAGSNGEELFEDLSKIKETC  
DYSCVCGYKREPTITTEPPRPTKSTVSTISLETIMKASSASPSIKSPSTTEP  
SPLOASSRATPEPLIRPESTRASSASAKREVOTTITTEIRISLPEFLKSTTVT  
TTTPEPATVDVGDHDMIGDDEYDESNNKVGKIDRIVGFFVLLVTE"  
complement(join(25359..25414,25792..26337,26389..26506,  
26554..26633,26676..26793,26862..26943,26989..27235,  
27279..27402))  
/gene="Y116A8A.6"  
complement(join(25359..25414,25792..26337,26389..26506,  
26554..26633,26676..26793,26862..26943,26989..27235,  
27279..27402))  
/gene="Y116A8A.6"  
/standard\_name="Y116A8A.6"  
/note="CDNA EST YK8246.5 comes from this gene  
CDNA EST YK471a12.3 comes from this gene  
CDNA EST YK290b7.5 comes from this gene  
CDNA EST YK339e8.5 comes from this gene  
CDNA EST YK471a12.5 comes from this gene







GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2003, 19:48:32 ; Search time 586.536 Seconds  
(without alignments)  
9113.362 Million cell updates/sec

Title: US-09-700-770-3

Perfect score: 2060  
Sequence: 1 cttagagcctcaataact.....ttccatgtaaaaaaaaaa 2060

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 1731049 seqs, 1297405648 residues

Total number of hits satisfying chosen parameters: 3462098

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published\_Applications\_NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PC7\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PC7US\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2060	100.0	2061	12	US-10-180-719-16
2	1352	65.6	1425	10	US-09-964-899-10
3	1345.2	65.3	1365	14	US-10-288-222A-29
4	1199.2	58.2	1299	13	US-10-094-080-4
5	984	47.8	1487	10	US-09-969-384-4
6	797.2	38.7	1360	9	US-09-789-919-13
7	797.2	38.7	1360	9	US-09-789-919-43
8	757.8	36.8	794	10	US-09-915-582-27
9	678.4	32.9	1823	11	US-09-909-567B-12
10	678	32.9	741	10	US-09-915-582-48
11	614.2	29.2	723	10	US-09-915-582-49
12	602.4	29.2	1041	9	US-09-925-302-227
13	436	21.2	534	10	US-09-860-670-43
14	413	20.0	414	11	US-09-918-995-6261
15	401	19.5	412	11	US-09-918-995-6282
16	361.8	17.6	371	11	US-09-918-995-30293

17	325	15.8	408	13	US-10-040-739-177
18	316.6	15.4	2038	12	US-10-101-510-25
19	316.6	15.4	2076	14	US-10-084-817-172
20	315	15.3	1988	12	US-10-007-926A-128
21	298.8	14.5	530	10	US-09-867-701-1436
22	289.2	14.0	299	9	US-09-745-288-42
23	287.8	14.0	1365	10	US-09-938-842A-2423
24	286	13.9	526	10	US-09-867-701-1437
25	274.6	13.3	1234	14	US-10-106-698-2040
26	269.8	13.1	2201	12	US-10-101-510-457
27	267.6	13.0	1341	12	US-10-220-083-1
28	224	10.9	1414	11	US-09-822-846-571
29	223.8	10.9	1194	14	US-10-168-425-27
30	221.6	10.8	3352	14	US-10-128-714-184
31	214.8	10.4	1420	10	US-09-971-392-43
32	212.2	10.3	1386	12	US-09-971-392-41
33	206.4	10.0	1352	14	US-10-128-714-1184
34	197	9.6	1530	10	US-09-887-576-795
35	189.4	9.2	1784	12	US-10-339-351-4
36	187.8	9.1	1784	12	US-10-339-351-6
37	181	8.8	1227	14	US-10-128-714-2184
38	173.2	8.4	1366	10	US-09-969-708-441
39	173.2	8.4	1366	10	US-09-470-954A-45
40	173.2	8.4	1366	12	US-09-873-319-641
41	172.4	8.4	1366	12	US-09-960-706-984
42	172.4	8.4	575	9	US-09-864-761-15916
43	168.2	8.2	2733	11	US-09-893-525-6
44	163.6	7.9	180	12	US-10-101-510-236
45	157	7.6	1828	12	US-10-339-351-5

#### ALIGNMENTS

RESULT 1  
US-10-180-719-16  
Sequence 16, Application US/10180719  
Publication No. US20030166246A1  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
Hillman, Jennifer L.  
Yue, Henry  
Guegley, Karl J.  
Corley, Neil C.  
Tang, Tom Y.  
Shah, Purvi  
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/180,719  
FILING DATE: 25-Jun-2002  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/008,271  
FILING DATE: 16-Jan-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Mohan-Peterson, Sheela  
REGISTRATION NUMBER: 41,201  
REFERENCE/DOCKET NUMBER: PF-0458 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166

Sequence 177, App  
Sequence 175, App  
Sequence 128, App  
Sequence 128, App  
Sequence 1436, App  
Sequence 42, App  
Sequence 2423, App  
Sequence 1437, App  
Sequence 2040, App  
Sequence 457, App  
Sequence 1, App  
Sequence 571, App  
Sequence 27, App  
Sequence 184, App  
Sequence 43, App  
Sequence 41, App  
Sequence 1184, App  
Sequence 795, App  
Sequence 6, App  
Sequence 2184, App  
Sequence 441, App  
Sequence 45, App  
Sequence 641, App  
Sequence 984, App  
Sequence 15916, App  
Sequence 6, App  
Sequence 236, App  
Sequence 5, App



Db 1921 GCGAGCGGACCTGGATGGGGAGAGACTGCGCAGCGCAAGTTCCTCCGGGTGACCCCAA 1980  
QY 1981 GTGAAGCGCATGCGCAGCGGGGTGCTCGCGAGGTCTGTACCCAGTAATAATCAGTAT 2040  
Db 1981 GTGAAGCGCATGCGCAGCGGGGTGCTCGCGAGGTCTGTACCCAGTAATAATCAGTAT 2040  
QY 2041 TTCCATTGAAAAA 2060  
Db 2041 TTCCATTGAAAAA 2060

RESULT 2  
US-09-964-899-10  
; Sequence 10, Application US/09964899  
; Patent No. US2002017446A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Dalia et al.  
; TITLE OF INVENTION: Identification of Genes Involved in  
; FILE REFERENCE: 4-31612 A  
; CURRENT APPLICATION NUMBER: US/09/964,899  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: 60/236,893  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/298,309  
; PRIOR FILING DATE: 2001-06-14  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 1425  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-09-964-899-10

Query Match 55.6%; Score 1352; DB 10; Length 1425;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1355; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 701 GTCCCAAGCATGTCTCCACACCCGCTGTCGCAACCCCTGCTGCTGCTGCTGCT 760  
Db 44 GTCCCAAGCATGTCTCCACACCCGCTGTCGCAACCCCTGCTGCTGCTGCTGCT 103  
QY 761 GAATGTGAGCCTTCGCGGGGCGACACATGATCCGATCCCTTTATGATGATCCAACTGG 820  
Db 104 GAAGTGTGAGCCTTCGCGGGGCGACACATGATCCGATCCCTTTATGATGATCCAACTGG 163  
QY 821 ACGCAGAGACCCCTGAACCTACTGAGGGATGAGAGAACACAGACAGCCCAAGTTGGG 880  
Db 164 ACGCAGAGATCTGAACTACTGAGGGATGAGAGAACACAGACAGCCCAAGTTGGG 223  
QY 881 GGCCCATCCCTGCGGGGCGACACATGATCCGATCCCTTTATGATGATCCAACTGG 940  
Db 224 GGCCCATCCCTGCGGGGCGACACATGATCCGATCCCTTTATGATGATCCAACTGG 283  
QY 941 GTATTTGGGGAATTTGGGCTGGGAGCGCTCCACAAAATCTCACTGTGGCTTTGACAC 1000  
Db 284 GTATTTGGGGAATTTGGGCTGGGAGCGCTCCACAAAATCTCACTGTGGCTTTGACAC 343  
QY 1001 TGGGCTCTCCAACTCTGGGCTGGGCTGCGAGAGATGACACTTCTCACTGTGGCTTGTG 1060  
Db 344 TGGGCTCTCCAACTCTGGGCTGGGCTGCGAGAGATGACACTTCTCACTGTGGCTTGTG 403  
QY 1061 GTTACACACCGATTTGATCCCAAGCCTTAGCTCTCTTCCAGGCGCAATGGGACCAATTT 1120  
Db 404 GTTACACACCGATTTGATCCCAAGCCTTAGCTCTCTTCCAGGCGCAATGGGACCAATTT 463  
QY 1121 TGGCATTCATATGAACTGGGCGGGTAGATGAACTCTGAGCGAGCAAGTAGTACTAT 1180  
Db 464 TGGCATTCATATGAACTGGGCGGGTAGATGAACTCTGAGCGAGCAAGTAGTACTAT 523  
QY 1181 TGGTGAGATCAAGGCTGATGATGATTTTGGGGAAGCGCTCTGCGAGCCCAAGCTGTGT 1240  
Db 524 TGGTGAGATCAAGGCTGATGATGATTTTGGGGAAGCGCTCTGCGAGCCCAAGCTGTGT 583

QY 1241 CTTCGCTTTTGGCCCATTTTGAATGGGATTTGGGCTCGGTTTCCATTTCTGTGTGA 1300  
Db 584 CTTCGCTTTTGGCCCATTTTGAATGGGATTTGGGCTCGGTTTCCATTTCTGTGTGA 643  
QY 1301 AGGAGTTGGCCCGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1360  
Db 644 AGGAGTTGGCCCGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 703  
QY 1361 CTCTTTTACCTCAAGGAGGAGCCCTGAAGAGCCCTGATGATGATGATGATGATGATGAT 1420  
Db 704 CTCTTTTACCTCAAGGAGGAGCCCTGAAGAGCCCTGATGATGATGATGATGATGATGAT 763  
QY 1421 CTGAGACCCGCGACATACATCCACCCCTGATGATGATGATGATGATGATGATGATGAT 1480  
Db 764 CTGAGACCCGCGACATACATCCACCCCTGATGATGATGATGATGATGATGATGATGAT 823  
QY 1481 CTGCGAGATCCATGAGAGCCTGTGAAAGTGGGCGCCAGGCGCTGATCTGTGCTCAAGG 1540  
Db 824 CTGCGAGATCCATGAGAGCCTGTGAAAGTGGGCGCCAGGCGCTGATCTGTGCTCAAGG 883  
QY 1541 CTGTCGTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1600  
Db 884 CTGTCGTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 943  
QY 1601 GGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1660  
Db 944 GGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1003  
QY 1661 CTGCGAAATCCCAAGCTCCCGCAGTCTCTCTCTTCTTGGGGGGCTGTGTTAACT 1720  
Db 1004 CTGCGAAATCCCAAGCTCCCGCAGTCTCTCTCTTCTTGGGGGGCTGTGTTAACT 1063  
QY 1721 CAGGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1780  
Db 1064 CAGGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1133  
QY 1781 TTTCAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1840  
Db 1124 TTTCAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1183  
QY 1841 CTGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1900  
Db 1184 CTGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1243  
QY 1901 CCGGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1960  
Db 1244 CCGGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1303  
QY 1961 GTTCCCGGCTGAGCGCCCAAGTGAAGCGATGCGAGCGGCTGTGCGGAGTCTGCT 2020  
Db 1304 GTTCCCGGCTGAGCGCCCAAGTGAAGCGATGCGAGCGGCTGTGCGGAGTCTGCT 1363  
QY 2021 ACCAGTAAAAATCCATTTTCCATTTGAAAAA 2060  
Db 1364 ACCAGTAAAAATCCATTTTCCATTTGAAAAA 1403

RESULT 3  
US-10-288-222A-29  
; Sequence 29, Application US/10288222A  
; Publication No. US20030119742A1  
; GENERAL INFORMATION:  
; APPLICANT: Logan, Thomas Joseph  
; APPLICANT: Galvin, Katherine  
; TITLE OF INVENTION: Methods and Compositions to treat  
; TITLE OF INVENTION: Cardiovascular Disease Using 139, 258, 1261, 1486, 2398, 2414  
; FILE REFERENCE: MPI2001-286PIR(M)  
; CURRENT APPLICATION NUMBER: US/10/288,222A  
; NUMBER OF SEQ ID NOS: 30



```

;
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; IMMEDIATE SOURCE:
; LIBRARY: LUNGMOT02
; CLONE: 312099
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-094-080-4

Query Match      58.28; Score 1199.2; DB 13; Length 1299;
Best Local Similarity 94.38; Pred. No. 0;
Matches 1286; Conservative 0; Mismatches 3; Indels 75; Gaps 1;

QY 697  ACGGCTCCCAAGGATGCTTCACACACCGGTGCTGCAACCCCTGCTGCTGCTGCTC 756
DB 3    ACGGCTCCGAGAGATGCTTCACACACCGGTGCTGCAACCCCTGCTGCTGCTGCTC 62
QY 757  TGCCTGAATGAGACCTTCGCGGGCCACACTGATCCGCATCCCTTCATCGAGTCCAC 816
DB 63   TGCCTGAATGAGACCTTCGCGGGCCACACTGATCCGCATCCCTTCATCGAGTCCAC 122
QY 817  CTGACCCAGAGACCTTAACCTACTGAGGGATGAGAGAACCAAGAGCTCCCAAGT 876
DB 123  CTGACCCAGAGATCTTAACCTACTGAGGGATGAGAGAACCAAGAGCTCCCAAGT 182
QY 877  TGGGGGCCCCATCCCTCGGGGACAAAGCCCATCTTCGTACCTCTCGAACTACAGGANTG 936
DB 183  TGGGGGCCCCATCCCTCGGGGACAAAGCCCATCTTCGTACCTCTCGAACTACAGGANTG 242
QY 937  TGCAGATATTTGGGGAATTTGGGCTGGGAACGCCCTCCAAACCTTCACTGTTGCCTTG 996
DB 243  TGCAGATATTTGGGGAATTTGGGCTGGGAACGCCCTCCAAACCTTCACTGTTGCCTTG 302
QY 997  ACACTGGCTCTCCCAATCTCTGGGTCCCGTCCAGGAATGCACTTCTGAGTGGCCT 1056
DB 303  ACACTGGCTCTCCCAATCTCTGGGTCCCGTCCAGGAATGCACTTCTGAGTGGCCT 362
QY 1057  GCTGGTTACACACACGATTTGATCCCAAGCCTTACTCTCTCCAGGCCAATGGAGCA 1116
DB 363  GCTGGTTACACACACGATTTGATCCCAAGCCTTACTCTCTCCAGGCCAATGGAGCA 422
QY 1117  AGTTTGCCATTAATGAGAACTGGGCGGTAGATGGAATCTCGAGGAGACAAGTGA 1176
DB 423  AGTTTGCCATTAATGAGAACTGGGCGGTAGATGGAATCTCGAGGAGACAAGTGA 482
QY 1177  CTATTTGGTAATCAAGGATGCACTGATTTTCGGGAGGCTCTCGGAGCCCAAGCC 1236
DB 483  CTATTTGGTAATCAAGGATGCACTGATTTTCGGGAGGCTCTCGGAGGCCCAAGCC 542
QY 1237  TGGTCTTCGCTTTTGGCCATTTTATGAGGATTTGGGCTCGGTTTCCATTCGTCTG 1296
DB 543  TGGTCTTCGCTTTTGGCCATTTTATGAGGATTTGGGCTCGGTTTCCATTCGTCTG 602
QY 1297  TCGAAGAGATTTGGGCCCCGATGATGATGCTGAGAGAGGGGCTATTTGATTAAGCCTG 1356
DB 603  TCGAAGAGATTTGGGCCCCGATGATGATGCTGAGAGAGGGGCTATTTGATTAAGCCTG 662
QY 1357  TCTTCTCCCTTTTACCTTAACAAGGACCTTAAGAGCCTGATGAGAGAGAGCTGCTGG 1416
DB 663  TCTTCTCCCTTTTACCTTAACAAGGACCTTAAGAGCCTGATGAGAGAGAGCTGCTGG 722
QY 1417  GGGGCTGGAGCCGGACACTATACATCCACCCCTCACTTCGTGCTCAAGTCCGCTCTG 1476
DB 723  GGGGCTGGAGCCGGACACTATACATCCACCCCTCACTTCGTGCTCAAGTCCGCTCTG 782
QY 1477  CTTACTGGAGATCCACATGAGGCTGTGAAGTGGGCCCAAGGGCTGACTCTCTGTGCA 1536
DB 783  CTTACTGGAGATCCACATGAGGCTGTGAAGTGGGCCCAAGGGCTGACTCTCTGTGCA 842
QY 1537  AGGGCTGTGCTGCTGCTGATGAGGAGAGCTGCTCAATCAAGAGCCCACTGAGAGA 1596
DB 1537  AGGGCTGTGCTGCTGCTGATGAGGAGAGCTGCTCAATCAAGAGCCCACTGAGAGA 1596
```

```

DB 843  AGGGCTGTGCTGCTGCTGATGAGGAGAGCTGCTCAATCAAGAGCCCACTGAGAGA 902
QY 1597  TCCGGGCTCTGCATGACGACCATTTGGGGGAATCCCTTGTGCTGCTGGGAGATACATCC 1656
DB 903  TCCGGGCTCTGCATGACGACCATTTGGGGGAATCCCTTGTGCTGCTGGGAGATACATCC 962
QY 1657  TGTGCTGGGAATCCCAAGCTCCCGCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1716
DB 963  TGTGCTGGGAATCCCAAGCTCCCGCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1022
QY 1717  ACCTCAGGCCCCATGATTAAGTCAATCCAGTCACTCAAGTCAAGTCAAGTCAAGTCA 1776
DB 1023  ACCTCAGGCCCCATGATTAAGTCAATCCAGTCACTCAAGTCAAGTCAAGTCAAGTCA 1062
QY 1777  CCGGTTTCAAGGCCCCCTGATGCTCCGCTCGAGGGCCCTTCTGATCTCGGTGACG 1836
DB 1063  CCGGTTTCAAGGCCCCCTGATGCTCCGCTCGAGGGCCCTTCTGATCTCGGTGACG 1067
QY 1837  TCTTCTTGGGAGCTGATGCTGCTCTTTCGACCGCGGGGACATGAAGACAGCCCGGG 1896
DB 1068  TCTTCTTGGGAGCTGATGCTGCTCTTTCGACCGCGGGGACATGAAGACAGCCCGGG 1127
QY 1897  TGGGCTGTGGCGCGGCTTCGCACTGCGGAGGAGCTCGATGGGAGAGACTGCGAGG 1956
DB 1128  TGGGCTGTGGCGCGGCTTCGCACTGCGGAGGAGCTCGATGGGAGAGACTGCGAGG 1187
QY 1957  CGCAGTTCGCCGGGTGAGCGCCCAAGTGAAGGCGATGCGGAGGCTGCGGAGGTCC 2016
DB 1188  CGCAGTTCGCCGGGTGAGCGCCCAAGTGAAGGCGATGCGGAGGCTGCGGAGGTCC 1247
QY 2017  TGTACCCAGTAAATTCACATTTTCATTTGAAAAA 2060
DB 1248  TGTACCCAGTAAATTCACATTTTCATTTGAAAAA 1291

RESULT 5
US-09-969-384-4
; Sequence 4, Application US/09969384
; Publication No. US20020192749A1
; GENERAL INFORMATION:
; APPLICANT: Moore, et al.
; TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: P7055P1
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10542
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/236,384
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/194,118
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1487
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-969-384-4

Query Match      47.88; Score 984; DB 10; Length 1487;
Best Local Similarity 88.6%; Pred. No. 1,5e-307;
Matches 1210; Conservative 0; Mismatches 25; Indels 131; Gaps 8;

QY 693  CAGAAAGGCTCCCGAGGATGCTTCACACACCGGTGCTGCAACCCCTGCTGCTGCTG 752
DB 236  CAGAAAGGCTCCCGAGGATGCTTCACACACCGGTGCTGCAACCCCTGCTGCTGCTG 294
QY 753  CCTCTGTGATGAGAGCTTCCGGGCGACACTGATCCGATCCCTCTTCAATGAGTCC 812
DB 295  CCTCTGTGATGAGAGCTTCCGGGCGACACTGATCCGATCCCTCTTCAATGAGTCC 353
QY 813  CAACCTGAGCAGAGACCTTAACCTACTGAGGGGATGAGAGAACCAAGACAGACTCCC 872
DB 813  CAACCTGAGCAGAGACCTTAACCTACTGAGGGGATGAGAGAACCAAGACAGACTCCC 872
```

Db	354	CAACCTGGACGAGGATGCTGTGAACCTACTGAGGGGATGAGAGAACACACGAACTCCCC	413
QY	873	AAGTTGGGGGGCCCCATCCCTCTGGGACAAGCCCATCTTGTAACCTCTCGAATCAAG	932
Db	414	AAGTTGGGGGGCCCCATCCCTGTAGAGACAAGCCCATCTTGTAACCTCTCGAATCAAG	473
QY	933	GATGTGCAAGTATTTTGGGGAAATTTGGGCTGGGAAGCCTCCACAAACTGTCACTGTGCC	992
Db	474	G-----	474
QY	993	TTTGACACTGGCTCCTCCAACTCTGGATCCGTCAGAGAGATGCCACTTCTAGTGTG	1052
Db	475	-----	474
QY	1053	CCCTGTGGTTACACACGCAATTTGATCCAAAGCCTTAGCTCTCCAGGCCMAATGG	1112
Db	475	-----GATGTTACACACCGATTTTATCCAAAGCCTTA-CTCTTCCAGCCATATGG	528
QY	1113	ACCAAGTTTGGCCATTCAAATATGGAATCTGGGGGTAGATGGAATCTGAGCGAGACAAG	1172
Db	529	ACCAA-TTTGGCAATTCAAATATGGAATCTGGGGGTAGATGGAATCTGAGCGAGACAAG	587
QY	1173	CTGACTATTGGTGAATCAAGGGTGCATCACTGANTTTTCGGGGAGGCTCTCTGGAGACC	1232
Db	588	CTGACTATTGGTGAATCAAGGGTGCATCACTGANTTTTCGGGGAG-GCCTCTGGGA-CCC	645
QY	1233	AGCCTGATCTTCGCTTTTGCCATTTTGATGGGATATTTGGGACCTTGCTTCCATCTG	1292
Db	646	AGCCTGATCTTCGCTTTTGCCCA-TTTGATGGGATATTTGGGACCTTGCTTCCATCTG	704
QY	1293	TCTGTGGAAAGAGTTCCGGCCCCCGCATGATGTACTGCTGTGGACAGCGGCTATTGGATAG	1352
Db	705	TCTGTGGAAAGAGTTCCGGCCCCCGCATGATGTACTGCTGTGGACAGCGGCTATTGGATAG	764
QY	1353	CGTGTCTCTCTCTTTTACCTCAACAGGAGCCTGTGAAGAGCCTGATGGAGAGAGCTGTC	1412
Db	765	CGTGTCTCTCTCTTTTACCTCAACAGGAGCCTGTGAAGAGCCTGATGGAGAGAGCTGTC	824
QY	1413	CTGGGGGGCTGGACCCGGGACACTACTCCACCCCTACCTTGTCAGTCAAGCTC	1472
Db	825	CTGGGGGGCTGGACCCGGGACACTACTCCACCCCTACCTTGTCAGTCAAGCTC	884
QY	1473	CTGTGCTCTGTGGAGATCCATATGAGAGGAGGCTGTGAAGGGGGCCAGGGCTGACTCTGT	1532
Db	885	CTGTGCTCTGTGGAGATCCATATGAGAGGAGGCTGTGAAGGGGGCCAGGGCTGACTCTGT	944
QY	1533	GCCAAAGGCTGTGCTCCCATCTGGATACGGGGACGCTCCTCATACAGAACCACTGAG	1592
Db	945	GCCAAAGGCTGTGCTCCCATCTGGATACGGGGACGCTCCTCATACAGAACCACTGAG	1004
QY	1593	GAGATCCGGGGCCCTGCATGCAAGCATTTGGGGGAATCCCTTGTCGGGCTGGGAGTACATC	1652
Db	1005	GAGATCCGGGGCCCTGCATGCAAGCATTTGGGGGAATCCCTTGTCGGGCTGGGAGTACATC	1064
QY	1653	ATTCGTGTCTGGAATCCCAAAGCTCCCGCAGATCTCTCTCTTCTTTGGGGGGGTCTGG	1712
Db	1065	ATTCGTGTCTGGAATCCCAAAGCTCCCGCAGATCTCTCTCTTCTTTGGGGGGGTCTGG	1124
QY	1713	TTTAAACCTCAACGGGCCATGATTAGTCACTCCAGACTACTGAAATGGCGTCCGCTCTGC	1772
Db	1125	TTTAAACCTCAACGGGCCATGATTAGTCACTCCAGACTACTGAAATGGCGTCCGCTCTGC	1184
QY	1773	TTGTCCGGTTTCCAGGCCCTGGATGTGCCTCCGCTGAGAGGCCCTTGATCTCTGGGT	1832
Db	1185	TTGTCCGGTTTCCAGGCCCTGGATGTGCCTCCGCTGAGAGGCCCTTGATCTCTGGGT	1244
QY	1833	GACGTCTTCTTGGGAGCGTATGTGGCGCTTTTGACCGCGGGGACATGAAGCAGCGCC	1892
Db	1245	GACGTCTTCTTGGGAGCGTATGTGGCGCTTTTGACCGCGGGGAGATGAAGACAGCGCC	1304
QY	1893	CGGGTGGGGCCGGGGGGGCTCGACACTGCGGAGACCGAACCCTCGGATGGGGAGACTGTGG	1952
Db	1305	CGGGTGGGGCCGGGGGGGCTCGACACTGCGGAGACCGAACCCTCGGATGGGGAGACTGTGG	1364

```

RESULT 6
US-09-789-919-13
: Sequence 13, Application US/09789919
: Patent No. US20020064855A1
: GENERAL INFORMATION:
: APPLICANT: Lemischka, Ihor
: TITLE OF INVENTION: GENES THAT REGULATE HEMATOPOIETIC BLOOD FORMING STEM
: TITLE OF INVENTION: CELLS AND USES THEREOF
: FILE REFERENCE: 2275-1-005
: CURRENT APPLICATION NUMBER: US/09/789,919
: CURRENT FILING DATE: 2001-02-21
: NUMBER OF SEQ ID NOS: 96
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 13
: LENGTH: 1360
: TYPE: DNA
: ORGANISM: Mus musculus
US-09-789-919-13

```

Query Match	38.7%;	Score 797.2;	DB 9;	Length 1360;
Best Local Similarity	75.8%;	Pred. No. 5.2e-247;		
Matches 1014;	Conservative	0;	Mismatches 317;	Indels 7; Gaps 2

QY		724	CAGGCTGCACAAACCCTGTGGTGTGGTCCTGTGCAATGTTGGAGACTTTCCGGGGACA	783
Db		22	CGCACACTACCTGCTCTGTGCTGTGCTGTGCTGCTGCTGCTGGGAATTGTAAGCTGAGGAGCCA	81
QY		784	CACGTATCCGCATCCCTCTTCATGAGTCCAACTGGACGAGGACCCCTGAACCTACTGA	843
Db		82	AACGTATCCGHTGCCCTCTTCAAGAAATCCACCTTGGACACAGAATTTAACCACATGA	141
QY		844	GGGATGTGAGAAACCAAGCAGAGTCCCCCAAATTTGGGGCCCCCATCCCCTGGGACAAGC	903
Db		142	ATGGATGGGAACACTGGCACAGACTTTCTA-----GACCTCCACCTCTGTGGTGCAAC	195
QY		904	CAATCTTCGAACTCTCTCGAATACAGAGGATGTGAGTATTTTGGGGAAATGGGTGG	963
Db		196	CTCTCTTTGTGCTCTCTCTCCAACTTCAATGAACACCCAGATATTTTGGAACTATATGTTTT	255
QY		964	GAACGCTCCACAATACTGATCTGTGCTCTTTCACCTGGCTCCCAATCTCGGGTCC	1023
Db		256	GAAGCCTCTCAGAAATTCACGGTGTCTTTTGACAGGGGTCTTCCAACTGTGGGTTTC	315
QY		1024	CGTCCAGGAATGCGCACTTTCTTAGTGTGCCCTGTGCTGTTACACCAACCGATTTGATCCA	1083
Db		316	CGTCCAGGAATGCAATTTCTTCAATTTGGATCTGTGTACCAATCGCTTATATCCA	375
QY		1084	AAGCCTTACTCCTTCACAGGCCAATGGGAOCAAATTTGCCATTCATATGAACTGGC	1143
Db		376	AGGCTCTCACTCTTATAGGCCCAATGGAGCAAGTTTGGCATTCACATATGGGACCGGGC	435
QY		1144	GGGTAGATGAAATCCTGAGCAGAGACAAAGCTGATTTGGTGGAAATGAAGGTGCATCAG	1203
Db		436	GGCTGAGCGGAATCTTAGCCAGGACAAATGTGACTATCGGGGGGATCAAGATGCTTTTG	495
QY		1204	TGATTTTCGGGGAGGCTCTCTGGGAGCCACAGCCTGTCTTCGCTTTTGGCCATTTGATG	1263
Db		496	TGACATTTGGAGAGGCTCTGTGGGAGCCACGACCTGATCTTTGTGTTAGCCACTTTATG	555
QY		1264	GGATATTTGGGCTCTGGTTTCCATCTGTCTGTGGAAGAGTTCCGGCCCCCATGTAGT	1323
Db		556	GGATCTTGGGGCTTCGGCTTCCACACTCTGGCTGTGGGCGAGATTCACGCTCCCTGTGAT	615



QY	1324	TACGTCGTGACAGGAGGCTATGGATAAGACCTGCTCTTCCTTTTACTTAAACAGGGAC	1383
Db	616	CGATGCTGAGCAAGGGCTGCTGGAGAAACCGCTCTTCTCTTTTAACTCAACAGGGATT	675
QY	1384	CTGAAGAGCCTGATGTAGAGAGAGCTGTGCTCTGGGGGGGCTCGAGACCAGGACACTACATCC	1443
Db	676	CTGAAGAGGTCTGATGTGGGGAGAGCTGGTGTCTTAGGGGGGCTCAGACCCGCTCACTAGTAC	735
QY	1444	CACCCCTCACCCTTGTGTCGCACTCAGCGTCCCTGCTTACTGGCAGATTCACATGGAGCTG	1503
Db	736	CTCCCTCACCCTTATACAGACTACATCCCTGCTACTGTGCAGGTCCACATGGAGATG	795
QY	1504	TGAAGTGGGGCCAGGGGCTGACTCTCTGTGCAAGGGGCTGTGCTGCCATCTCGATTAGG	1563
Db	796	TGAAGTGGGCGACAGGGGCTGAGCCTCTGTGTGCCAGGGGCTGAGTGTCCATCTTAGACACAG	855
QY	1564	GCAGCTCCCTCATCAGAGAGACCACATGAGAGATCCGGGGCCCTGCATGCAGCAATTGGGG	1623
Db	856	GCACATCCCTCATCAGAGAGACTGTAGGAGATCCGGGGCTTGAAATTAAGCAATTGGGG	915
QY	1624	GAATCCCTTGTCTGTGGCTGGGAGTACATCATCTGTGTGCTCGGAATTCGCAAGCTCCCG	1683
Db	916	GATATCCCTTCTTAATGGGACAGTACTTCACTGATTCAGTGTCCAGAGCCAGCTTCCCTCC	975
QY	1684	CAGTCTCCTTCTTGTGGGGGGGTCTGTGTTAACTCAGAGGCCATGATTACGCAATCC	1743
Db	976	CTGTCTCTTCCACTTGT	1035
QY	1744	AGACTACTCGAATAGGCGTCCGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1803
Db	1036	AGATTCTTCAAGAGGATGT	1095
QY	1804	CGCCTGCAAGGGCCTTCTGTGATTCCTGCTGTACGCTTCTTGTGGGACGATATGTGGCGCT	1866
Db	1096	AGCCTGTGGGGACCCCTCTGTGATCTTGTGGGAGCTTCTTGTGGGGCCCTATGTGTGTCT	1155
QY	1864	TCGACCGCGGGACATGAGAGACAGCGCCGGGTGGGCTGGCGGCGCTGCACTGCG	1923
Db	1156	TTGACCGGTGGGACAAACACGTCCGGCCCGCGGTGGGACGTGGCGCTGTCAATGTCTT	1215
QY	1924	GAGCGACCTTGGATGGGGAGAGACTGTGCGAGGGCGCATTCGCCGGGTGAGCGCCCAAGTG	1983
Db	1216	CACAGACCGGGGACGAAAGAGGACTACGACAGGCGGAGTCTTCAAAAGACGCCCTGT	1275
QY	1984	A-AACCGATGGCGACGGGTGTGGCGAGGTCTCTGCTACCCAGTAAATTCACATATT	2042
Db	1276	AGGCTACAGCTCACCGGGGACAGCAGCTATGCTTCTTCCAAATTAACAACTAAATAA	1335
QY	2043	CCATTGAAAAAAAAAAAAA 2060	
Db	1336	AAAAAAAAAAAAAAAAAAAA 1353	
RESULT 7			
US-09-789-919-43			
: Sequence 43, Application US/09789919			
: Patent No. US20020064855A1			
: GENERAL INFORMATION:			
: APPLICANT: Lemischka, Thor			
: APPLICANT: Moore, Kaleli			
: TITLE OF INVENTION: GENES THAT REGULATE HEMATOPOIETIC BLOOD FORMING STEM			
: FILE REFERENCE: 2275-1-005			
: CURRENT APPLICATION NUMBER: US/09/789, 919			
: CURRENT FILING DATE: 2001-02-21			
: NUMBER OF SEQ ID NOS: 96			
: SOFTWARE: Patentin Ver. 2.0			
: SEQ ID NO 43			
: LENGTH: 1360			
: TYPE: DNA			
: ORGANISM: Mus musculus			
US-09-789-919-43			

[illegible]













GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2003, 12:41:16 ; Search time 607.912 Seconds

(Without alignments)  
9147.448 Million cell updates/sec

Title: US-09-700-770-3

Perfect score: 2060  
Sequence: 1 ctctgagagcttcaataact.....ttccattgaaaaaataa 2060

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

N.Geneseq\_19Jun03:\*

1: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*  
2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*  
3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*  
4: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*  
5: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*  
6: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*  
7: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:\*  
8: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*  
9: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*  
10: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*  
11: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:\*  
12: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:\*  
13: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:\*  
14: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*  
15: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:\*  
16: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:\*  
17: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:\*  
18: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:\*  
19: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*  
20: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:\*  
21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*  
22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*  
23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*  
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*  
25: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2060	100.0	2060	21	AAZ29722 Human lung specific
2	2060	100.0	2061	20	AAK87152 Human protease HUP
3	1356.8	65.9	1910	19	AAV27038 Human napsin B CDN
4	1352	65.6	1425	24	AAK99391 DNA of NAPI from a
5	1261.4	61.2	1263	21	AAZ50231 Human Aspartic pro
6	1199.2	58.2	1298	19	AAV31665 Nucleotide sequenc
7	1151.8	55.9	1375	19	AAV28623 Human aspartic pro
8	1142	55.4	1353	19	AAV27036 Human napsin A CDN

9	1122.6	54.5	1329	21	AAZ50232 Human Aspartic Pro
10	1100.4	53.4	1370	24	AAZ38693 Human Lp191 secret
11	984	47.8	1487	22	AAZ14882 Human CDNA encoding
12	949.2	46.1	1347	19	AAZ28624 Human aspartic pro
13	936.2	45.4	1387	22	AAH98322 Human EST-derived
14	839.6	40.8	865	22	AAZ40936 Human encoding nove
15	797.2	38.7	1360	21	AAZ94089 Haematopoietic ste
16	797.2	38.7	1360	21	AAZ94118 Haematopoietic ste
17	757.8	36.8	794	22	AAH46949 Human secreted pro
18	757.8	36.8	794	24	AAZ58485 Human secreted pro
19	716.4	34.8	1645	19	AAV27037 Human napsin A gen
20	678.4	32.9	1823	24	AAZ32339 Human lung specific
21	678.4	32.9	1840	23	AAH471264 Human nucleic acid
22	678	32.9	741	22	AAH46970 Human secreted pro
23	678	32.9	741	24	AAZ58506 Human secreted pro
24	676.8	32.9	1844	24	AAZ05172 Human DEAE and DEA
25	614.2	29.8	723	22	AAH46971 Human secreted pro
26	614.2	29.8	723	24	AAZ58507 Human secreted pro
27	602.4	29.2	1041	21	AAZ18208 Lung cancer associ
28	596.8	29.0	673	22	AAZ40937 CDNA encoding nove
29	502.8	24.4	693	24	AAZ30266 Human G-protein-co
30	493.6	24.0	866	23	AAZ84221 DNA encoding novel
31	462.4	22.4	663	24	AAZ30495 Human G-protein-co
32	436	21.2	534	22	AAZ41501 CDNA encoding nove
33	436	21.2	534	22	AAZ62784 Human CDNA SEQ ID
34	397.2	19.3	481	19	AAZ28634 Human aspartic pro
35	387.6	18.8	407	21	AAZ00579 Human secreted pro
36	386.6	18.8	407	20	AAZ28633 Human secreted pro
37	360.2	17.5	474	19	AAV28633 Human aspartic pro
38	339.6	16.5	466	24	AAZ86526 Human protease CDN
39	335	15.8	408	20	AAZ87699 Human protease CDN
40	323.2	15.7	442	23	AAZ84214 DNA encoding novel
41	322.6	15.7	402	19	AAZ28632 Human aspartic pro
42	319.4	15.5	1666	23	AAZ03379 Drosophila melanog
43	319.4	15.5	3915	23	AAZ03378 Human secreted pro
44	319	15.5	2131	22	AAZ03492 Human secreted pro
45	319	15.5	2131	25	AAZ50578 Human secreted pro

#### ALIGNMENTS

AAZ29722	AAZ29722 standard; DNA; 2060 BP.
ID	AAZ29722
AC	AAZ29722;
XX	
DT	27-MAR-2000 (first entry)
XX	
DE	Human lung specific gene Lng105.
XX	
KW	Lung Specific Gene; LSG; Lng105; human; diagnostic marker;
KW	prognosticate; Lung cancer; diagnosis; ds.
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	711..1973
FT	/tag= a
FT	/product= "LSG Lng105 protein"
PN	MO9960160-Al.
XX	
PD	25-NOV-1999.
XX	
PF	12-MAY-1999; 99MO-US10344.
XX	
PR	21-MAY-1998; 98US-0086212.
XX	
PA	(DIAD-) DIADEXUS LLC.
XX	
PI	Yang F, Macina RA, Sun Y;

xx WPI: 2000-116320/10.  
 DR P-PSDB; AAY44457.  
 xx  
 PT A new method for diagnosing, monitoring and staging lung cancer -  
 xx  
 PS Claim 6; Pages 34-35; 40pp; English.  
 xx  
 CC The present sequence is a lung specific gene (LSG) lmg105 from human  
 CC clone ID 3107312. The LSG has high level of tissue specificity for lungs  
 CC and is overexpressed in cancerous tissues. The sequence serves as a lung  
 CC diagnostic marker for detecting, monitoring, staging and prognosticating  
 CC lung cancer. The diagnosis involves comparing levels of LSG in samples  
 CC obtained from patient and normal control.  
 xx  
 xx Sequence 2060 BP; 458 A; 573 C; 537 G; 492 T; 0 other;

Query Match 100.0%; Score 2060; DB 21; Length 2060;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2060; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGAGAGCTCTCAATCTGTGTCATGATGAAGCCGACGAATCTGATATGATTT 60  
 Db 1 CTTGAGAGCTCTCAATCTGTGTCATGATGAAGCCGACGAATCTGATATGATTT 60  
 OY 61 TGAGACAGAGGTTGACAGAGCTCGAGATCGGAAAAACATTCCTCTCTGACACCATGAC 120  
 Db 61 TGAGACAGAGGTTGACAGAGCTCGAGATCGGAAAAACATTCCTCTCTGACACCATGAC 120  
 OY 121 CAAGAAGTTCAAAAACCTTCAGCGAGAGCTGTGAAGAACTCTGGAATGTCGGCTTTC 180  
 Db 121 CAAGAAGTTCAAAAACCTTCAGCGAGAGCTGTGAAGAACTCTGGAATGTCGGCTTTC 180  
 OY 181 CTCTAATATACAGACAGTGTGAAAAATACACAAATATATATTTTATCCCTTAATTT 240  
 Db 181 CTCTAATATACAGACAGTGTGAAAAATACACAAATATATATTTTATCCCTTAATTT 240  
 OY 241 CAAGATACCTACCTGCTGTTTATATCTTAATGAATGGCTGGAACCTCTTATGATATT 300  
 Db 241 CAAGATACCTACCTGCTGTTTATATCTTAATGAATGGCTGGAACCTCTTATGATATT 300  
 OY 301 CTGACGACCTGTATATATACCGAGAAAGCTTTGTACTGCGAAATCTTGCTTAC 360  
 Db 301 CTGACGACCTGTATATATACCGAGAAAGCTTTGTACTGCGAAATCTTGCTTAC 360  
 OY 361 TGCCATCCCTCCATGACAAATGATGAGTAAGCGCTAGAGTCCCTTAATGATT 420  
 Db 361 TGCCATCCCTCCATGACAAATGATGAGTAAGCGCTAGAGTCCCTTAATGATT 420  
 OY 421 TAAAGCCAAAGCCGCTTCATTTCTTAGCAACTGACGTTGCCAGCGAGTTTGACAT 480  
 Db 421 TAAAGCCAAAGCCGCTTCATTTCTTAGCAACTGACGTTGCCAGCGAGTTTGACAT 480  
 OY 481 AACTCATGTAGATGTTGTTCACTTGCATTCCTACCTCCATTCAGAGATTAATCA 540  
 Db 481 AACTCATGTAGATGTTGTTCACTTGCATTCCTACCTCCATTCAGAGATTAATCA 540  
 OY 541 TCGAGTAGTGAACAGCTAGAGTGGCGCTCCGGAAGGCTATTACTTTTGTACACA 600  
 Db 541 TCGAGTAGTGAACAGCTAGAGTGGCGCTCCGGAAGGCTATTACTTTTGTACACA 600  
 OY 601 GTATGATGTGAACCTTCACAGCGCATGAACACTTAATTTGGAGAACTACAGTTT 660  
 Db 601 GTATGATGTGAACCTTCACAGCGCATGAACACTTAATTTGGAGAACTACAGTTT 660  
 OY 661 TCCAAACAGAGATGATGAGTTATGATGCTGACAGAAAGCGTCCCAAGCATGTCTCAC 720  
 Db 661 TCCAAACAGAGATGATGAGTTATGATGCTGACAGAAAGCGTCCCAAGCATGTCTCAC 720  
 OY 721 CACGCTCTGCAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
 Db 721 CACGCTCTGCAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780

OY 781 CCACACTGATCCGATCCCTCTTTCATGAGTCCAACTGACGAGAGACCTGAACTTAC 840  
 Db 781 CCACACTGATCCGATCCCTCTTTCATGAGTCCAACTGACGAGAGACCTGAACTTAC 840  
 OY 841 TGAGGGATGAGAGAACACAGACAGCTCCCAAGTTGGGGGCCCATCCCTGGGACACA 900  
 Db 841 TGAGGGATGAGAGAACACAGACAGCTCCCAAGTTGGGGGCCCATCCCTGGGACACA 900  
 OY 901 AGCCATCTTCGTCACCTCTCTGCAACTACAGAGATGTCAGTATTTTGGGAAATTTGGG 960  
 Db 901 AGCCATCTTCGTCACCTCTCTGCAACTACAGAGATGTCAGTATTTTGGGAAATTTGGG 960  
 OY 961 TGGAAGCCTCCACAAACTTCACTGTGCTTTGACACTGCTCTGCAATCTGCG 1020  
 Db 961 TGGAAGCCTCCACAAACTTCACTGTGCTTTGACACTGCTCTGCAATCTGCG 1020  
 OY 1021 TCCCGTCCAGAGATGTCACCTCTTTCAGTGTGCTCTGCTTACACCCGATTTTATC 1080  
 Db 1021 TCCCGTCCAGAGATGTCACCTCTTTCAGTGTGCTCTGCTTACACCCGATTTTATC 1080  
 OY 1081 CCAAGCCTTCAGCTCTCTCCAGGCAATGGGACCAAGTTGCCATTCATATGAACTG 1140  
 Db 1081 CCAAGCCTTCAGCTCTCTCCAGGCAATGGGACCAAGTTGCCATTCATATGAACTG 1140  
 OY 1141 GCGGGTAGATGGAATCTGAGGACAGCAAGTACTATTGTGGAATCAAGGTGCAT 1200  
 Db 1141 GCGGGTAGATGGAATCTGAGGACAGCAAGTACTATTGTGGAATCAAGGTGCAT 1200  
 OY 1201 CAGTATTTTGGGGAGGCTCTGCGGAGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260  
 Db 1201 CAGTATTTTGGGGAGGCTCTGCGGAGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260  
 OY 1261 ATGGATATTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320  
 Db 1261 ATGGATATTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320  
 OY 1321 ATGTACTGTGAGACAGGGGCTATTGATTAAGCTGTCTTCTCTTTACTCAAGAGG 1380  
 Db 1321 ATGTACTGTGAGACAGGGGCTATTGATTAAGCTGTCTTCTCTTTACTCAAGAGG 1380  
 OY 1381 ACCCTGAAGACCTGATGAGAGAGAGCTGCTGCGGGGGCTCGAGACCGGACACATCA 1440  
 Db 1381 ACCCTGAAGACCTGATGAGAGAGAGCTGCTGCGGGGGCTCGAGACCGGACACATCA 1440  
 OY 1441 TCCACCCCTACCTTCGTGCAAGTACAGCTCCCTGCTACTGSCAGATCCATGAGC 1500  
 Db 1441 TCCACCCCTACCTTCGTGCAAGTACAGCTCCCTGCTACTGSCAGATCCATGAGC 1500  
 OY 1501 GTGTGAAGTGGGCCCAAGGCTGACTCTCTGCTGCAAGGCTGTGCTGCTGCTGCTG 1560  
 Db 1501 GTGTGAAGTGGGCCCAAGGCTGACTCTCTGCTGCAAGGCTGTGCTGCTGCTGCTG 1560  
 OY 1561 CGGGACGCTCCCTCATACAGAGACCCACTGAGAGATCCGGGCCCTGATCAGCATTTG 1620  
 Db 1561 CGGGACGCTCCCTCATACAGAGACCCACTGAGAGATCCGGGCCCTGATCAGCATTTG 1620  
 OY 1621 GGGGATCCCTTGTGCTGGGAGTACATATCTGCTGCGAAATTCCAAAGCTCC 1680  
 Db 1621 GGGGATCCCTTGTGCTGGGAGTACATATCTGCTGCGAAATTCCAAAGCTCC 1680  
 OY 1681 CCGGATCTCTCTCTTCTTGGGGGGCTGTGTTTAACTACAGGCCCCATATTAACGCA 1740  
 Db 1681 CCGGATCTCTCTCTTCTTGGGGGGCTGTGTTTAACTACAGGCCCCATATTAACGCA 1740  
 OY 1741 TCCAGATACAGGAATGGGCTCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800  
 Db 1741 TCCAGATACAGGAATGGGCTCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800  
 OY 1801 CTCGCTCTGAGGGCCCTTCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860  
 Db 1801 CTCGCTCTGAGGGCCCTTCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860  
 OY 1861 TCTTCCAGCCGGGGGACATGAAGACAGCGCCCGGGTGGCTGGCGCGCTGACATC 1920

Dd		1861 TCTTCGACCGGGAGACAATGAAGACAGCCGCCCGGTGGCCTTGCACTC	1920
Oy		1921 GCGGAGCGGCACCTCGGATGGGAGAGACTGCGCAGCGCACATTCCC GG GTGACGCCAA	1980
Dd		1921 GCGGAGCGGCACCTCGGATGGGAGAGACTGCGCAGCGCACATTCCC GG GTGACGCCAA	1980
Oy		1981 GTGAAGCGCATGCGCAGCGGGTGGTCCGCGGAGTCTGCTACCAGTAATAATCACTAT	2040
Dd		1981 GTGAAGCGCATGCGCAGCGGGTGGTCCGCGGAGTCTGCTACCAGTAATAATCACTAT	2040
Oy		2041 TTCCATTGAAAAAATAAAA 2060	
Dd		2041 TTCCATTGAAAAAATAAAA 2060	
	RESULT 2		
ID	AAX87152		
XX	AAX87152 standard; cDNA; 2061 BP.		
XX			
XX	AAX87152;		
XX			
Dt	27-SEP-1999 (first entry)		
XX			
De	Human protease HUPM-4 cDNA.		
XX			
KW	Aspartic protease; human; HUPM-4; cell proliferation; cancer;		
RW	immune disorder; inflammation; therapy; ss.		
OS	Homo sapiens.		
FH			
FH	Key Location/Qualifiers		
FT	CDS 711..1973		
FT	/tag= a		
FT	sig_peptide 711..773		
FT	/tag= b		
FT	/note= "putative signal peptide sequence"		
FT	mat_peptide 774..1970		
FT	/tag= b		
XX	MO9936550-AZ.		
Pd	22-JUL-1999.		
XX			
Pf	12-JAN-1999; 99WO-US00655.		
XX			
PR	16-JAN-1998; 98US-0008271.		
PA	(INCYTE) INCYTE PHARM INC.		
PI	Bandman O, Corley NC, Guegler KJ, Hillman JL, Shah P;		
PI	Tang YF, Yue H;		
DR	WPI: 1999-430616/36.		
DR	P-PsDB: AAY06435.		
PF	Novel human protease molecules useful in the treatment of		
PT	developmental disorders and/or cancers		
PS	Claim 8; Page 85; 90pp; English.		
XX			
XX	This nucleotide sequence codes for HUPM-4 (see AAY06435), a novel		
CC	human protease. HUPM-4 cDNA was initially identified in Incyte		
CC	Clone 877617 from the lung cDNA library LUNGAST01 using a computer		
CC	search for amino acid sequence alignments. The present sequence		
CC	is a consensus sequence derived from the following overlapping		
CC	and/or extended nucleic acid sequences: Incyte Clones 372314		
CC	(LUNGNOR02), 698335 (SYNORAT03), 692718 (LUNGRUT02), 877617		
CC	(LUNGST01) and 13994470 (BRAIRU08). A fragment comprising		
CC	nucleotides 1609-1692 of the present sequence can be used for		
CC	hybridisation. This sequence encompasses a leucine zipper domain.		
CC	Northern analysis shows expression of HUPM-4 in cardiovascular,		
CC	haematopoietic, and male an female reproductive cDNA libraries.		

	Query Match	100.0%	Score 2060;	DB 20;	Length 2061;	
	Best Local Similarity	100.0%;	Pred. No. 0;			
	Matches 2060;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0	
QY	1	CTTGGAGGCTCTCAAAATCTTGGTCTCATGGATGAGGCGGACCGGAATCTGAAATGTGGATTT	60			
DB	1	CTTGGAGGCTCTCAAAATCTTGGTCTCATGGATGAGGCGGACCGGAATCTGAAATGTGGATTT	60			
QY	61	TGAGACAGAGGTTTGACAAAGCCTCGAGATGGAAAACATTCCTCTCTGCGACCAATGAC	120			
DB	61	TGAGACAGAGGTTTGACAAAGCCTCGAGATGGAAAACATTCCTCTCTGCGACCAATGAC	120			
QY	121	CAGAAGGTTTCAAAAACTTCAGCGAGACGCTCTGAAAGAACTCTGTAAGATGTGCGGTTTC	180			
DB	121	CAGAAGGTTTCAAAAACTTCAGCGAGACGCTCTGAAAGAACTCTGTAAGATGTGCGGTTTC	180			
QY	181	CTCTAAATATCCAGACAGAGTTGAAAAATTAACGCAATTTATATTTTATTTCCCTCTAAAT	240			
DB	181	CTCTAAATATCCAGACAGAGTTGAAAAATTAACGCAATTTATATTTTATTTCCCTCTAAAT	240			
QY	241	CAAGATACCTACCTGCGTTTATATCTTAATGAATTTGGCGTGAAGACCTCTTATGATAT	300			
DB	241	CAAGATACCTACCTGCGTTTATATCTTAATGAATTTGGCGTGAAGACCTCTTATGATAT	300			
QY	301	CTGCAGACACCTGTAAATATATACCAGAAACAGCTTTGCTACGCGGAATCTTGCGTTTCAC	360			
DB	301	CTGCAGACACCTGTAAATATATACCAGAAACAGCTTTGCTACGCGGAATCTTGCGTTTCAC	360			
QY	361	TGGCCATCCCTCCCATATGACCAATATGATGATAGAGCTAGGCGCTTAGATCCCTTAATAAGTT	420			
DB	361	TGGCCATCCCTCCCATATGACCAATATGATGATAGAGCTAGGCGCTTAGATCCCTTAATAAGTT	420			
QY	421	TAAAGCCAAAGCCCGCTTCATTCTTCTAGCAACTGACGTTGCCAGCGGAGGTTTGACAT	480			
DB	421	TAAAGCCAAAGCCCGCTTCATTCTTCTAGCAACTGACGTTGCCAGCGGAGGTTTGACAT	480			
QY	481	ACCTCATGTAGATGTGGTTGTCAACTTTGACATTTCTTACCATTCCCAAGATTATACATCA	540			
DB	481	ACCTCATGTAGATGTGGTTGTCAACTTTGACATTTCTTACCATTCCCAAGATTATACATCA	540			
QY	541	TGCAATAGGTTCGAACAGCTTAGAGCTGGGGGCTTCGGAAAAGGCTATTAATCTTTGTACACA	600			
DB	541	TGCAATAGGTTCGAACAGCTTAGAGCTGGGGGCTTCGGAAAAGGCTATTAATCTTTGTACACA	600			
QY	601	GTATGATGGGAACCTTTCACAGCGCATTAACACTTAATTTGGGAAGAAACTACCAAGTTT	660			
DB	601	GTATGATGGGAACCTTTCACAGCGCATTAACACTTAATTTGGGAAGAAACTACCAAGTTT	660			
QY	661	TCCAACACAGATGTATGAGTTATGATGCTGACAGAACGCGTCCCGCAGGATGTCTCCAC	720			
DB	661	TCCAACACAGATGTATGAGTTATGATGCTGACAGAACGCGTCCCGCAGGATGTCTCCAC	720			
QY	721	CACGCGTGTGCAACCCCTGCTGTGCTGCTGCTCTGCTGAATGTGAGACCTTCGGGG	780			
DB	721	CACGCGTGTGCAACCCCTGCTGTGCTGCTGCTCTGCTGAATGTGAGACCTTCGGGG	780			
QY	781	CCAGACTATCCGCAATCCCTCTTCAATCAGATGCCAACTGTGACAGAGACCTGAAACCTTAC	840			
DB	781	CCAGACTATCCGCAATCCCTCTTCAATCAGATGCCAACTGTGACAGAGACCTGAAACCTTAC	840			
QY	841	TGAGGGATGTGAGAACACAGACAGCTCCCAAGTTGGGGGGCCCATCCCTGGGGGACA	900			



```

Db      841 TGGGGGATGAGAGACAGCAGAGAGCTCCCAAGTGGGGGCCCATCCCTGGGAGACA 900
QY      901 AGCCATCTTCTGACCTCTCTGCACTACAGGAGATGAGATGTTTGGGAAATGGGC 960
Db      901 AGCCATCTTCTGACCTCTCTGCACTACAGGAGATGAGATGTTTGGGAAATGGGC 960
QY      961 TGGGAAAGCCTCCACAAATTCCTACTGTTGCCCTTGGACATGGCTCTCCATCTCTGGG 1020
Db      961 TGGGAAAGCCTCCACAAATTCCTACTGTTGCCCTTGGACATGGCTCTCCATCTCTGGG 1020
QY      1021 TCCGCTCCAGGAGATGCACTTCTTCAAGTGTGCTGCTGCTGCTTACACACCGATTGATC 1080
Db      1021 TCCGCTCCAGGAGATGCACTTCTTCAAGTGTGCTGCTGCTGCTTACACACCGATTGATC 1080
QY      1081 CCAGAGCCTCTAGCTCTCTCCAGGCAATGGGACCAAGTTGGCATTAATATGGAACG 1140
Db      1081 CCAGAGCCTCTAGCTCTCTCCAGGCAATGGGACCAAGTTGGCATTAATATGGAACG 1140
QY      1141 GCGGGGTAGATGGAATCTGAGCGAGACAGCTGACTATGTTGGTGAATCAAGGTGAT 1200
Db      1141 GCGGGGTAGATGGAATCTGAGCGAGACAGCTGACTATGTTGGTGAATCAAGGTGAT 1200
QY      1201 CAGTATTTTGGGGAGGCTCTCTGGAGCCAGCCTGCTTCCGCTTGGCCATTG 1260
Db      1201 CAGTATTTTGGGGAGGCTCTCTGGAGCCAGCCTGCTTCCGCTTGGCCATTG 1260
QY      1261 ATGGATATTTGGGCTCGGTTTCCCATCTCTCTGTTGGAAGAGTTGCGCCCGATG 1320
Db      1261 ATGGATATTTGGGCTCGGTTTCCCATCTCTCTGTTGGAAGAGTTGCGCCCGATG 1320
QY      1321 ATGTCCTGTGAGAGAGGGGCTATGGAATACCTGCTCTCTTCACTCAACAGG 1380
Db      1321 ATGTCCTGTGAGAGAGGGGCTATGGAATACCTGCTCTCTTCACTCAACAGG 1380
QY      1381 ACCCTGAAGAGCCTATGAGAGAGAGCTGCTCTGGGGGCTCGGACCGGAGACTCA 1440
Db      1381 ACCCTGAAGAGCCTATGAGAGAGAGCTGCTCTGGGGGCTCGGACCGGAGACTCA 1440
QY      1441 TCCCAACCCCTACCTCTGTCAGTACAGGCTCCCTGCTACTGAGAGATCCACATGAGC 1500
Db      1441 TCCCAACCCCTACCTCTGTCAGTACAGGCTCCCTGCTACTGAGAGATCCACATGAGC 1500
QY      1501 GTGTGAAGTGGGGCCAGAGGCTGACTCTGTGCTGCTGCTGCTGCTGCTGCTGATA 1560
Db      1501 GTGTGAAGTGGGGCCAGAGGCTGACTCTGTGCTGCTGCTGCTGCTGCTGCTGATA 1560
QY      1561 CGGCGACGCTCCCTCATACAGAGACCCACTGAGAGATCCGGGCTCTGATGAGCATG 1620
Db      1561 CGGCGACGCTCCCTCATACAGAGACCCACTGAGAGATCCGGGCTCTGATGAGCATG 1620
QY      1621 GGGGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
Db      1621 GGGGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
QY      1681 CCGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1740
Db      1681 CCGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1740
QY      1741 TCCAGACTACTGGAATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
Db      1741 TCCAGACTACTGGAATGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
QY      1801 CTCCGCTGCAAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1860
Db      1801 CTCCGCTGCAAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1860
QY      1861 TCTTGAACCGGGGAGATGAAGAGAGCGCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
Db      1861 TCTTGAACCGGGGAGATGAAGAGAGCGCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920
QY      1921 GCGAGCGGAGCTCTGATGGGAGAGACTGCGAGGGCGAGTTCCCGGGGTGAGCGCCAA 1980

```

```

Db      1921 GCGAGCGGAGCTCGGATGGGGAGAGACTGCGCAGCGCGAGTTCCCGGCTGACGCCAA 1980
QY      1981 GTGAAGCGCATGCGCAGCGGGTGTGCGGAGGCTCTGCTACCAATAAAATCCACTAT 2040
Db      1981 GTGAAGCGCATGCGCAGCGGGTGTGCGGAGGCTCTGCTACCAATAAAATCCACTAT 2040
QY      2041 TTCCATTGAAAAA 2060
Db      2041 TTCCATTGAAAAA 2060

RESULT 3
AAV27038
ID AAV27038 standard; DNA; 1910 BP.
XX
AC AAV27038;
XX
DT 26-OCT-1998 (first entry)
XX
DE Human napsin B cDNA.
XX
KW Napsin B; splicing; clone; screening; human liver cDNA library;
KW aspartic protease; N-terminal; C-terminal; genomic clone; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 526..1788
FT /tag= "a
FT /product= "napsin B protein"
XX
PD WO9822597-A2.
XX
PD 28-MAY-1998.
XX
PF 20-NOV-1997; 97WO-US21684.
XX
PR 09-MAY-1997; 97US-0046126.
PR 20-NOV-1996; 96US-0031196.
XX
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX
PI Keolsch G, Lin X, Tang JUN;
XX
DR WPI; 1998-312482/27.
XX
DR P-PSDB; AAM54878.
XX
PT New isolated aspartic protease, napsin, from human liver.
XX
PS potentially useful for, e.g. diagnosis and treatment of disease
XX
PS Claim 6; Figure 4; 24pp; English.
XX
CC The present sequence represents the human napsin B cDNA. The N-terminus
CC of this cDNA was obtained by splicing together isolated napsin cDNA
CC clones, which had been found by screening a human liver cDNA library,
CC whereas the C-terminus was obtained by using genomic clones. Napsin B is
CC an aspartic protease which was isolated from human liver.
XX
SQ Sequence 1910 BP; 437 A; 538 C; 522 G; 412 T; 1 other;

Query Match 65.9%; Score 1356.8; DB 19; Length 1910;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1358; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 701 GTCCCGCAGCATGCTCCACACCGCTGCTGCAACCCCTCTGCTGCTGCTGCTGCTGCT 760
Db 516 GTCCCGCAGCATGCTCCACACCGCTGCTGCAACCCCTCTGCTGCTGCTGCTGCTGCT 575
QY 761 GAATGTGAGCCTTCCGCGGCAACATGATCGGATCCCTTCATCGATGATCAACCTGG 820
Db 576 GAATGTGAGCCTTCCGCGGCAACATGATCGGATCCCTTCATCGATGATCAACCTGG 635
QY 821 AGCGAGACCTGAACTACTGAGGGGATGAGAGAACAGCAGAGCTCCCAAGTTGGG 880

```



```

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db ACAGAGAGTCTGAACCTACTGAGGGGATGAGAGAAACACAGAGCTCCCAATTTGGG 695
OY GGGCCCATCCCTGGGGACAAGCCATCTTGTAACCTCTGCAACTACAGAGATGTGA 940
Db GGGCCCATCCCTGGGGACAAGCCATTTTGTAACCTCTGCAACTACAGAGATGTGA 755
OY GTATTTTGGGAAATTTGGGCTGGGAAGCCCTCCACAAACCTTCACTGTTGCTTTGACAC 1000
Db GTATTTTGGGAAATTTGGGCTGGGAAGCCCTCCACAAACCTTCACTGTTGCTTTGACAC 815
OY TGGCTCCCTCCCAATCTCTGGGCTCCGCTCCAGAGATGCCACTTCTCACTGTTGCTTTG 1060
Db TGGCTCCCTCCCAATCTCTGGGCTCCGCTCCAGAGATGCCACTTCTCACTGTTGCTTTG 875
OY GTTACACACGAGATTTGATTTCCCAAAAGCCTTAGCTCTTCCAGGCGCAATGGGACCAAGTT 1120
Db GTTACACACGAGATTTGATTTCCCAAAAGCCTTAGCTCTTCCAGGCGCAATGGGACCAAGTT 935
OY TGGCATTCATATGGAAGTGGGGGGTATGGAATCTTGAGCGAGACAAAGCTGACTAT 1180
Db TGGCATTCATATGGAAGTGGGGGGTATGGAATCTTGAGCGAGACAAAGCTGACTAT 995
OY TGGTGGAATCAAGGCTGATAGTATTTTGGGGAGGCTCTCTGGGAGCCAGCTGCT 1240
Db TGGTGGAATCAAGGCTGATAGTATTTTGGGGAGGCTCTCTGGGAGCCAGCTGCT 1055
OY CTTCGCTTTTCCCATTTTGAATGGGATATTTGGGCTCTGCTTTCCATTTCTGTGTGA 1300
Db CTTCGCTTTTCCCATTTTGAATGGGATATTTGGGCTCTGCTTTCCATTTCTGTGTGA 1115
OY AGAGATTCGAGCCCGGATGATGTAAGTGTGAGAGAGAGGAGGCTATGATTAAGCTGTCTT 1360
Db AGAGATTCGAGCCCGGATGATGTAAGTGTGAGAGAGAGGAGGCTATGATTAAGCTGTCTT 1175
OY CTCTTTTAACTCAACAGGAGCCCTGGAAGAGCTGATGAGAGAGAGCTGTCTGGGGGG 1420
Db CTCTTTTAACTCAACAGGAGCCCTGGAAGAGCTGATGAGAGAGAGCTGTCTGGGGGG 1235
OY CTGCGACCCGGCACACTATACCTCCACCCCTCACTTCTGCGACAGTCAAGTCTGCTCA 1480
Db CTGCGACCCGGCACACTATACCTCCACCCCTCACTTCTGCGACAGTCAAGTCTGCTCA 1295
OY CTGCGACATCCACATGAGAGCTGTGAGAGTGGGGCCAGGCGCTGACTCTGTGCCAAGGG 1540
Db CTGCGACATCCACATGAGAGCTGTGAGAGTGGGGCCAGGCGCTGACTCTGTGCCAAGGG 1355
OY CTGTGCTGCCATCCCTGATACGGGACGCTCCCTCATCAACAGAGACCACTGAGAGATCCG 1600
Db CTGTGCTGCCATCCCTGATACGGGACGCTCCCTCATCAACAGAGACCACTGAGAGATCCG 1415
OY GGGCCCTGATGAGAGATTTGGGGGAATCCCTTGTGCTGGGAGTACATCATCTGTG 1660
Db GGGCCCTGATGAGAGATTTGGGGGAATCCCTTGTGCTGGGAGTACATCATCTGTG 1475
OY CTGCGAAATCCCAAAAGCTCCCGCAGTCTCTCTTCTTGGGGGGGCTGGTTAACTT 1720
Db CTGCGAAATCCCAAAAGCTCCCGCAGTCTCTCTTCTTGGGGGGGCTGGTTAACTT 1535
OY CACGGCCCATATGATACGATACCAAGTCACTCACTCACTCACTCACTCACTCACTCACT 1780
Db CACGGCCCATATGATACGATACCAAGTCACTCACTCACTCACTCACTCACTCACTCACT 1595
OY TTTTCAGGCGCTGATGTCCTTCCGCTGACAGGAGGCTTCTTGATCTCTGAGTGAAGTCT 1840
Db TTTTCAGGCGCTGATGTCCTTCCGCTGACAGGAGGCTTCTTGATCTCTGAGTGAAGTCT 1655
OY CTGCGGAGATGATGCGCTTCTTGCACCGGGGAGACATGAAGACAGCGCCGGGGTGG 1900
Db CTGCGGAGATGATGCGCTTCTTGCACCGGGGAGACATGAAGACAGCGCCGGGGTGG 1655
OY CTGCGGAGATGATGCGCTTCTTGCACCGGGGAGACATGAAGACAGCGCCGGGGTGG 1715
Db CTGCGGAGATGATGCGCTTCTTGCACCGGGGAGACATGAAGACAGCGCCGGGGTGG 1901
OY CTTGGCGGGCGCTGCCACTCCCGGAGCGGAGCTCGGATGGGAGAGACTGCCAGGCGCA 1960

```

```

Db 1716 CTTGGCGGGCGCTCGCACTCCGCGAGCGGACCTCGGATGGGAGAGACTCCGACGGCA 1775
OY 1961 GTTCCCGGGGTGACGCGCCCAAGTGAAGCGCATGCGAGCGGGGTGCGGGAGATCTGCT 2020
Db 1776 GTTCCCGGGGTGACGCGCCCAAGTGAAGCGCATGCGAGCGGGGTGCGGGAGATCTGCT 1835
OY 2021 ACCCAGTAAAAATCCACTATTTTCATTTGAAAAA 2060
Db 1836 ACCCAGTAAAAATCCACTATTTTCATTTGAAAAA 1875

RESULT 4
AAK9391
ID AAK9391 standard; DNA; 1425 BP.
XX
AC AAK9391;
XX
DI 27-JUN-2002 (first entry)
XX
DE DNA of NAPI from aspartyl protease-related family.
XX
KW Neuropeptide; neuropeptide; transgenic fly; Alzheimer's disease; Abeta;
KW amyloid precursor protein; tissue-specific expression control; human APP;
KW APP pathway modulator; gene therapy; gene; ds.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT 15..1316
FT CDS /*tag= "Protein of NAPI from an aspartyl protease-
FT related family"
FT /*note= "No start codon"
PN MO200226820-A2.
XX
PD 04-APR-2002.
XX
PF 01-OCT-2001; 2001WO-EP11345.
XX
PR 29-SEP-2000; 2000US-236893P.
PR 14-JUN-2001; 2001US-298309P.
XX
PA (NOVS ) NOVARTIS AG.
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERM GES MBH.
PI Cohen D, Dengler UJ, Finelli AL, Freuler F, Konsolaki M;
PI Reinhardt MWH, Zusan S;
PI WPI; 2002-315796/35.
DR P-PSDB; AAO20497.
XX
PS The invention relates to a transgenic fly whose genome comprises DNA
XX encoding a polypeptide having the Abeta portion of human amyloid
XX precursor protein (APP), fused to a signal sequence. The DNA sequence
XX encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in
XX the specification. The DNA sequence is operably linked to a tissue-
XX specific expression control sequence. Expression of the sequence gives
XX the fly an altered phenotype. The purpose of the invention is for
XX identifying agents that inhibit or promote the expression and/or function
XX of genes or encoded polypeptides which modify the APP pathway. The agent
XX is a compound, triple helix DNA, antisense oligonucleotide, double
XX stranded RNA molecule, ribozyme, or particularly an antibody. It is used
XX to treat conditions such as Alzheimer's disease. The agent can be used as
XX an APP pathway modulator or in gene therapy. This polynucleotide sequence
XX represents the DNA of the APP related NAPI from the aspartyl protease-
XX related family.

```







		/transl_except=	(pos:1325..1327,aa:Ala)	
Ft	Pt	/transl_except-	(pos:1328..1330,aa:Ser)	
Ft	Pt	/transl_except-	(pos:1331..1333,aa:Ala)	
Ft	Pt	/transl_except-	(pos:1334..1336,aa:Thr)	
Ft	Pt	/transl_except-	(pos:1337..1339,aa:Gln)	
Ft	Pt	/note=-	"no stop codon given; the CDS is marked according to the protein given in the specification but could decode for its full length"	
Ft	Pt			
Xx	Pn			
Xx	Pn	MO98II236-AL.		
Xx	Pd			
Xx	Pd	19-MAR-1998.		
Xx	Pf			
Xx	Pf	09-SEP-1997;	97WO-GB02426.	
Xx	Pr			
Xx	Pr	11-SEP-1996;	96GB-0018966.	
Pa	Pa	(SMIK ) SMITHKLINE BEECHAM PLC.		
Pa	Pa	(UYMA-) UNIV WALES.		
Xx	Pi	Hill J, Kay J, Powell D;		
Xx	Pi			
Xx	Dk	WPI; 1998-207396/18.		
Xx	Dr	P-PSDB; AAM57042.		
Pt	Pt	Human aspartic protease and related DNA - which may be involved in processing of endothelin and pro-opiomelanocortin pro-hormone(s)		
Ps	Ps	Claim 2; Page 20; 32pp; English.		
Xx	Cc	The present sequence encodes a human aspartic protease. The present invention describes novel human aspartic proteases and also ESTs from human cDNA libraries having partial DNA sequences which encode an aspartic protease. Compounds which inhibit aspartic protease, especially antibodies can be used in therapy where needed. The protease can also be used in therapy where needed. Important functions of aspartic proteases are the processing of endothelin and pro-opiomelanocortin prohormones. They may also be involved in the processing of serum amyloid A protein.		
Sq	Sq	Sequence 1375 BP; 255 A; 419 C; 396 G; 305 T; 0 other;		
		Query Match	55.9%; Score 1151.8; DB 19; Length 1375; Best Local Similarity 90.8%; Pred. No. 5.4e-309; Matches 1238; Conservative 0; Mismatches 122; Indels 3; Gaps 14;	
Oy	Oy	CGCGTCCGCACAGATGTCTCCACCACGCCGTCGTCAACCCCTGGTGCTGTCGCCCT	757	
Db	Db	13 CGGCTCCCCAAGCATGTCTCCACCACGCCCTCTGTACTTTGCTGCTGCTGCTCT	72	
Oy	Oy	758 GCTGAATGTGGAGCCTTCCGGGGCACACTGATCCGATCCCCTCTTCATGAGTCCAAC	817	
Db	Db	73 GCTGAATGTGGAGCCTGTGGGGCACATGATCCGATCCCTCTTCATGAGTCCAAC	132	
Oy	Oy	818 TGAGACGAGAGACCTGAACTACTGAGGGATGAGAGAACACAGAGAGCTCCCAAGTT	877	
Db	Db	133 TGGACGAGAGAGCCCTGAACTACTGAGGGATGAGAGAAACAAGAGAGCTCCCAAGTT	192	
Oy	Oy	878 GGGGGCCCAATCCCTGGGGACAAGCCCATPTTGTAATTCTCTGCAACTACAGGAGAT	937	
Db	Db	193 GGGGGCCCAATCCCTGGGGACAAGCCCTGCTCGGTACTCTCTCCAAATTCGTGAATGC	252	
Oy	Oy	938 GCAGTATTTTTGGGAAAATTGGGCTTGGGAACGCTCCACAAAACTTCACTGTGGCTTTGA	997	
Db	Db	253 CCAGTATTTTTGGGAAAATTGGGCTTGGGAACGCTCCACAAAACTTCACTGTGGCTTTGA	312	
Oy	Oy	998 CACTGCGCTCTCAATCTCTGGGTCGGCTCCAGAGATGCACTTCTTCACTGTGGCTGTG	1057	
Db	Db	313 CACTGCGCTCTCAATCTCTGGGTCGGCTCCAGAGATGCACTTCTTCACTGTGGCTGTG	372	
Oy	Oy	1058 CTGGTTACACACAGGATTTGATTCCAAAGCCTCTAGAAGCTTCACAGGCGCATTTGGACCAA	1117	
Db	Db	373 CTGGTTACACACAGGATTTGATTCCAAAGCCTCTAGAAGCTTCACAGGCGCATTTGGACCAA	432	

OY	1118	GTGTGGCAATCAATATGGAACACTGGGGGGGTAGATGGAATCCTGAGCGAGACAAAGCTGAC	1177
Db	433	GTGTGGCAATTCAGTATGGAACATGGGGGGGTAGATGGAATCCTGATAGGCAAGACTGAC	492
OY	1178	TATTGGTGGAAATCAAGGGTGCATCAGTATTTTGGGGAGAGCCTCTGGGAGCCACGCT	1237
Db	493	TATTGGTGGAAATCAAGGGTGCATCCGTGATTTTGGGGAAAGCTCTGGGAAATCCAGCT	552
OY	1238	GGTCTTGGCTTTTGGCCCATTTTGTATGGGAAATTTGGGGCCTGGTTTTTCCCATTTCTGTCTGT	1297
Db	553	GGTCTTCACTGTTTTCCGGCCCGCATGGGAAATTTTGGGCTGGTTTTTCCCATTTCTGTCTGT	612
OY	1298	GGAAGGAGTTTGGGCCCCCGATGATGTACTGTGTGTAGACAGAGGCTATTGGATTAAGCTGT	1357
Db	613	GGAAGGAGTTTGGGCCCCCGCTGTGATGTACTGTGTAGACAGAGGCGCTATTGGATTAAGCTGT	672
OY	1358	CTTCTCCGTTTACCTCAACAGGGACCGTGAAAGACCTGATGGAGAGAGGCTGGTCCGGG	1417
Db	673	CTTCTCCGTTTACTTCAACAGGGACCGCTGAAGTGGCTGATGAGAGAGAGCTGGTCCGGG	732
OY	1418	GGGCTCGGACCCGGGACACACTACATCCACCCCTCACTTCGTGCAGTCAAGCGTCCCTGC	1477
Db	733	GGGCTCGAAGCCGGGACACACTACATCCACCCCTCACTTCGTGCAGTCAAGCTCCCGC	792
OY	1478	CTACTGCGAGATCCACATGAGAGCGTGTGAAGGTGGGCCCAAGGCTGACTCTCTGTGCCAA	1537
Db	793	CTACTGCGAGATCCACATGAGAGCGTGTGAAGGTGGGCTCAAGGCTGACTCTCTGTGCCAA	852
OY	1538	GGGCTGTGCTGCCATCCTCGGATTAAGGGGACGTCCTCCCTATCAACAGACCCCATGTAGAGAT	1597
Db	853	GGGCTGTGCTGCCATCCTCGGATTAAGGACACACGCTGATCTGTAGAGCCCATGTAGAGAT	912
OY	1598	CCGGGCCCCCTGATCGACAGCATTTGGGGGAAATCCCTTCTGTGGCTGGGGAGTACATACCT	1657
Db	913	CCGGGCCCCCTGATCGACAGCATTTGGGGGAAATCCCTTCTGTGGCTGGGGAGTACATACCG	972
OY	1658	GTGCTCGGAAATCCCAAGACTCCCGCAGTCTCCTTCTTGGGGGGGTCTGTGTAA	1717
Db	973	GTGCTCGAAGAAATCCCAAGACTCCCGCAGTCTCCTTCTTGGGGGGGTCTGTGTAA	1032
OY	1718	CCCTACGGGCCCATATTACCTGCATCCACAGACTACACTCGAAATGGGCTCCGCCCTCTGTCTC	1777
Db	1033	TCTACGGGCCCATGAGATTACGTCAATCCAACTTGTGTCAAGGTGACGTCGCCCTCTGTCTC	1092
OY	1778	CGGTTTCCAGGCCCCGATGTCCTCTCCGCTCGACAGGGGCCCTTTGGATTCCTCGGTGAGCT	1837
Db	1093	CGGCTTCCGGGCTCTTGGACATCGCTTCGCTCTCCAGTACTGTGTGATCTCTCGGCGAGCT	1152
OY	1838	CTTCTTGGGGAGTATGTGGGCCGTCTTCGACAGCGGGGACATGAAGAGACAGCGCCGAGT	1897
Db	1153	TTTCTTGGGGGCGTATGTGACCGTCTTCGACAGCGGGGACATGAAGAGCGCGACGAGT	1212
OY	1898	GGGCTGTGGCGCGCGCTGCACTCGCGGAGCGGACCTGGATGGGAGACAGACTGCGCAGC	1957
Db	1213	GGGACTGTGCGCGCGCTGCACTCGCGGAGCGGACCTGGGAAAGCGCGAGACCGCGCAGGC	1272
OY	1958	GCACTTCCCCGGGGTGAAGCCCAAGTGAAGGAGCATGCGAGCGGGGTGGTGGCGGAGGTCT	2017
Db	1273	GCACTTCCCCGGGGTGGCGGCCCAAGTGAAGGAGCATGCGAGCGGGGTAGCC--GAGCTAGC	1329
OY	2018	GCTACCCAGTAAAAATCCACTATTTCATTTGAAAAAATAAAAA 2060	
Db	1330	GCTACCTGATAAAAATCCAAATATTTCATTTGAAAAAATAAAAA 1372	
RESULT 8			
AAV27036			
AAV27036 standard; DNA; 1353 BP.			
AC	AAV27036;		
XX			
DT	26-Oct-1998 (first entry)		
XX			

DE	Human napsin A cDNA.
xx	
KW	Napsin A; splicing; clone; screening; human liver cDNA library;
KM	aspartic protease; ss.
xx	
OS	Homo sapiens.
xx	
FT	Key Location/Qualifiers
FT	CDS 1..1353
FT	/tag- a
FT	/product= "napsin A protein"
FT	/note= "no stop codon at 3' end"
xx	
PN	WO9822597-A2.
xx	
PD	28-MAY-1998.
xx	
PF	20-NOV-1997; 97MO-US21684.
xx	
PR	09-MAY-1997; 97US-0046126.
PR	20-NOV-1996; 96US-0031196.
xx	
PA	(OKLA-) OKLAHOMA MEDICAL RES FOUND.
xx	
PL	Keolsch G, Lin X, Tang JTN;
xx	
DR	WPI; 1998-312482/27.
xx	P-PSDB; AAM54877.
xx	
PT	New isolated aspartic protease, napsin, from human liver -
xx	potentially useful for, e.g. diagnosis and treatment of disease
xx	
PS	Claim 4; Figure 1; 24pp; English.
xx	
CC	The present sequence represents the human napsin A cDNA, which does not
CC	contain an in-frame stop codon in the entire coding region. This
CC	sequence was obtained by splicing together isolated napsin cDNA clones,
CC	which had been found by screening a human liver cDNA library. Napsin A
CC	is an aspartic protease which was isolated from human liver.
xx	
SQ	Sequence 1353 BP; 255 A; 408 C; 389 G; 301 T; 0 other;
	Query Match 55.4%; Score 1142; DB 19; Length 1353;
	Best Local Similarity 90.9%; Pred. No. 2.8e-306;
	Matches 1227; Conservative 0; Mismatches 120; Indels 3; Gaps 1;
OY	711 ATGTCCTCACACCGCTGCTCAACCCCCTGTCTGCTGCTGCTGCTGTAATGTGGAG 770
Db	1 ATGTCCTCACACCGCTGCTGCTAACCCTTGCTGCTGCTGCTGCTGCTGAATGTGGAG 60
OY	771 CCTTCCGGGGGCACACTGATCCGCCATCCCTTTTCATGCAATGCCACTTGGACGCGAGACC 830
Db	61 CCTGTGGGGGCACACTGATCCGCCATCCCTTTTCATGCAATGCCACTTGGACGCGAGACC 120
OY	831 CTGAACCTACTGAGGGGATGAGAGAAACACAGAGAGCTCCCCAATTGGGGGCCCATCC 890
Db	121 CTGAACCTACTGAGGGGATGAGAGAAACACAGAGAGCTCCCCAATTGGGGGCCCATCC 180
OY	891 CCTGGGGACAACGCCATCTTGCTGACTCTTCGAACTCAGAGGATGTCAGATATTTTGGG 950
Db	181 CCTGGGGACAACGCCATCTTGCTGACTCTTCGAAATTCCTGGAGTCCAGATATTTTGGG 240
OY	951 GAATTTGGGGCTGGGGAAGCTCTCAACAAAATTCATGTGTGCTTGGACTGAGCGCTCCGCC 1010
Db	241 GAATTTGGGGCTGGGGAAGCTCTTCACAAACTTCACTGTGGCTTTGACACTGCTCTCTCC 300
OY	1011 AATCTCTGGTCCGCTCCAGAGATGACACTTCTTCACTGTGTGCCCTGTGTTACACCAAC 1070
Db	301 AATCTCTGGTCCGCTCCAGAGATGACACTTCTTCACTGTGTGCCCTGTGTTACACCAAC 360
OY	1071 CGATTGTATCCCAAAGCCTCTAGCTCTCTCCACAGGCATGGGACCAATGTTGCCATTCAA 1130
Db	361 CGTTTCATATCCCAAAGCCTCTAGCTCTCTCCAAAGCCCACTGGGACCAATGTTGCCATTGAG 420

QY	1131	TATGAACTGGGGGGAGATGAAATCTGTGACGAGGCAAGGCACTATTGGTGAATC	1190
Db	421	TATGGAACTGGGGGGATGATGAATCTGTGATGAGGCAAGGCACTATTGGTGAATC	480
QY	1191	AAGGGTGCATCAGTATTTTCGGGGAGAGCTCTCTGGAGGCCACCGCTGTTCGCTTTT	1250
Db	481	AAGGGTGCATCAGTATTTTCGGGGAGAGCTCTGTGGAGATCAGCGTGTTCAGTGT	540
QY	1251	GCCCATTTTGAATGGGATATTGGCCCTCGGTTTCCATTTCTGTGTGGAAGAGTTCCG	1310
Db	541	TCCCGCCCCGATGGGAATATTGGGCTCGGTTTCCATTTCTGTGTGGAAGAGTTCCG	600
QY	1311	CCCCGATGATGATGACTGGTGGAGCAGGGGCTATTGGATAGACCTGTCTTCCTTTTAC	1370
Db	601	CCCCCGCTGGATGATGATGATGGAGCAGGGGCTATTGGATAGACCTGTCTTCCTTTTAC	660
QY	1371	CTCAACAGGAGCCCTGAAAGACCTGATGAGAGAGCTGTGTCTGGGGGGGCTCGGACCG	1430
Db	661	TTCAACAGGAGCCCTGAAAGTGGTGTGATGAGAGAGCGTGTGTCTGGGGGGGCTCAGACCG	720
QY	1431	GCACACTATATCCCAACCCCTTACCTTGTGCTGCACGTCAAGGTTCCTGCTACTGCAATC	1490
Db	721	GCACACTATATCCCAACCCCTTACCTTGTGCTGCACGTCAAGGTTCCTGCTACTGCAATC	780
QY	1491	CACATGAGAGCTGTGAGAGTGGGGCCAGAGGCTGTACTCTGTGCAAGAGGCTGTGCTGCC	1550
Db	781	CACATGAGAGCTGTGAGAGTGGGGCCAGAGGCTGTACTCTGTGCAAGAGGCTGTGCTGCC	840
QY	1551	ATCTGTGATACGGGACGCTCCCTCATATCAGAGGACCCACTGAGAGATCCGGGCCCTGCAT	1610
Db	841	ATCTGTGATACGGGACGACCTGTGATCATGTAGAGCCCACTGAGAGATCCGGGCCCTGCAT	900
QY	1611	GCAGGCATTTGGGGGAATCCCTTGTGCTGGCTGGGAGATACATATCTGTGTCCGGAATC	1670
Db	901	GCAGGCATTTGGGGGAATCCCTTGTGCTGGCTGGGAGATACATATCTGTGTCCGGAATC	960
QY	1671	CCAAAGTCCCCGAGAGTCTCCTCTCTTGGGGGGGTCTGTTTAACTTCACGACCCTAT	1730
Db	961	CCAAAGTCCCCGAGAGTCTCCTCTCTTGGGGGGGTCTGTTTAACTTCACGACCCTAG	1020
QY	1731	GATTACGTATCAGACTACTTCGAAATGGGCTCGGCTGTGCTGTTCGGTTCCAGGCC	1790
Db	1021	GATTACGTATCAGACTTTGCTCAGGGTACGTCGCGCTCTCTGTTCGGTTCCAGGCC	1080
QY	1791	CTGATGTGCTCCGCGCTGACAGGGGCCCTTGTGAAATCCCGGTGAGAGCTTCTTGGGGACG	1850
Db	1081	TTGGGCAATGCTTTCGCTCTCCAGTACTCTGTGATCTCTGCGCGAGCTTTTCTTGGGGGCG	1140
QY	1851	TATGAGCGCTTCTGACACGCGGGGACATGAAAGACAGCGCCGCGGTGGGCTTGCGCGC	1910
Db	1141	TATGAGCACTGCTTCTGACACGCGGGGACATGAAAGCGCGCGACGAGTGGGACTGGCGGC	1200
QY	1911	GCTGCACTCGCGAGGCGGAGCTCGGATGGGAGAGACTGCGCAGGCGCACTTCCCGGG	1970
Db	1201	GCTGCGCTCTCGCGAGGCGGAGCTCGGAGAGGCGCGCAGGCGCGCACTTACCGCGGG	1260
QY	1971	TGAGCGCCCAAGGAGAGCGCATGCGGAGGGGGGTGCGCGGAGAGGTCGTACCCAGTAA	2030
Db	1261	TGCGCGCCCAAGGATGCGCATGCGCACCGGGGTAGCC---GAGCTAGCGCTACTCAGTAA	1317
QY	2031	AATCCACTATTTCCATTGAAAAAATAAAAA 2060	
Db	1318	AATCCAAATATTTCCATTGAAAAAATAAAAA 1347	
RESULT 9			
AAZ50232			
ID AAZ50232 standard; cDNA; 1329 BP.			
XX AAZ50232;			
DT 18-MAY-2000 (first entry)			





Db 1097 CCGGCTCCGGGCGCTTGACATCGCTTCCTCCAGTACTGTGTGATTCCTCGCGACG 1156  
 QY 1837 TCTTCTTGAGGACGATGTGGCCGCTTCGACCGGGGACATGAAGACGACGCCGG 1896  
 Db 1157 TTTTCTTGAGGACGATGTGGCCGCTTCGACCGGGGACATGAAGACGACGCCGG 1216  
 QY 1897 TGGGCTTGAGGACGCTTCGACCGGGGACGCTTCGATGGGGAGAGACTGCGCAGG 1956  
 Db 1217 TGGGACTGGCGCGCTCGCTCGCGGAGCGAGACTGGGAAGGCGGAGACCGCGCAGG 1276  
 QY 1957 CGCAGTCCCGGGGACGCGGACGATGAAGGACGATGGCGACGGGTGTCCG 2009  
 Db 1277 CGCAGTACCGGCGCTCGCGGACGATGCGCAGTGGCGACCGGGGTAGCAGAG 1329  
 RESULT 10  
 AAD38693  
 ID AAD38693 standard; cDNA; 1370 BP.  
 AC AAD38693;  
 XX  
 DT 23-SEP-2002 (first entry)  
 DE Human LP191 secreted protein encoding cDNA.  
 KW Human; secreted protein; atherosclerosis; Alzheimer's disease; LP191;  
 KW diabetic retinopathy; severe combined immunodeficiency; pancreatitis;  
 KW rheumatoid arthritis; colorectal adenoma; hemolytic anaemia; cancer;  
 KW reperfusion injury; arteriosclerosis; wound healing; transgenic animal;  
 KW gene therapy; neoplasm; transgenic; psoriasis; ischemia; carcinoma;  
 KW gene; ss.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 95..409  
 FT /tag- a  
 FT /product- "Human LP191 secreted protein"  
 FT sig\_peptide 95..160  
 FT /tag- b  
 FT mat\_peptide 161..406  
 FT /tag- c  
 FT /product- "Mature human LP191 secreted protein"  
 XX  
 PN WO200226801-A2.  
 XX  
 PD 04-APR-2002.  
 XX  
 PR 14-SEP-2001; 2001WO-US26026.  
 XX  
 PA 28-SEP-2000; 2000US-236088P.  
 XX  
 PA (ELIL ) LILLY & CO ELI.  
 XX  
 PI Su EW, Wang H;  
 XX  
 DR WPI; 2002-471259/50.  
 DR P-PSDB; AAE23978.  
 XX  
 PT Novel proteins and polynucleotides of secreted proteins useful for  
 PT treating various diseases e.g. Rheumatoid arthritis, cancer, psoriasis,  
 PT diabetic retinopathy, arteriosclerosis, ischemia or reperfusion injury  
 PT  
 PS Claim 1: Page 107-108; 145pp; English.  
 XX  
 CC The invention relates to human secreted polypeptides designated LP095,  
 CC LP191, LP217, LP220, LP221, LP222, LP229, LP237 or LP238 and nucleic  
 CC acid molecules encoding such polypeptides. Novel secreted proteins of  
 CC the invention are used for treating diseases such as atherosclerosis,  
 CC Alzheimer's disease, diabetic retinopathy, psoriasis, pancreatitis,  
 CC arteriosclerosis, rheumatoid arthritis, colorectal adenomas, severe  
 CC combined immunodeficiency, ischemia, carcinoma, haemolytic anaemia,

CC reperfusion injury, neoplasms and cancer especially liver cancer. They  
 CC are also used for wound healing. Polynucleotides of the invention can  
 CC be used to generate transgenic animals or knock out animals, which in  
 CC turn, are useful in the development and screening of therapeutically  
 CC useful reagents for use in the treatment of diseases associated with  
 CC LP polypeptide associated activity. They are also used in gene therapy.  
 CC The present sequence is human LP191 secreted protein encoding cDNA.  
 SQ Sequence 1370 BP; 303 A; 401 C; 389 G; 277 T; 0 other;  
 Query Match 53.4%; Score 1100.4; DB 24; Length 1370;  
 Best Local Similarity 90.8%; Pred. No. 1e-294;  
 Matches 1235; Conservative 0; Mismatches 1; Indels 124; Gaps 1;  
 QY 701 GTCCCAAGCATGTCTCCACACCGCTGCTGCAACCCCTGCTGCTGCTGCTGCT 760  
 Db 85 GTCCCAAGCATGTCTCCACACCGCTGCTGCAACCCCTGCTGCTGCTGCTGCT 144  
 QY 761 GAATGTGAGGCTTCGCGGGGCGACACTGATCCGATCCCTTCATGAGTCAACCTG 820  
 Db 145 GAATGTGAGGCTTCGCGGGGCGACACTGATCCGATCCCTTCATGAGTCAACCTG 204  
 QY 821 ACGGAGACCTGAACTGACCTGAGGGATGAGAGAACACAGAGCTCCCAAGTGGG 880  
 Db 205 ACGGAGATCCTGAACTGACCTGAGGGATGAGAGAACACAGAGCTCCCAAGTGGG 264  
 QY 881 GGCCCATCCCTGCGGGGCAAGCCCATCTTGTACTCTCTGCACTACAGAGATGCA 940  
 Db 265 GGCCCATCCCTGCGGGGCAAGCCCATCTTGTACTCTCTGCACTACAGAGATGCA 318  
 QY 941 GTATTTGGGGAATTTGGGCTGGGAGCGCTCCACAAACTTCACTGTGCTTTGACAC 1000  
 Db 319 ----- 318  
 QY 1001 TGGCTCCTCAATCTCTGGTCCGCTCCAGAGATGCCACTTCTCAAGTGTGCTGCTG 1060  
 Db 319 -----TG 320  
 QY 1061 GTTACACACCGATTTGATTCACCAAGCCCTAGCTCTTCAGGACCAATGGACCAAGTT 1120  
 Db 321 GTTACACACCGATTTGATTCACCAAGCCCTAGCTCTTCAGGACCAATGGACCAAGTT 380  
 QY 1121 TGGCATTAATATGAACTGGGCGGTGATGAAATCTGTAGCGAGCAAGCTGACTAT 1180  
 Db 381 TGGCATTAATATGAACTGGGCGGTGATGAAATCTGTAGCGAGCAAGCTGACTAT 440  
 QY 1181 TGGTGAATCAAGGTCATGATGATTTTGGGAGGCTCTTGAGAGCCACGCTGCT 1240  
 Db 441 TGGTGAATCAAGGTCATGATGATTTTGGGAGGCTCTTGAGAGCCACGCTGCT 500  
 QY 1241 CTTCGCTTTGCCCATTTTGTATGGGATATGGGCTCGGTTTCCATTTCTGTGGA 1300  
 Db 501 CTTCGCTTTGCCCATTTTGTATGGGATATGGGCTCGGTTTCCATTTCTGTGGA 560  
 QY 1301 AGGAGTTGGGCGCCGATGATGATCTGTGTGAGAGGCGCTATTTGATAGCTGTCT 1360  
 Db 561 AGGAGTTGGGCGCCGATGATGATCTGTGTGAGAGGCGCTATTTGATAGCTGTCT 620  
 QY 1361 CTTCCTTTACCTCAACAGAGGACCTGAAAGAGCTGATGAGAGAGCTGCTGGGGGG 1420  
 Db 621 CTTCCTTTACCTCAACAGAGGACCTGAAAGAGCTGATGAGAGAGCTGCTGGGGGG 680  
 QY 1421 CTGCGACCCGCGACACTATCATCCACCCCTCACTTCTGTGCAGTCAAGGTCCTGCTA 1480  
 Db 681 CTGCGACCCGCGACACTATCATCCACCCCTCACTTCTGTGCAGTCAAGGTCCTGCTA 740  
 QY 1481 CTGCGAGATCCACATGAGAGCTGTGAAGTGGGCGCCAGAGCTGACTCTGTGCCAAGG 1540  
 Db 741 CTGCGAGATCCACATGAGAGCTGTGAAGTGGGCGCCAGAGCTGACTCTGTGCCAAGG 800  
 QY 1541 CTGTCTCGCATCTCGATACGAGGACGCTCCCTATCAACAGAGCCACTGAGAGATCG 1600  
 Db 801 CTGTCTCGCATCTCGATACGAGGACGCTCCCTATCAACAGAGCCACTGAGAGATCG 860



QY	1601	GGCCCTGATGCACCAATTGGGGGAAATCCCTTCCTGTGCGNCGGAGATCAATCAATCGTGTG	1660		
QY	1601	GGCCCTGATGCACCAATTGGGGGAAATCCCTTCCTGTGCGNCGGAGATCAATCAATCGTGTG <td>1660</td>	1660		
Db	861	GGCCCTGATGCACCAATTGGGGGAAATCCCTTCCTGTGCGNCGGAGATCAATCAATCGTGTG	920		
QY	1661	CTCGGAAATCCCAAGCTCCCGCAGACTCTCTTCCTCTTGGGGGGGCTGGTTAACT	1720		
Db	921	CTCGGAAATCCCAAGCTCCCGCAGACTCTCTTCCTCTTGGGGGGGCTGGTTAACT	980		
QY	1721	CACGGCCCATGATTAAGTCAATCCAGACTCTGAAATGGCGTCCGCTCTGTGTCGG	1780		
Db	981	CACGGCCCATGATTAAGTCAATCCAGACTCTGAAATGGCGTCCGCTCTGTGTCGG	1040		
QY	1781	TTTTCACAGCCCTGGATGTGCCCTCCGCGCTGCAGGGCCCTTCGGAATCCGTTGACGCTT	1840		
Db	1041	TTTTCACAGCCCTGGATGTGCCCTCCGCGCTGCAGGGCCCTTCGGAATCCGTTGACGCTT	1100		
QY	1841	CTTGGGGGACGATGTGGCCCTCTTTCGACCCGCGGGGACATGAAGACAGCCGCCGGTGGG	1900		
Db	1101	CTTGGGGGACGATGTGGCCCTCTTTCGACCCGCGGGGACATGAAGACAGCCGCCGGTGGG	1160		
QY	1901	CTTGGGGGCGGCTGTGCACCTGCGGAGGGGACCTGGATGGGGAAGACTGGCGAGCGCA	1960		
Db	1161	CTTGGGGGCGGCTGTGCACCTGCGGAGGGGACCTGGATGGGGAAGACTGGCGAGCGCA	1220		
QY	1961	GTTTCCCGGGGAGACGCCCAAGTGAAGGCGATGCGCAGCGGGTGGTCGGGGAGTCTGCT	2020		
Db	1221	GTTTCCCGGGGAGACGCCCAAGTGAAGGCGATGCGCAGCGGGTGGTCGGGGAGTCTGCT	1280		
QY	2021	ACCCAGTAAAAATCCACTATTTCATTGTAATGAAAAA 2060			
Db	1281	ACCCAGTAAAAATCCACTATTTCATTGTAATGAAAAA 1320			
RESULT 11					
ID	AA514882	AA514882 standard; cDNA: 1487 BP.			
AC	AA514882;				
XX	20-DEC-2001	(first entry)			
XX	Human cDNA encoding novel human protein NHP #3.				
DE	Human: novel human protein: NHP; ss: antidiabetic; antirheumatic;				
KW	antiarthritic; cytosolic; antiarteriosclerotic; vulnery;				
KW	neuroprotective; nootropic; antiParkinsonian;				
KW	anti-human immunodeficiency virus; antilastemic; vasotropic; cardiant;				
KW	hypertensive; anorectic; antihfertility; neuroleptic; anticonvulsant;				
KW	antimanic; immunosuppressive; cerebroprotective; antimicrobial;				
KW	antiflammatory; antibacterial; antiparasitic; thymimetic;				
KW	immunomodulator; antiseborrheic; dermatological; vasoconstriction;				
KW	gastrointestinal disorder; cardiovascular disorder; hypertension;				
KW	coronary heart disease; arteriosclerosis; anorexia; obesity; bulimia;				
KW	cachexia; male infertility; impotence; testicular cancer; lung tumour;				
KW	hyperproliferative disorder; pulmonary system disorder;				
KW	central nervous system disorder; bone disorder;				
KW	neurodegenerative disease; Alzheimer's disease; Parkinson's disease;				
KW	Huntington's disease; schizophrenia; mania; dementia; paranoia;				
KW	panic disorder; learning disability; amyotrophic lateral sclerosis;				
KW	psychosis; autism; sleep disorder; immune system disorder;				
KW	Hashimoto's thyroiditis; musculo-skeletal system disorders;				
KW	multiple sclerosis; ischaemic brain injury; stroke; infectious disease;				
KW	diabetes mellitus; immunological disorder; asthma; AIDS;				
KW	acquired immunodeficient syndrome; leukaemia; Rheumatoid arthritis;				
KW	inflammatory bowel disease; sepsis; acne; psoriasis; lupus erythematosus;				
KW	neural system disorder; respiratory disorder; olfactory disorder;				
XX	wound healing.				
OS	Homo sapiens.				
XX					
XX					
Key	Location/Qualifiers				
FT	CDS	213..1385			

	FT	/*tag=	a
	FT	/product=	"NHP #3"
XX	MO200174896-A1.		
XX	11-OCT-2001.		
XX	02-APR-2001; 2001WO-US10542.		
XX	03-APR-2000; 2000US-19411BP.		
XX	29-SEP-2000; 2000US-236384P.		
XX	(HUMA-) HUMAN GENOME SCI INC.		
XX	Moore PA, M J, Soppet DR, Coleman TA, Gentz RL, Endress GA;		
XX	Ll Y, Dillon PJ;		
DR	WPI; 2001-626394/72.		
XX	P-PSDB; AAU09094.		
PT	New human proteins, useful for diagnosing, treating, preventing and/or		
PT	prognosing disorders related to the proteins, including cardiovascular		
PT	disorders, autoimmune disorders and reproductive disorders -		
PS	Claim 1; Page 293; 318pp; English.		
CC	The invention relates to novel human proteins (NHP) and the		
CC	nucleic acids that encode them and antibodies raised against them.		
CC	The proteins, antibodies and nucleic acids are useful in the diagnosis,		
CC	prognosis, prevention and/or treatment or diseases and/or disorders		
CC	involving vasoconstriction, gastrointestinal disorders, cardiovascular		
CC	disorders (e.g. hypertension, erectile dysfunction, high blood pressure,		
CC	coronary heart disease and arteriosclerosis), anorexia, obesity, bulimia,		
CC	cachexia, disorders of small intestine, disorders of reproductive system		
CC	(e.g. male infertility and/or impotence), testicular cancer, lung tumours		
CC	and other hyperproliferative disorders, disorders of pulmonary system,		
CC	central nervous system disorders, bone disorders, neurodegenerative		
CC	diseases and behavioural disorders (e.g. Alzheimer's disease, Parkinson's		
CC	disease, Huntington's disease, schizophrenia, mania, dementia, paranoia,		
CC	panic disorder, learning disabilities, amyotrophic lateral sclerosis,		
CC	psychoses, autism, sleep disorders), immune system disorders (e.g.		
CC	Hashimoto's thyroiditis), renal and musculo-skeletal system disorders,		
CC	central nervous system disorders (e.g. multiple sclerosis, ischemic		
CC	brain injury and/or stroke), infectious diseases, diabetes mellitus,		
CC	immunological disorders (e.g. asthma, acquired immunodeficient syndrome		
CC	(AIDS), leukaemia, rheumatoid arthritis, inflammatory bowel disease,		
CC	sepsis, acne, psoriasis and lupus erythematosus), neural system		
CC	disorders, respiratory disorders, olfactory disorders and wound		
CC	healing. The present sequence encodes an NHP of the invention.		
XX	Sequence 1487 BP; 305 A; 450 C; 420 G; 312 T; 0 other:		
Query Match	47.8%; Score 984; DB 22; Length 1487;		
Best Local Similarity	88.6%; Pred. No. 2.le-262;		
Matches 1210; Conservative	0; Mismatches 25; Indels 131; Gaps 8;		
OY	693 CAGAACGCGTCCCACGAGATGTCTCACACCOCGTCTGCACAACCCCTGCTGCTGCTG	752	
Db	236 CACACGCCGTCGCCAGCATGTCTCCACACCGGCTGT-CAACCCCTGCTGCTGCTG	294	
OY	753 CCTCGCGAGATGGAGACCTTCGGGGGCCACACMGATCGCATTCCCTTCATCGACTC	812	
Db	295 CCTCTGCTGAATGGGA-CCTTCGGGGGCCACACTGATCCGATCCCTTCATCGACTC	353	
OY	813 CAACCTGAGCAGAGACCCCTGAACCTACTGAGGGATGGAGAAGCAACGACGAGATCC	872	
Db	354 CAACCTGAGCAGAGATCCGTAACCTACTGAGGGATGGAGAAGCAACGAGAACTCCC	413	
OY	873 AAGTTGGGGGCCCATCCCCCTGGGGGACAAGCCCATCTTGATCTCTTGCATACTACAG	932	
Db	414 AAGTTGGGGGCCCATCCCCCTGGAGACAAGCCCATCTTGATCTCTTGCATACTACAG	473	
OY	933 GATGTGACGATATTTTGGGGAATTTGGGCTGGGAAGCGCTCCACAACAACTTACTGTGCC	992	

Db	474	G-----	474
OY	993	TTTGGACACTGGCTCCTCCAAATCTGAGGTCCGCTCCAGAGATGCCACTTCTTCAGTGTG	1052
Db	475	-----	474
OY	1053	CCCTGCTGGTTACACACCGAATTGATGCCAAAGCCTTACTCTTCCAGGCCAATGGG	1112
Db	475	----GATGGTTACACACCGAATTGATGCCAAAGCCTTCA--CTTCCTTCAGCCAAATGGG	528
OY	1113	ACCAAGTTGCCATTCAATATGAACTGGGGGAGATGGAATCCTAGAGAGACAAAG	1172
Db	529	ACCAA--TTTGCCATTCAATATGAACTGGGGGAGTACATGGAATCCTAGAGAGACAAAG	587
OY	1173	CTGACTAATTGGTGGCATCAAGGGTGCATCACTGATTTTTCGGGGAGGCTCTTCGGAGACC	1232
Db	588	CTGACTAATTGGTGGCATCAAGGGTGCATCACTGATTTTTCGGGGAG--GCCTCTGGGA--CCC	645
OY	1233	AGCCGTGCTTCGCTTTTGGCCATTGATGGGAATATGGGCTCCGGTTTCCCATTTCTG	1292
Db	646	AGCCGTGCTTCGCTTTTGGCCCA--TTTATGAGGAATATGGGCTCCGGTTTCCCATTTCTG	704
OY	1293	TCTGTGGAAGAGTTCCGGCCCCGATGATGTACTGTGTGAGAGAGGGGCTATTGATTAAG	1352
Db	705	TCTGTGGAAGAGAGTTCCGGCCCCCATGATGTACTGTGTGAGAGAGGGGCTATTGATTAAG	764
OY	1353	CCGTGCTTCTCCTTTTACCTCAACAGGAGACCTTAAGAGCTGATGAGAGAGCTGTGC	1412
Db	765	CCGTGCTTCTCCTTTTACCTCAACAGGAGACCTTAAGAGCTGATGAGAGAGAGCTGTGC	824
OY	1413	CTGGGGGGCTCGAGCCGGGCACACTAGATCCACCCCTCACTCGTGTGCCAGTACAGGTC	1472
Db	825	CTGGGGGGCTCGAGACCGGGCACACTAGATCCACCCCTCACTCGTGTGCCAGTACAGGTC	884
OY	1473	CCTGCGTACTGGCAGATTCACATGAGCGTGTGAAGTGGGCCAGGGCTGTACTCTGT	1532
Db	885	CCTGCGTACTGGCAGATTCACATGAGCGTGTGAAGTGGGCCAGGGCTGTACTCTGT	944
OY	1533	GCCAAAGGCGTGTGCGCATCTGTGATACGGGGCAGTCCGTCCTCACTCAACAGGACCACTGAG	1592
Db	945	GCCAAAGGCGTGTGCGCATCTGTGATACGGGGCAGTCCGTCCTCACTCAACAGGACCACTGAG	1004
OY	1593	GAGATCCGGGCCCTGTGATGACAGCCATTGGGGGAATCCCTTGTGCGTGGGGAGTACATC	1652
Db	1005	GAGATCCGGGCCCTGTGATGACAGCCATTGGGGGAATCCCTTGTGCGTGGGGAGTACATC	1064
OY	1653	ATCTGTGCTCGGAAATCCCAAAAGCTCCCGGCACTCTCTTCTTCTTGGGGGGGTGTG	1712
Db	1065	ATCTGTGCTCGGAAATCCCAAAAGCTCCCGGCACTCTCTTCTTCTTGGGGGGGGTGTG	1124
OY	1713	TTTAACTCAACGGGCCATGATTACGTATCCAGACTACTGGAATGGCGTCCGCTGTG	1772
Db	1125	TTTAACTCAACGGGCCATGATTACGTATCCAGACTACTGGAATGGCGTCCGCTGTG	1184
OY	1773	TTTCCCGGTTTCCAGGCGCCCTGATGTCCCTCCGCTGACAGGCGCTTCTGATCTCGGT	1832
Db	1185	TTTCCCGGTTTCCAGGCGCCCTGATGTCCCTCCGCTGACAGGCGCTTCTGATCTCGGT	1244
OY	1833	GACCTCTTCTTGGGGAAGTATGAGCGGCTTGTGACCGGGGGAACATGAAAGACACAGCC	1892
Db	1245	GACCTCTTCTTGGGGAAGTATGAGCGGCTTGTGACCGGGGGAAGTATGAAAGACACAGCC	1304
OY	1893	CGGGTGGGCTTGAGCGCGCTGCACTCCGGAGAGCGGAGCTCGGATGGGAGAGACTGTGG	1952
Db	1305	CGGGTGGGCTTGAGCGCGCGCTGCACTCCGGAGAGCGGAGCTCGGATGGGAGAGACTGTGG	1364
OY	1953	CAGGCGAGATTCCCGGGGTGAGCGCCAAATGAAAGCCATGTGCGAGCGGGTGTGCGGAG	2012
Db	1365	CAGGCGAGATTCCCGGGGTGAGCGCCAAATGAAAGCCATGTGCGAGCGGGTGTGCGGAG	1424
OY	2013	GTCCTGTACCGATGAAATCCACTATTTCATTGAAAAAAA 2058	

[illegible]

```

Db      44  CGGCTCCCCAGCAATCTCTCCACACTGCTGCTCAACCTTCACTGCTGCTCTGCTC 103
      757  TGGTGAATGAGAGCCCTCCGAGGAGACACTGATCCGCATCCCTTTCATCGATGAC 816
      104  TCGTGAATGAGAGCCCTGCTGAGGAGACACTGATCCGCATCCCTTTCATCGATGAC 163
      817  CTGGAGCAGAGAGCCCTGAACCTTACTAGAGGATGAGAGAACGAGAGAGCTCCCAAGT 876
      164  CTGGAGCAGAGAGCCCTGAACCTTACTAGAGGATGAGAGAACGAGAGAGCTCCCAAGT 223
      877  TGGAGGAGCCCATCCCTGAGGAGAACCCATCTTCTACTCTCTGAACTACAGGATG 936
      224  TGGAGGAGCCCATCCCTGAGGAGAACCCATCTTCTACTCTCTGAACTACAGGATG 283
      937  TGGAGATTTTGGGAAATTTGGGCTGGGAAAGCCCTCCACAAAACCTTCACTGCTCT 996
      284  CCGAGATTTTGGGAAATTTGGGCTGGGAAAGCCCTCCACAAAACCTTCACTGCTCT 343
      997  ACAGTGGCTCTCCAAATCTCTGGGCTCCGTCAGAGAGATCCCACTTCTTCAAGTGCCT 1056
      344  ACAGTGGCTCTCCAAATCTCTGGGCTCCGTCAGAGAGATCCCACTTCTTCAAGTGCCT 403
      1057  GCGGTACACCAACCGATTTGATCCCAAGCCCTCTAGCTCTTCCAGGCCAATGGAGCA 1116
      404  GCGGTACACCAACCGATTTGATCCCAAGCCCTCTAGCTCTTCCAGGCCAATGGAGCA 463
      1117  AGTTGCCATCAATATGGAATGGAGGAGGAGGATAGATGAATCCAGAGAGAGACAGTGA 1176
      464  AGTTGCCATCAATATGGAATGGAGGAGGAGGATAGATGAATCCAGAGAGAGACAGTGA 523
      1177  CTATTTGGGAAATCAAGGGTGCATCATATTTTCGGGAGGCTCTCTGGAGCCCAAGCC 1236
      524  CTATTTGGGAAATCAAGGGTGCATCATATTTTCGGGAGGCTCTCTGGAGGATTCACAGCC 583
      1237  TGGTCTTCGCTTTGCCCCATTTTGAATGGATATTTGGGCTCTGCTTTCCATCTGCTG 1296
      584  TGGTCTTCGCTTTGCCCCATTTTGAATGGATATTTGGGCTCTGCTTTCCATCTGCTG 643
      1297  TGGAGAGATTTGGGAGGAGGAGGATGATGATGATGATGATGATGATGATGATGATGAT 1356
      644  TGGAGAGATTTGGGAGGAGGAGGATGATGATGATGATGATGATGATGATGATGATGAT 703
      1357  TCTTCTCTCTTTTACTCAACAGGAGCCCTGAGAGAGCTGATGAGAGAGAGCTGCTG 1416
      704  TCTTCTCTCTTTTACTCAACAGGAGCCCTGAGAGAGCTGATGATGATGATGATGATGAT 763
      1417  GGGGCTCGAGCCCGGAGACATACATCCACCCCTGACCTTCTGCTGCTGCTGCTGCTG 1476
      764  GGGGCTCGAGCCCGGAGACATACATCCACCCCTGACCTTCTGCTGCTGCTGCTGCTG 823
      1477  CTTACTGAGATTCACATGAGAGCGTGTGAAGT-GAGCCAGAGGCTGACTCTGCTGCTG 1535
      824  CTTACTGAGATTCACATGAGAGCGTGTGAAGT-GAGCCAGAGGCTGACTCTGCTGCTG 883
      1536  AAGGCTGTGCTCATCTGATAGAGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1592
      884  AAGGCTGTGCTCATCTGATAGAGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 942
      1593  GAATCCGAGGCTGCTGATGAGAGGATTTGGGGAATCCCTTCTGCTGCTGCTGCTGCTG 1652
      943  GAATCCGAGGCTGCTGATGAGAGGATTTGGGGAATCCCTTCTGCTGCTGCTGCTGCTG 1002
      1653  ATCTGTGCTGAGAAATCCCAAGCTCCCGGAGTCCCTTCTGCTGCTGCTGCTGCTGCTG 1712
      1003  ATCTGTGCTGAGAAATCCCAAGCTCCCGGAGTCCCTTCTGCTGCTGCTGCTGCTGCTG 1062
      1713  TTTAATCTCAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1769
      1063  TTTAATCTCAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1122
      1770  TGGTGTCCGCTTTCAGAGGCTGAGATGCTCTGCTGCTGAGGAGGCTTCTGATCTCTC 1829

```

```

Db      1123  TGGTGTCCGGCTTCAGAGGCTTGAACATCGCTCGGGCTGAGAGAGCTGTGATCTTC 1182
      1830  GGTGAGCTCTTCTTGGGAGATGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1889
      1183  GGGGAGTTTGGGGGAA--TATGTACCGCTTTTACCGGGGAGATGAAGAGCGGCA 1240
      1890  GCCCGGCTGGGCTGCGCG 1909
      1241  ACCGAGTTGACTTGGCGGG 1260

RESULT 13
AAH98322/c
ID   AAH98322 standard; cDNA; 1387 BP.
XX
XX   AAH98322;
AC
XX
XX   12-OCT-2001 (first entry)
DT
XX
XX   Human EST-derived coding sequence SEQ ID NO: 179.
DE
XX
XX   Human: sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW   tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW   diagnostics; forensic test; gene mapping; genetic disorder;
KW   biodiversity; gene therapy; nutrition; ss.
OS   Homo sapiens.
XX
XX   NO200154477-A2.
PN
XX
XX   02-AUG-2001.
PD
XX
XX   25-JAN-2001; 2001MO-US02687.
PE
XX
XX   25-JAN-2000; 2000US-0491404.
PR   17-JUL-2000; 2000US-0617746.
PR   03-AUG-2000; 2000US-0631451.
PR   15-SEP-2000; 2000US-0663870.
XX
XX   (HYSE-) HYSEQ INC.
PA
XX
XX   Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI   Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
XX   WPI; 2001-476164/51.
DR   P-PSDB; AAM23663.
XX
XX   Isolated polypeptide for treatment of diseases, diagnostics, raising
PT   antibodies and research use -
XX
XX   Claim 1; Page 302; 1275bp; English.
XX
XX   The present invention provides the protein and coding sequences of novel
CC   proteins from a variety of organisms, including human, dog, cat, horse,
CC   cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC   urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC   from the organism of interest. They can be used in diagnostics,
CC   forensics, gene mapping, identification of mutations, to assess
CC   biodiversity and for nutritional purposes. The present sequence is a cDNA
CC   of the invention.
XX
XX   Sequence 1387 BP; 310 A; 396 C; 421 G; 260 T; 0 other;

Query Match      45.4%; Score 936.2; DN 22; Length 1387;
Best Local Similarity 86.7%; Pred. No. 3.8e-249;
Matches 1197; Conservative 0; Mismatches 158; Indels 26; Gaps 14;

      703  CCCGAGAGATGCTCACAACCGCTGCTGCAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 762
      1378  CCCGAGAGATGCTCACAACCGCTGCTGCAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1319
      763  ATGTGAGACCTTCGGGGCCCACTGATTCGCATCCCTTTCATGAGTCCAACTGGAC 822

```

Db 1318 ATGTGAGACCTGCTGGGGCCACACTGATCCGATGCCCTCTCTGTCAGTCCACCCCTGGAC 1259  
QY 823 GCAGAGACCTGTAACCTACTAGAGGGATGAGAGAAACAGACAGAGTCCCAAGTTGGGG 882  
Db 1258 GCAGAGACCTGTAACCTACTAGAGGGATGAGAGAAACAGAGAGTCCCAAGTTGGGG 1199  
QY 883 CCCCATCCCCCTGGGGCAAGCCCATTTGTGATCTCTCTGCAACTACAGAGATGTCAGT 942  
Db 1198 CCCCATCCCCCTGGGGCAAGCCCTGCTGCTCTCTCAAAATTCGTGATGCCCACT 1139  
QY 943 ATTTGGGGAATTTGGGCTGGGAGCCCTCCACAAAACCTCACTGTGCTTGTGACACTG 1002  
Db 1138 ATTTGGGGAATTTGGGCTGGGAGCCCTCCACAAAACCTCACTGTGCTTGTGACACTG 1079  
QY 1003 GCTCTCAATCTCTGGGTCCTCCAGAGATGCCACTTCTCACTGTGCTTGTGACACTG 1062  
Db 1078 GCTCTCAATCTCTGGGTCCTCCAGAGATGCCACTTCTCACTGTGCTTGTGACACTG 1019  
QY 1063 TACACACCCGATTTGATCCCAAGCCTTAAGTCTCTCTCCAGGCAATGGGACCAAGTTG 1122  
Db 1018 TCCACACCCGATTTGATCCCAAGCCTTAAGTCTCTCTCCAGGCAATGGGACCAAGTTG 959  
QY 1123 CCATTCATATGGAAGTGGGAGGATGATGAAATCCTGAGGAGACAGACAGTCACTATG 1182  
Db 958 CCATTCATATGGAAGTGGGAGGATGATGAAATCCTGAGGAGACAGACAGTCACTATG 899  
QY 1183 GTGGAATCAGGGGTCATCATGATTTTCGGGGAGGCTCTGGG--AGCCAGCCGTGT 1240  
Db 898 GTGGAATCAGGGGTCATCATGATTTTCGGGGAGGCTCTGGGAGGCTCTGGG 839  
QY 1241 CTTCGCTTTGGCCATTTTGAAGGATANT--GGGCTCTGGTTTCCCATTC--GTC 1295  
Db 838 CTTCGCTTTGGCCATTTTGAAGGATANTGGGGCTCTGGTTTCCCATTCGTTCTGT 779  
QY 1236 GTGGAAGAGTTGCGGCCCCCGATGATGATGATGATGATGATGATGATGATGATGAT 1355  
Db 778 GGAAGAGATTTGCGGCCCCCGATGATGATGATGATGATGATGATGATGATGATGAT 719  
QY 1356 GTCTCTCTCTTTACTCAACAGGACCTGTAAGACCTGATGAGAGAGCTGTCTGT 1415  
Db 718 GTCTCTCTCTTTACTCAACAGGACCTGTAAGACCTGATGAGAGAGCTGTCTGT 659  
QY 1416 GGGGGCTCG--GACCCGGGACACTACATCCACCCC--TCACCTGTGCTCCACTCAGGT-- 1471  
Db 658 GGGGGCTCAAGACCTGACACACTACATCCACCCCCTCAACTTGTGCTCCACTCAGT 599  
QY 1472 CCCTGCTACTGAGATCACA--TGGAGGCTGTGAAGTGGG--CCAGGGCTACTCT 1528  
Db 598 CCCGACTACTGAGATCACAATGAGAGAGTGTGAAGTGTGCTCAACGCTACTCT 539  
QY 1529 CTGTGCAAGGCTGTGCTGCTCACTCTGATACAGGAGCTGCTCATACAGACCCAC 1588  
Db 538 CTGTGCAAGGCTGTGCTGCTCACTCTGATACAGGAGCTGCTCATACAGACCCAC 479  
QY 1589 TGAGAGATCCGGGCGCTGATGAGGATGGGGGATCCCTGCTGCTGGGAGATA 1648  
Db 478 TGAGAGATCCGGGCGCTGATGAGGATGGGGGATCCCTGCTGCTGGGAGATA 419  
QY 1649 CATCATCTGTGCTGGAATCCCAAGCTCCCGCATCTCTCTCTTGGGGGGGT 1708  
Db 418 CATCATCTGTGCTGGAATCCCAAGCTCCCGCATCTCTCTCTTGGGGGGGT 359  
QY 1709 CTGCTTTAATCTCAAGGCGCCAGGATACGATCAGTTCTCAGGGTGTGACGCC 299  
Db 358 CTGCTTTAATCTCAAGGCGCCAGGATACGATCAGTTCTCAGGGTGTGACGCC 299  
QY 1769 CT---GCTTGTCCGGTTTC--AGGCGCTGATGTCCTCCGCGGAGGCGCTTCGGA 1824  
Db 298 CTCTGCTTGTCCGGTTTC--AGGCGCTGATGTCCTCCGCGGAGGCGCTTCGGA 239  
QY 1825 TCCT--CGGTGAGCTCTCTTGGGAGCTATGTGCGCTCTTGCACCGCGGAGATCA-- 1881  
Db 238 TCCTCCGCGAGCTTTCTTGGGCGATGTGACCGCTTTCGACCGCGGAGATCA 179

QY 1882 -AGAGAGCGCCCGGGTGGGCTGGGCGGCGCTCCGACCTGCGGAGCGGAGCTCG--GATG 1939  
Db 178 GAGCGCGACGAGAGTGGGCTGGGCGGCGCTCCGACCTGCGGAGCGGAGCTGCGGATA 119  
QY 1940 GGGAGAGACTGGCGAGCGCACTTCCCGGCTGAGCGCCCAATGTAAGCGCATGCGCAGCG 1999  
Db 118 TGGGAGAGCGCGGCGCACTTACCGCGGCTGCGCGCAGGTGATGCGCATGCGCAGCG 59  
QY 2000 GGTGTGCGGCGGAGTCTGCTACCAATGTAATCCACTATTTCATTGAAAAA 2059  
Db 58 ---GGTAGAGAGCTAGCGCTACTCAGTAAATCAATATTCATTGAAAAA 2  
QY 2060 A 2060  
Db 1 A 1  
RESULT 14  
AAS40936  
ID AAS40936 standard; cDNA; 865 BP.  
XX  
AC AAS40936;  
XX  
DT 17-DEC-2001 (first entry)  
XX  
DE cDNA encoding novel human enzyme polypeptide #152.  
XX  
KW Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;  
KW ligase; hyperproliferative disorder; immunodeficiency disorder;  
KW autoimmune disorder; neurological disorder; metabolic disorder;  
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;  
KW blood-related disorder; infectious disorder; gene therapy; cytostatic;  
KW anti arthritic; nephrotropic; antitumor; 85.  
OS Homo sapiens.  
XX  
PN W020015301-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01239.  
XX  
PR 31-JAN-2000; 2000US-0179065.  
XX  
PR 04-FEB-2000; 2000US-0180628.  
XX  
PR 24-FEB-2000; 2000US-0184664.  
XX  
PR 02-MAR-2000; 2000US-0186350.  
XX  
PR 16-MAR-2000; 2000US-0189874.  
XX  
PR 17-MAR-2000; 2000US-0190076.  
XX  
PR 18-APR-2000; 2000US-0198123.  
XX  
PR 19-MAY-2000; 2000US-0205515.  
XX  
PR 07-JUN-2000; 2000US-0209467.  
XX  
PR 28-JUN-2000; 2000US-0214886.  
XX  
PR 30-JUN-2000; 2000US-0215135.  
XX  
PR 07-JUL-2000; 2000US-0216647.  
XX  
PR 07-JUL-2000; 2000US-0216880.  
XX  
PR 11-JUL-2000; 2000US-0217487.  
XX  
PR 11-JUL-2000; 2000US-0217496.  
XX  
PR 14-JUL-2000; 2000US-0218290.  
XX  
PR 26-JUL-2000; 2000US-0220963.  
XX  
PR 26-JUL-2000; 2000US-0220964.  
XX  
PR 14-AUG-2000; 2000US-0224518.  
XX  
PR 14-AUG-2000; 2000US-0224519.  
XX  
PR 14-AUG-2000; 2000US-0225213.  
XX  
PR 14-AUG-2000; 2000US-0225214.  
XX  
PR 14-AUG-2000; 2000US-0225266.  
XX  
PR 14-AUG-2000; 2000US-0225267.  
XX  
PR 14-AUG-2000; 2000US-0225268.  
XX  
PR 14-AUG-2000; 2000US-0225270.  
XX  
PR 14-AUG-2000; 2000US-0225447.  
XX  
PR 14-AUG-2000; 2000US-0225757.  
XX  
PR 14-AUG-2000; 2000US-0225758.  
XX  
PR 14-AUG-2000; 2000US-0225759.

PR 18-AUG-2000; 2000US-0226279.  
 PR 22-AUG-2000; 2000US-0226681.  
 PR 22-AUG-2000; 2000US-0226868.  
 PR 22-AUG-2000; 2000US-0227182.  
 PR 23-AUG-2000; 2000US-0227009.  
 PR 30-AUG-2000; 2000US-0228924.  
 PR 01-SEP-2000; 2000US-0229287.  
 PR 01-SEP-2000; 2000US-0229343.  
 PR 01-SEP-2000; 2000US-0229344.  
 PR 01-SEP-2000; 2000US-0229345.  
 PR 05-SEP-2000; 2000US-0229509.  
 PR 05-SEP-2000; 2000US-0229513.  
 PR 06-SEP-2000; 2000US-0230437.  
 PR 06-SEP-2000; 2000US-0230438.  
 PR 08-SEP-2000; 2000US-0231243.  
 PR 08-SEP-2000; 2000US-0231244.  
 PR 08-SEP-2000; 2000US-0231244.  
 PR 08-SEP-2000; 2000US-0231413.  
 PR 08-SEP-2000; 2000US-0231414.  
 PR 08-SEP-2000; 2000US-0232080.  
 PR 08-SEP-2000; 2000US-0232081.  
 PR 12-SEP-2000; 2000US-0231968.  
 PR 14-SEP-2000; 2000US-0232397.  
 PR 14-SEP-2000; 2000US-0232398.  
 PR 14-SEP-2000; 2000US-0232399.  
 PR 14-SEP-2000; 2000US-0232401.  
 PR 14-SEP-2000; 2000US-0232401.  
 PR 14-SEP-2000; 2000US-0233063.  
 PR 14-SEP-2000; 2000US-0233064.  
 PR 14-SEP-2000; 2000US-0233065.  
 PR 21-SEP-2000; 2000US-0234223.  
 PR 21-SEP-2000; 2000US-0234274.  
 PR 25-SEP-2000; 2000US-0234997.  
 PR 25-SEP-2000; 2000US-0234998.  
 PR 26-SEP-2000; 2000US-0235484.  
 PR 27-SEP-2000; 2000US-0235834.  
 PR 27-SEP-2000; 2000US-0235835.  
 PR 29-SEP-2000; 2000US-0236327.  
 PR 29-SEP-2000; 2000US-0236367.  
 PR 29-SEP-2000; 2000US-0236368.  
 PR 29-SEP-2000; 2000US-0236369.  
 PR 29-SEP-2000; 2000US-0236370.  
 PR 02-OCT-2000; 2000US-0236802.  
 PR 02-OCT-2000; 2000US-0237037.  
 PR 02-OCT-2000; 2000US-0237038.  
 PR 02-OCT-2000; 2000US-0237039.  
 PR 02-OCT-2000; 2000US-0237040.  
 PR 13-OCT-2000; 2000US-0239935.  
 PR 13-OCT-2000; 2000US-0239937.  
 PR 20-OCT-2000; 2000US-0240960.  
 PR 20-OCT-2000; 2000US-0241221.  
 PR 20-OCT-2000; 2000US-0241785.  
 PR 20-OCT-2000; 2000US-0241786.  
 PR 20-OCT-2000; 2000US-0241787.  
 PR 20-OCT-2000; 2000US-0241808.  
 PR 20-OCT-2000; 2000US-0241809.  
 PR 20-OCT-2000; 2000US-0241826.  
 PR 01-NOV-2000; 2000US-0244617.  
 PR 01-NOV-2000; 2000US-0244617.  
 PR 08-NOV-2000; 2000US-0246475.  
 PR 08-NOV-2000; 2000US-0246476.  
 PR 08-NOV-2000; 2000US-0246477.  
 PR 08-NOV-2000; 2000US-0246478.  
 PR 08-NOV-2000; 2000US-0246523.  
 PR 08-NOV-2000; 2000US-0246524.  
 PR 08-NOV-2000; 2000US-0246525.  
 PR 08-NOV-2000; 2000US-0246526.  
 PR 08-NOV-2000; 2000US-0246527.  
 PR 08-NOV-2000; 2000US-0246528.  
 PR 08-NOV-2000; 2000US-0246532.  
 PR 08-NOV-2000; 2000US-0246609.  
 PR 08-NOV-2000; 2000US-0246610.  
 PR 08-NOV-2000; 2000US-0246611.

PR 08-NOV-2000; 2000US-0246613.  
 PR 17-NOV-2000; 2000US-0249207.  
 PR 17-NOV-2000; 2000US-0249208.  
 PR 17-NOV-2000; 2000US-0249209.  
 PR 17-NOV-2000; 2000US-0249210.  
 PR 17-NOV-2000; 2000US-0249211.  
 PR 17-NOV-2000; 2000US-0249212.  
 PR 17-NOV-2000; 2000US-0249213.  
 PR 17-NOV-2000; 2000US-0249214.  
 PR 17-NOV-2000; 2000US-0249215.  
 PR 17-NOV-2000; 2000US-0249216.  
 PR 17-NOV-2000; 2000US-0249217.  
 PR 17-NOV-2000; 2000US-0249218.  
 PR 17-NOV-2000; 2000US-0249244.  
 PR 17-NOV-2000; 2000US-0249245.  
 PR 17-NOV-2000; 2000US-0249264.  
 PR 17-NOV-2000; 2000US-0249265.  
 PR 17-NOV-2000; 2000US-0249267.  
 PR 17-NOV-2000; 2000US-0249297.  
 PR 17-NOV-2000; 2000US-0249299.  
 PR 17-NOV-2000; 2000US-0249300.  
 PR 01-DEC-2000; 2000US-0250160.  
 PR 01-DEC-2000; 2000US-0250391.  
 PR 05-DEC-2000; 2000US-0251030.  
 PR 05-DEC-2000; 2000US-0251988.  
 PR 05-DEC-2000; 2000US-0251988.  
 PR 06-DEC-2000; 2000US-0251479.  
 PR 08-DEC-2000; 2000US-0251856.  
 PR 08-DEC-2000; 2000US-0251868.  
 PR 08-DEC-2000; 2000US-0251869.  
 PR 08-DEC-2000; 2000US-0251989.  
 PR 08-DEC-2000; 2000US-0251990.  
 PR 11-DEC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2001US-0259676.

#### (HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;  
 WPI; 2001-465566/50.  
 DR XX  
 DR XX  
 DR P-PSDB; AAU23066.

Novel polypeptides and polynucleotides useful for diagnosing,  
 preventing, treating neural, immune system, muscular, reproductive,  
 PT pulmonary, cardiovascular, renal, proliferative disorders and cancerous  
 PT diseases -

PS Claim 4; SEQ ID No 162; 1180bp; English.

XX The present invention relates to the isolation of novel human enzyme  
 CC polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences  
 CC encoding them. The enzyme polypeptides of the invention may comprise the  
 CC functional classes of oxidoreductases, transferases, hydrolases, lyases,  
 CC isomerases or ligases. The sequences of the invention are useful in the  
 CC diagnosis, treatment, prevention and/or prognosis of a wide range of  
 CC disorders including hyperproliferative disorders (e.g. cancer),  
 CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders  
 CC (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),  
 CC metabolic disorders (e.g. phenylketonuria), inflammatory disorders  
 CC (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis),  
 CC blood-related disorders (e.g. haemophilia), reproductive disorders  
 CC (e.g. infertility) and infectious disorders (e.g. influenza). The  
 CC polynucleotides of the invention can also be used in gene therapy.  
 CC AAU40785-AAU41684 represent cDNA sequences encoding for the novel human  
 CC enzyme polypeptides of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pcl\_sequences.

CC Sequence 865 BP; 163 A; 254 C; 245 G; 201 T; 2 other;

Query Match 40 8%; Score 839.6; DB 22; Length 865;  
 Best Local Similarity 99.4%; Pred. No. 1.9e-222;  
 Matches 861; Conservative 2; Mismatches 1; Indels 2; Gaps 2;









GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2003, 12:42:26 ; Search time 7930.98 Seconds

(without alignments)  
10625.902 Million cell updates/sec

Title: US-09-700-770-3

Perfect score: 2060

Sequence: 1 ctgagagctcctaataact.....ttccattgaaaaaaaaaaaaa 2060

Scoring table: IDENTITY\_NUC

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

```

1:  gb_Da:*
2:  gb_Htg:*
3:  gb_In:*
4:  gb_Om:*
5:  gb_Ov:*
6:  gb_Pat:*
7:  gb_Pt:*
8:  gb_Pl:*
9:  gb_Pr:*
10: gb_Ro:*
11: gb_Sts:*
12: gb_Sy:*
13: gb_Un:*
14: gb_Vl:*
15: em_Da:*
16: em_Fun:*
17: em_Hum:*
18: em_In:*
19: em_Mu:*
20: em_Om:*
21: em_Or:*
22: em_Ov:*
23: em_Pat:*
24: em_Ph:*
25: em_Pl:*
26: em_Ro:*
27: em_Sts:*
28: em_Un:*
29: em_Vl:*
30: em_Htg_Hum:*
31: em_Htg_Inv:*
32: em_Htg_Other:*
33: em_Htg_Mus:*
34: em_Htg_Pln:*
35: em_Htg_Rod:*
36: em_Htg_Man:*
37: em_Htg_Vrt:*
38: em_Sy:*
39: em_Htgo_Hum:*
40: em_Htgo_Mus:*
41: em_Htgo_Other:*

```

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2060	100.0	2061	6	ARI42618
2	2060	100.0	2061	6	BD137127
3	1358.4	65.9	1438	9	AF098484
4	1356.8	65.9	1389	9	BC017842
5	1356.8	65.9	1910	6	ARI48427
6	1352	65.6	1425	6	AX429547
7	1351.8	65.6	1358	9	AF200345
8	1350.4	65.6	1519	6	E33553
9	1350.4	65.6	1648	6	E33552
10	1345.2	65.3	1365	9	AF090386
11	1199.2	58.2	1299	6	AR016588
12	1199.2	58.2	1299	6	AR078758
13	1199.2	58.2	1299	6	AR242712
14	1199.2	58.2	1299	6	BD082059
15	1151.8	55.9	1375	6	A70198
16	1151.8	55.9	1375	6	A70213
17	1142	55.4	1353	6	ARI48425
18	1140.4	55.4	1350	9	AF090387
19	1140.4	55.4	1352	9	AF200344
20	1140.4	55.4	1353	9	AF098485
21	1138.4	55.3	1367	9	BC032360
22	1131.8	54.9	1398	9	BC040958
23	1127	54.7	1347	9	BC006149
24	949.2	46.1	1347	6	A70212
25	797.2	38.7	1360	6	AX046346
26	797.2	38.7	1360	6	AX046376
27	793.2	38.5	1479	10	D88899
28	791.8	38.4	1332	10	BC014813
29	791.4	38.4	1520	10	AB038144
30	788.8	38.3	1331	10	RNO251299
31	747	36.3	1651	6	ARI48426
32	678.4	32.9	1801	9	BC009379
33	678.4	32.9	1823	6	AX375625
34	678.4	32.9	1840	6	AX086222
35	678.4	32.9	1840	9	HSMB01634
36	676.8	32.9	1796	6	AX1713323
37	676.8	32.9	1796	6	AK054574
38	673.6	32.7	1804	9	HS276704
39	502.8	24.4	693	6	AR263858
40	462.4	22.4	663	6	AR264087
41	397.2	19.3	481	6	A70208
42	396.4	19.2	1448	5	S49650
43	387.6	18.8	407	6	BD024324
44	386.6	18.8	407	6	BD075934
45	374.4	18.2	1647	9	AF078843

# ALIGNMENTS

RESULT 1  
ARI42618  
LOCUS ARI42618 2061 bp DNA  
DEFINITION Sequence 16 from patent US 6203979. linear PAT 08-AUG-2001  
ACCESSION ARI42618  
VERSION ARI42618.1 GI:15103904  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2061)  
AUTHORS Bandman O., Hillman J.L., Yue H., Guegler, K.J., Corley, N.C.,  
Tang, Y.Tom. and Shah, P.  
TITLE Human protease molecules  
JOURNAL Patent: US 6203979-A 16 20-MAR-2001;

FEATURES		Location/Qualifiers	
Source	1. .2061	/organism="unknown"	
BASE COUNT	459 a	573 c	537 g
ORIGIN		492 t	
Query Match	100.0%;	Score 2060;	DB 6; Length 2061;
Best Local Similarity	100.0%;	Pred. No. 0;	
Matches 2060;	Conservative	0; Mismatches	0; Indels
			Gaps 0;
OY	1	CTTGAGACCTCTGCAAAATCTGTCATATGAGTGAAGCCGACCGAATACTGAATATGATTT	60
Db	1	CTTGAGACCTCTCAAAATCTGTCATATGAGTGAAGCCGACCGAATACTGAATATGATTT	60
OY	61	TGAGACAGAGTTGACAAAGCTCGAGATCGGAAACATTCCTCTCTCGCACCATGAC	120
Db	61	TGAGACAGAGTTGACAAAGCTCGAGATCGGAAACATTCCTCTCTCGCACCATGAC	120
OY	121	CACAGAGTTCAAAAACCTTCACGCGACAGCTCTGAAGAACTCTGTAATGTGCCGTTTC	180
Db	121	CACAGAGTTCAAAAACCTTCACGCGAGCAGCTCTGAAGAACTCTGTAATGTGCCGTTTC	180
OY	181	CTCTAAATACACAGACAGTTGAAAAATTCAGCAATATATATTTTATTTCCCTCTCAAT	240
Db	181	CTCTAAATACACAGAGTTGAAAAATTCAGCAATATATATTTTATTTCCCTCTCAAT	240
OY	241	CAAGGATACCTACCTCGTGTATATCTCTAAATGAATGGCTGGAACTCCTTATGATAT	300
Db	241	CAAGGATACCTACCTCGTGTATATCTCTAAATGAATGGCTGGAACTCCTTATGATAT	300
OY	301	CTGCAGCACCTGTATTAATTAATCCACAGAAACAGCTTGTCTACTGCGAATCTTGGCTTAC	360
Db	301	CTGCAGCACCTGTATTAATTAATCCACAGAAACAGCTTGTCTACTGCGAATCTTGGCTTAC	360
OY	361	TGCCATCCCCCCTCCATGGACAAATAGTCAGAGTAAGGCGCTAGGATCCCTAATAGTT	420
Db	361	TGCCATCCCCCCTCCATGGACAAATAGTCAGAGTAAGGCGCTAGGATCCCTAATAGTT	420
OY	421	TAAAGCCAAAGGCCGCTTCATCTTCTAGCAACTAGCTTGGCAGCCGAGTTTGGACAT	480
Db	421	TAAAGCCAAAGGCCGCTTCATCTTCTAGCAACTAGCTTGGCAGCCGAGTTTGGACAT	480
OY	481	ACCTCATGTAGATGTGGTTGTCACTTGACATTCCTACCATTCGAAAGATTACATCA	540
Db	481	ACCTCATGTAGATGTGGTTGTCACTTGACATTCCTACCATTCGAAAGATTACATCA	540
OY	541	TGAGTAGGTGCAACAGTAGAGTGGGGGCGTCGGAAAGGATTAATCTTTGTACACA	600
Db	541	TGAGTAGGTGCAACAGTAGAGTGGGGGCGTCGGAAAGGATTAATCTTTGTACACA	600
OY	601	GTATGATGTGNAACCTTCACAGCGGATAGAACCTTAATTTGGGAAGAACTACAGGTTT	660
Db	601	GTATGATGTGNAACCTTCACAGCGGATAGAACCTTAATTTGGGAAGAACTACAGGTTT	660
OY	661	TCCAACACAGAGTGAAGGTTTATGATGCTGACAAAGCGCTCCACAGAGATGTCCAC	720
Db	661	TCCAACACAGAGTGAAGGTTTATGATGCTGACAAAGCGCTCCACAGAGATGTCCAC	720
OY	721	CACGCGTCTGGAACCCCTGCTGCTGCTGCTCCCTCTGTAATGTGAGCCTTCCGGGG	780
Db	721	CACGCGTCTGGAACCCCTGCTGCTGCTGCTCCCTCTGTAATGTGAGCCTTCCGGGG	780
OY	781	CCACACTATCCGATCCCTCTTATTCAGAGTCCAACTGGAAGCAGACCCGAACTAC	840
Db	781	CCACACTATCCGATCCCTCTTATTCAGAGTCCAACTGGAAGCAGACCCGAACTAC	840
OY	841	TGAGGGATGAGAGAACAGCAGAGCTCCCAAGTTGGGGGCCCATTCCTCGGGACA	900
Db	841	TGAGGGATGAGAGAACAGCAGAGCTCCCAAGTTGGGGGCCCATTCCTCGGGACA	900
OY	901	AGCCATCTTGTACTCTCTCGAACTACAGGATGTGCAGTATTTTGGGAAATTTGGCC	960
Db	901	AGCCATCTTGTACTCTCTCGAACTACAGGATGTGCAGTATTTTGGGAAATTTGGCC	960

QY	961	TGGGAGGCCCTCCACAAAATCTCACTGTGGCTTTGACACTGGCTCTCCAAATCTCTGGG	1020
Dp	961	TGGGAAGCCCTCCACAAAATCTCACTGTGGCTTTGAOACAGGGCTCTCCAAATCTCTGGG	1020
QY	1021	TCGGCTCCAGAGATGACACTCTCTCAAGTGTGCCCTGTGGTTACACACACGATTTATATC	1080
Dp	1021	TCGGCTCCAGAGATGACACTCTCTCAAGTGTGCCCTGTGGTTACACACACGATTTATATC	1080
QY	1081	CCAAAGCCTTAGCTCTCTCCAGGCCAATGGGACCAAGTTGCCATTCATATGGAACGTG	1140
Dp	1081	CCAAAGCCTTAGCTCTCTCCAGGCCAATGGGACCAAGTTGCCATTCATATGGAACGTG	1140
QY	1141	GGGGGTTGATGATGATCCCTGAGCCAGAGCAAGCTGACATATTTGGGGAATCAAGGTCAT	1200
Dp	1141	GGGGGTTGATGATGATCCCTGAGCCAGAGCAAGCTGACATATTTGGGGAATCAAGGTCAT	1200
QY	1201	CAGTGAATTTTGSGGGAGGCTCTCTGGAGCCACGCTGTCTTGCTTGCTTTGGCCATTTTG	1260
Dp	1201	CAGTGAATTTTGSGGGAGGCTCTCTGGAGCCACGCTGTCTTGCTTGCTTTGGCCATTTTG	1260
QY	1261	ATGGGATATTTGGGCTCGGTTTTCCCATTTGTGTGGGAAGAGATTCGGCCCCGATGG	1320
Dp	1261	ATGGGATATTTGGGCTCGGTTTTCCCATTTGTGTGGGAAGAGATTCGGCCCCGATGG	1320
QY	1321	ATGTACTGTGGAGCAGAGGGCTATTTGGATAGCGCTGTCTTCTCTTTTACTCTCAACAGG	1380
Dp	1321	ATGTACTGTGGAGCAGAGGGCTATTTGGATAGCGCTGTCTTCTCTTTTACTCTCAACAGG	1380
QY	1381	ACCTGGAAGAGCCTGATGAGAGAGAGCTGTCTTGSGGGGGCTCGGACCCGGACACTACA	1440
Dp	1381	ACCTGGAAGAGCCTGATGAGAGAGAGCTGTCTTGSGGGGGCTCGGACCCGGACACTACA	1440
QY	1441	TOCCACCCCTACACTGTGTGGCAGTCAAGCGCTGTCTACTGTGGCAGATCAATCTGAGC	1500
Dp	1441	TOCCACCCCTACACTGTGTGGCAGTCAAGCGCTGTCTACTGTGGCAGATCAATCTGAGC	1500
QY	1501	GTGTGAAGTGTGGGCCACGAGGCTGACATCTGTGTGCCAAGGCTGTGTCCATCTGTGATA	1560
Dp	1501	GTGTGAAGTGTGGGCCACGAGGCTGACATCTGTGTGCCAAGGCTGTGTCCATCTGTGATA	1560
QY	1561	CGGGAGGTCCTCCTATTCACAGAGACCCATGAGAGAGATCCGGGGCCCTGATCAGACCAATG	1620
Dp	1561	CGGGAGGTCCTCCTATTCACAGAGACCCATGAGAGAGATCCGGGGCCCTGATCAGACCAATG	1620
QY	1621	GGGGAAATCCCTTGTGTGGCTGGGAGTACATCATCTGTCTCGSAAATCCCAAAAGCTCC	1680
Dp	1621	GGGGAAATCCCTTGTGTGGCTGGGAGTACATCATCTGTCTCGSAAATCCCAAAAGCTCC	1680
QY	1681	CGGAGATCTCTCTCTTTGGGGGGGTCTGGTTAACCTAGAGGCCCATATTAAGTCA	1740
Dp	1681	CGGAGATCTCTCTCTTTGGGGGGGTCTGGTTAACCTAGAGGCCCATATTAAGTCA	1740
QY	1741	TCAGACTACTCGAAATGGGCTCGGCCCTGTCTTGTCCGGTTTTCAGAGCCCTGGATGTC	1800
Dp	1741	TCAGACTACTCGAAATGGGCTCGGCCCTGTCTTGTCCGGTTTTCAGAGCCCTGGATGTC	1800
QY	1801	CTCGGCTCTGACAGGGCCCTTCTTGATCTCCGGTGAAGCTTCTTTGGGGACATATGTGGCG	1860
Dp	1801	CTCGGCTCTGACAGGGCCCTTCTTGATCTCCGGTGAAGCTTCTTTGGGGACATATGTGGCG	1860
QY	1861	TCCTTGACACGGGGGACATGAAAGACAGCGCCGGGTGGGCTGTGGCGCGGCTGTGCATCTC	1920
Dp	1861	TCCTTGACACGGGGGACATGAAAGACAGCGCCGGGTGGGCTGTGGCGCGGCTGTGCATCTC	1920
QY	1921	GGGAGCGGAGCTCGGATGGGGAGAGACTGTGGACAGGGCAATCTCCCGGGGTAGCGCCAA	1980
Dp	1921	GGGAGCGGAGCTCGGATGGGGAGAGACTGTGGACAGGGCAATCTCCCGGGGTAGCGCCAA	1980
QY	1981	GTGAAGCGCATTCGCAAGCGGTGTGTCCGGAGGTCTGTCTACCCAGTAAAAATCCACTAT	2040
Dp	1981	GTGAAGCGCATTCGCAAGCGGTGTGTCCGGAGGTCTGTCTACCCAGTAAAAATCCACTAT	2040

OY	2041	TTCGATGGAAAAA	2060
Db	2041	TTCGATGGAAAAA	2060
RESULT 2			
Bd137127			
LOCUS	BD137127	Human protease molecule.	2061 bp
DEFINITION	BD137127		DNA
ACCESSION	BD137127.1	GI:23232072	linear
VERSION	JP 2002508970-A/4.		PAT 18-SEP-2002
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 2061)		
TITLE	Bandman,O., Hillman,J.L., Yue,H., Guegler,K.J., Corley,N.C.,		
JOURNAL	Tang,T.Y. and Shah,P.		
	Human protease molecule		
	Patent: JP 2002508970-A 4 26-MAR-2002;		
COMMENT	INCYTE PHARMACEUTICALS INC		
	OS Homo sapiens (human)		
	PN JP 2002508970-A/4		
	PD 26-MAR-2002		
	PF 12-JAN-1999 JP 2000540252		
	PR 16-JAN-1998 US 09/008271		
	PI OUGA BANDMAN,JENNIFER L HILLMAN,HENRY YUE,KARL J GUEGLER,NEIL		
	PI C CORLEY,		
	PI TOM Y TANG,PURVI SHAH		
	PC C12N15/09,A61K38/46,C07K16/40,C12N1/19,C12N1/21,C12N5/10 PC		
	,C12N9/48,C12N9/64,		
	PC C12Q1/68,C12N15/00,A61K37/54,C12N5/00		
	CC 877617		
	FH key	Location/Qualifiers	
	FT source	1..2061	
FEATURES		/Organism='Homo sapiens (human)'	
source		1..2061	
		/organism="Homo sapiens"	
		/mol_type="genomic DNA"	
		/db_xref="taxon:9606"	
BASE COUNT	459 a 573 c 537 g 492 t		
ORIGIN			
Query Match	100.0%; Score 2060; DB 6; Length 2061;		
Best Local Similarity	100.0%; Pred. NO. 0;		
Matches 2060; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
OY	1	CTTGAGAGCTCTCAAACTACTTGTGCATGATGAAGCGGACCGAATGATGATGATT	60
Db	1	CTTGAGAGCTCTCAAACTACTTGTGCATGATGAAGCGGACCGAATGATGATGATT	60
OY	61	TGAACAGAGTTGACAAGCTCGAGATCGGAAAACATCTCTTCTCTGCCACCATGAC	120
Db	61	TGAACAGAGTTGACAAGCTCGAGATCGGAAAACATCTCTTCTCTGCCACCATGAC	120
OY	121	CAGAAGGTTAAAAAAGCTTCAGCAGAGAGCTCTGAGAGATCTGTGAAAATGCGGTTTC	180
Db	121	CAGAAGGTTAAAAAAGCTTCAGCAGAGAGCTCTGAGAGATCTGTGAAAATGCGGTTTC	180
OY	181	CTCTAAATACAGACAGTTGAAAAATTACAGCATATTAATTTTTATTCCTTAATT	240
Db	181	CTCTAAATACAGACAGTTGAAAAATTACAGCATATTAATTTTTATTCCTTAATT	240
OY	241	CAAGGATACCTACTCGTTTATATCTTAAATGAATGGCTGGAACCTCTTATGATATT	300
Db	241	CAAGGATACCTACTCGTTTATATCTTAAATGAATGGCTGGAACCTCTTATGATATT	300
OY	301	CTGAGACACCTGTATAATATATACCCAGAGAACAGCTTGTCTACTGCGAAATCTGGCTTAC	360
Db	301	CTGAGACACCTGTATAATATATACCCAGAGAACAGCTTGTCTACTGCGAAATCTGGCTTAC	360

[illegible]

```

Db      1441  TCCACCCCTCACTCTGCGACGAGTCCCTGCTACGACGATCCACATGAGAGC 1500
OY      1501  GTGTGAAGGTGGGCGCCAGGCGTGACTCTGTGTCGCAAGGCGTGTGCGCATCTGGATA 1560
Db      1501  GTGTGAAGGTGGGCGCCAGGCGTGACTCTGTGTCGCAAGGCGTGTGCGCATCTGGATA 1560
OY      1561  CGGCGACGTCCCTCATCAACAGACCCACTGAGAGATCCGGGCGCTGCATGACGACATG 1620
Db      1561  CGGCGACGTCCCTCATCAACAGACCCACTGAGAGATCCGGGCGCTGCATGACGACATG 1620
OY      1621  GGGGAATCCCTGCTGGGCTGGGAGTACATCATCTGTGCTCGGAAATCCCAAGCTTC 1680
Db      1621  GGGGAATCCCTGCTGGGCTGGGAGTACATCATCTGTGCTCGGAAATCCCAAGCTTC 1680
OY      1681  CCGGACGTCTCTCTCTGTTGGGGGCTGTGTTTAACTCAAGGCGCATGATACGTA 1740
Db      1681  CCGGACGTCTCTCTCTGTTGGGGGCTGTGTTTAACTCAAGGCGCATGATACGTA 1740
OY      1741  TCCAGACTACTCGAAATGCGCTCGCTGTGCTTCCGGTTTCCAGGCGCTGATGTC 1800
Db      1741  TCCAGACTACTCGAAATGCGCTCGCTGTGCTTCCGGTTTCCAGGCGCTGATGTC 1800
OY      1801  CTCGCGCTGCAAGGCGCTTGTGATCTGCGAGTCTCTTCTTGGGAGATGTCGCG 1860
Db      1801  CTCGCGCTGCAAGGCGCTTGTGATCTGCGAGTCTCTTCTTGGGAGATGTCGCG 1860
OY      1861  TCTTCGACCGGCGGACATGAAGACAGCGCCGCGGTGGCGCTGCGCGCTGCACATC 1920
Db      1861  TCTTCGACCGGCGGACATGAAGACAGCGCCGCGGTGGCGCTGCGCGCTGCACATC 1920
OY      1921  GCGGACGCGGACCTCGATGCGGAGAGACTGCGCAGCGCAGTCCCGGCTGACGCCAA 1980
Db      1921  GCGGACGCGGACCTCGATGCGGAGAGACTGCGCAGCGCAGTCCCGGCTGACGCCAA 1980
OY      1981  GTGAAGCCATGCGGACGCGGTGTCGCGGAGGTCCTGCTACCCAGTAAATCCACTAT 2040
Db      1981  GTGAAGCCATGCGGACGCGGTGTCGCGGAGGTCCTGCTACCCAGTAAATCCACTAT 2040
OY      2041  TTCCATTGAAAAAATAAAAA 2060
Db      2041  TTCCATTGAAAAAATAAAAA 2060

RESULT 3
AF098484      1438 bp      mRNA      linear      PRI 08-FEB-1999
LOCUS      AF098484      Homo sapiens napsin 1 precursor, mRNA, complete cds.
DEFINITION      AF098484
ACCESSION      AF098484.1 GI:4235424
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1438)
Koelsch, G., Wu, S., Henthorn, J., Tang, J. and Lin, X.
New human aspartic proteases napsin 1 and napsin 2: Molecular
cloning and intracellular localization of napsin 1
Unpublished
2 (bases 1 to 1438)
Koelsch, G., Wu, S., Tang, J. and Lin, X.
Direct Submission
Submitted (13-OCT-1998) Protein Studies Program, Oklahoma Medical
Research Foundation, 825 N.E. 13th Street, Oklahoma City, OK 73104,
USA
FEATURES
SOURCE
1..1438      location/Qualifiers
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="liver"
54..1316

```

```

/function="aspartic protease"
/codon_start=1
/product="napsin 1 precursor"
/protein_id="A01325.1"
/db_xref="GI:4235425"
/translation="MSPPLLQPLLLPLLNVEPSGATLIRIPLHRVQGRRLINL
RGMREPAIPKIGAPSPDKPIEPLSNRYDQYGEIGLTPQNFVAADTSSNL
WPSRCHFEFSYPCWLIHRPDKASSSQANGTKFAIQYGRVGIISDKLTGSI
KQASVIFGEALWEPDLVFAFADGIIIGLGPILISBEGRPMVDVLRGILDKPVS
FYLNDRPEPDGGEIVLGGSDPAHYIPPLFTVPVPAVWQIMHMRVAVGRLTCAK
GCAALIDGTSLITPTPEIRLHAIGIPLAGEITIIISLPIKLPAVSLISGVW
ENLTHDVITQTRNGVRLCISFEALDVPVPAFGFWILGDFLGTVAVDRGDMKS
SARVLARARTRGADLGWETAQAQFPG"
sig_peptide
mat_peptide
240..1313
/product="napsin 1"
BASE COUNT      302 a      422 c      406 g      308 t
ORIGIN
Query Match      65.9%; Score 1358.4; DB 9; Length 1438;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1359; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
701  GTCCACAGATGTCTCCACACCGCTGCTGCAACCCCTGCTGCTGCTCTCTGCT 760
Db      44  GTCCACAGATGTCTCCACACCGCTGCTGCAACCCCTGCTGCTGCTCTCTGCT 103
OY      761  GAATGTGAGCTTCCGCGGCGCACACTGATCCGATCCCTCTTCAATCGAGTCAACCTGG 820
Db      104  GAATGTGAGCTTCCGCGGCGCACACTGATCCGATCCCTCTTCAATCGAGTCAACCTGG 163
OY      821  ACGCAGACCGTGAACCTACTGAGGAGATGAGAGACAGACAGAGAGCTCCCAAGTTGG 880
Db      164  ACGCAGAGTTCCTGAACCTACTGAGGAGATGAGAGACAGACAGAGAGCTCCCAAGTTGG 223
OY      881  GCGCCCATCCCTGGGAGACAGCCCATCTTGTACTCTCTCTGAACTACAGGAGATGCA 940
Db      224  GCGCCCATCCCTGGGAGACAGCCCATCTTGTACTCTCTCTGAACTACAGGAGATGCA 283
OY      941  GATTTTGGGGAATTTGGGCTGGGAGAGCGCTCCAAACCTCACTGTGCTTGGACAC 1000
Db      284  GATTTTGGGGAATTTGGGCTGGGAGAGCGCTCCAAACCTCACTGTGCTTGGACAC 343
OY      1001  TGGCTCTCCAAATCTGTGGTCCCTGCCAGAGATGCCACTTCTCACTGTGCTGCTG 1060
Db      344  TGGCTCTCCAAATCTGTGGTCCCTGCCAGAGATGCCACTTCTCACTGTGCTGCTG 403
OY      1061  GTTACACACCGATTTGATCCCAAGCCTCTAGCTCTTCCAGGCGCAATGGGACCAAGTT 1120
Db      404  GTTACACACCGATTTGATCCCAAGCCTCTAGCTCTTCCAGGCGCAATGGGACCAAGTT 463
OY      1121  TGCCATTCAATATGGAACCTGGGCGGTGATGAGATCTGAGCGGAGCAAGCTACAT 1180
Db      464  TGCCATTCAATATGGAACCTGGGCGGTGATGAGATCTGAGCGGAGCAAGCTACAT 523
OY      1181  TGGTGAATCAAGGCTGATGATGATTTTGGGAGGCTCTCTGGAGACCCAGCCTGAT 1240
Db      524  TGGTGAATCAAGGCTGATGATGATTTTGGGAGGCTCTCTGGAGACCCAGCCTGAT 583
OY      1301  AGGAGTTGGGCGCCCGATGAGATGATCTGTGTGAGAGAGGCGTATTTGATAGCCTGTT 1360
Db      644  AGGAGTTGGGCGCCCGATGAGATGATCTGTGTGAGAGAGGCGTATTTGATAGCCTGTT 703
OY      1361  CTCCTTTACCTCAACAGGAGACCCGAGAGAGCTGATGAGAGAGAGAGCTGCTGCTGG 1420
Db      704  CTCCTTTACCTCAACAGGAGACCCGAGAGAGCTGATGAGAGAGAGAGCTGCTGCTGG 763
OY      1421  CTCGAGCCGCGACACTACATCCACCCCTCACTCTGTGCAAGTCAAGGTCCTGCTCA 1480

```



```

Db      490 TGGTGGAATCAAGGGTGCATCAGTATTTTCGGGGAGGCTCTCTGTGGAGCCAGCCTGCT 549
OY      1241 CTTCGCTTTTGGCCATTTTGGATGGGATATTTGGGCCCGGTTTTCATTCGTGCTGTGA 1300
Db      550 CTTCGCTTTTGGCCATTTTGGATGGGATATTTGGGCCCGGTTTTCATTCGTGCTGTGA 609
OY      1301 AGGAGTTGGGGCCCCCGATGGATGTACTGTGTGAGCAGGGGCTATTGGATMAAGCTGTCTT 1360
Db      610 AGGAGTTGGGGCCCCCGATGGATGTACTGTGTGAGCAGGGGCTATTGGATMAAGCTGTCTT 669
OY      1361 CTTCCTTTTACCTCAACAGGAGGACCTTGAAAGCCTGATGAGAGAGAGCTGTCTGGGGG 1420
Db      670 CTTCCTTTTACCTCAACAGGAGGACCTTGAAAGCCTGATGAGAGAGAGCTGTCTGGGGG 729
OY      1421 CTTCGAGCCGGGACACTATACCTCAACCCCTCACTCTGTGCCAGTACAGGCTCCCTCTTA 1480
Db      730 CTTCGAGCCGGGACACTATACCTCAACCCCTCACTCTGTGCCAGTACAGGCTCCCTCTTA 789
OY      1481 CTTCGAGATCAACATGAGAGCTGTGAAGGTGGGCCCGAGGCTGACTCTGTGCCAAGG 1540
Db      790 CTTCGAGATCAACATGAGAGCTGTGAAGGTGGGCCCGAGGCTGACTCTGTGCCAAGG 849
OY      1541 CTTCGCTGCATCTCTGATACAGGGGACGTCCCTCATCACAGAGCCACTGAGAGATCCG 1600
Db      850 CTTCGCTGCATCTCTGATACAGGGGACGTCCCTCATCACAGAGCCACTGAGAGATCCG 909
OY      1601 GGCCCTGCATGAGAGCATTTGGGGGAATCCCTTTCCTGCTGGGAGATACATCATCTCTGTG 1660
Db      910 GGCCCTGCATGAGAGCATTTGGGGGAATCCCTTTCCTGCTGGGAGATACATCATCTCTGTG 969
OY      1661 CTTCGGAATCCCAAGCTCCCGCAGTCTCTCTTCTTGGGGGGGTCTGTTTAACCT 1720
Db      970 CTTCGGAATCCCAAGCTCCCGCAGTCTCTCTTCTTGGGGGGGTCTGTTTAACCT 1029
OY      1721 CAGGGCCCATGATTTAGCTATCAGACTACTGAAATGGGCTGTCGCTGCTGTCGCG 1780
Db      1030 CAGGGCCCATGATTTAGCTATCAGACTACTGAAATGGGCTGTCGCTGCTGTCGCG 1089
OY      1781 TTTTCCAGGGCCCTGATGTCTCTCCGCTTCAGAGGCCCTTCTGTGATCTCTGTGACCTCTT 1840
Db      1090 TTTTCCAGGGCCCTGATGTCTCTCCGCTTCAGAGGCCCTTCTGTGATCTCTGTGACCTCTT 1149
OY      1841 CTTCGGGAGCTATGTGGCCGTCTTCGACGCGGGGGACATGAAGAGCAGGCCCGGCTGG 1900
Db      1150 CTTCGGGAGCTATGTGGCCGTCTTCGACGCGGGGGACATGAAGAGCAGGCCCGGCTGG 1209
OY      1901 CCGGGGGGCGGCTCGGACCTCGGGGAGGAGACCTCGGATGGGGAGACTGCGCAGGCGGA 1960
Db      1210 CCGGGGGGCGGCTCGGACCTCGGGGAGGAGACCTCGGATGGGGAGACTGCGCAGGCGGA 1269
OY      1961 GTTCCCGGGGTGACGCCCAAGTGAAGCGCATGCGCAGCGGTTGTCGCGGAGGTCCTGCT 2020
Db      1270 GTTCCCGGGGTGACGCCCAAGTGAAGCGCATGCGCAGCGGTTGTCGCGGAGGTCCTGCT 1329
OY      2021 ACCCAGTAAATCCACTATTTCATTTGAAAAA 2060
Db      1330 ACCCAGTAAATCCACTATTTCATTTGAAAAA 1369

RESULT 5
ARI48427 1910 bp DNA linear PAT 08-AUG-2001
LOCUS ARI48427
DEFINITION Sequence 7 from patent US 6225103.
ACCESSION ARI48427
VERSION ARI48427.1 GI:15112517
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1910)
AUTHORS Keolsch, G., Lin, X. and Tang, J.
TITLE Cloning and characterization of napsin
JOURNAL Patent: US 6225103-A 7 01-MAY-2001;

```

```

FEATURES
    source          Location/Qualifiers
BASE COUNT      437 a 538 c 522 g 412 t 1 others
ORIGIN
Query Match      65.9%; Score 1356.8; DB 6; Length 1910;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1358; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      701 GTTCCAGCGATGTCTCCACACCGCTGCTGCAACCCCTGCTGCTGCTGCTGCT 760
Db      516 GTTCCAGCGATGTCTCCACACCGCTGCTGCAACCCCTGCTGCTGCTGCTGCTGCT 575
OY      761 GAATGGAGCCCTTCCGGGGGACACTGATTCGCACTCCCTCTTCATTCGAGTCAACCTGG 820
Db      576 GAATGGAGCCCTTCCGGGGGACACTGATTCGCACTCCCTCTTCATTCGAGTCAACCTGG 635
OY      821 ACGGAGACCTTGAACTACTAGAGGGATGAGAGAACCGACGAGACTCCCAAGTTGG 880
Db      636 ACGGAGATCTGGAACCTACTAGAGGGATGAGAGAACCGACGAGACTCCCAAGTTGG 695
OY      881 GGCCCATCCCTGGGGACAAAGCCATCTTCTGACTCTCTGGAATACAGGATGTGA 940
Db      696 GGCCCATCCCTGGGGACAAAGCCATCTTCTGACTCTCTGGAATACAGGATGTGA 755
OY      941 GTATTTTGGGAAATTTGGGCTGGGAAAGCCCTGCACAAAATTCACCTGTGCTTGACAC 1000
Db      756 GTATTTTGGGAAATTTGGGCTGGGAAAGCCCTGCACAAAATTCACCTGTGCTTGACAC 815
OY      1001 TGGCTCTTCCAAATCTGTGGGTCCTGTCAGAGATGCACTTCTCACTGTGCTGCTG 1060
Db      816 TGGCTCTTCCAAATCTGTGGGTCCTGTCAGAGATGCACTTCTCACTGTGCTGCTG 875
OY      1061 GTTAAACACCGAATTTGATCCCAAGCCCTGAGCTCTCTTCCAGGCAATGGGACCAAGTT 1120
Db      876 GTTAAACACCGAATTTGATCCCAAGCCCTGAGCTCTCTTCCAGGCAATGGGACCAAGTT 935
OY      1121 TGCATTTCAATATGAACTGGGCGGGTAGATGGAATCTGAGCAGAGCAAGCTGACTAT 1180
Db      936 TGCATTTCAATATGAACTGGGCGGGTAGATGGAATCTGAGCAGAGCAAGCTGACTAT 995
OY      1181 TGGTGAAATCAAGGTTGATCATGATTTTCGGGGAGGCTCTCTGAGAGCCAGCTGT 1240
Db      996 TGGTGAAATCAAGGTTGATCATGATTTTCGGGGAGGCTCTCTGAGAGCCAGCTGT 1055
OY      1241 CTTCGCTTTTGGCCATTTTATGAGGATATTGGGCGCGGTTTCCATCTGCTGTGA 1300
Db      1056 CTTCGCTTTTGGCCATTTTATGAGGATATTGGGCGCGGTTTCCATCTGCTGTGA 1115
OY      1301 AGGAGTTGGGGCCCCCGATGGATGTACTGTGTGAGCAGGGGCTATTGGATMAAGCTGTCTT 1360
Db      1116 AGGAGTTGGGGCCCCCGATGGATGTACTGTGTGAGCAGGGGCTATTGGATMAAGCTGTCTT 1175
OY      1361 CTTCCTTTTACCTCAACAGGAGCCTTGAAAGCCTGATGAGAGAGACTGTCTGTGGGGG 1420
Db      1176 CTTCCTTTTACCTCAACAGGAGCCTTGAAAGCCTGATGAGAGAGACTGTCTGTGGGGG 1235
OY      1421 CTTCGAGCCGGGACACTATACCTCAACCCCTCACTCTGTGCCAGTACAGGCTCCCTCTTA 1480
Db      1236 CTTCGAGCCGGGACACTATACCTCAACCCCTCACTCTGTGCCAGTACAGGCTCCCTCTTA 1295
OY      1481 CTTCGAGATCAACATGAGAGCTGTGAAGGTGGGCCCGAGGCTGACTCTGTGCCAAGG 1540
Db      1296 CTTCGAGATCAACATGAGAGCTGTGAAGGTGGGCCCGAGGCTGACTCTGTGCCAAGG 1355
OY      1541 CTTCGCTGCATCTCTGATACAGGGGACGTTCCTCATCACAGAGCCACTGAGAGATCCG 1600
Db      1356 CTTCGCTGCATCTCTGATACAGGGGACGTTCCTCATCACAGAGCCACTGAGAGATCCG 1415
OY      1601 GGCCCTGCATGAGAGCATTTGGGGGAATCCCTTTCCTGCTGGGAGATACATCATCTCTGTG 1660
Db      1416 GGCCCTGCATGAGAGCATTTGGGGGAATCCCTTTCCTGCTGGGAGATACATCATCTCTGTG 1475

```



QY 1661 CTCGGAATATCCCAAGCTCCCGCAGTCTCTTCTTGGGGGGGTGTGTTAACT 1720  
DB 1476 CTCGGAATATCCCAAGCTCCCGCAGTCTCTTCTTGGGGGGGTGTGTTAACT 1535  
QY 1721 CAGGGCCCATGATTAGCATACGACATCGAATAAGGCGTCCGGCTTCGCTGTCGG 1780  
DB 1536 CAGGGCCCATGATTAGCATACGACATCGAATAAGGCGTCCGGCTTCGCTGTCGG 1595  
QY 1781 TTTCCAGGCGCTGATGTCTCCCTCCGCTGACAGGCGCTTCTGATCTCGGTGACGCTT 1840  
DB 1596 TTTCCAGGCGCTGATGTCTCCCTCCGCTGACAGGCGCTTCTGATCTCGGTGACGCTT 1655  
QY 1841 CTGCGGACGATGTGCGCGCTCTTCGACCGCGGGGACATGAAGACAGCGCGGGTGGG 1900  
DB 1656 CTGCGGACGATGTGCGCGCTCTTCGACCGCGGGGACATGAAGACAGCGCGGGTGGG 1715  
QY 1901 CTTGGGCGCGGCTGACACTGCGGAGGACCTCGGATGGGAGAGAGATGCGGAGGCGCA 1960  
DB 1716 CTTGGGCGCGGCTGACACTGCGGAGGACCTCGGATGGGAGAGAGATGCGGAGGCGCA 1775  
QY 1961 GTTCCCGCGGTGACGCCCAAGTGAAGCGCATGCGCAGCGGGTGGTCCGCGAGTCTGCT 2020  
DB 1776 GTTCCCGCGGTGACGCCCAAGTGAAGCGCATGCGCAGCGGGTGGTCCGCGAGTCTGCT 1835  
QY 2021 ACCCAGTAAATCCACTATTTCATTGAAAAA 2060  
DB 1836 ACCCAGTAAATCCACTATTTCATTGAAAAA 1875

RESULT 6  
AX429547 1425 bp DNA linear PAT 21-JUN-2002  
LOCUS Sequence 10 from Patent WO0226820.  
DEFINITION AX429547  
ACCESSION AX429547  
VERSION GI:21540819  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Cohen, D., Dengler, U. J., Finelli, A. L., Freuler, F., Konsolaki, M.,  
Reinhardt, M. W., and Zisman, S.  
TITLE Transgenic drosophila melanogaster expressing beta amyloid  
JOURNAL Patent: WO 0226820-A 10 04-APR-2002;  
NOVARTIS ERFIND VERMALT GMBH (AT)  
FEATURES  
source 1. 1425  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 284 a 425 c 408 g 308 t  
ORIGIN

Query Match 65.6%; Score 1352; DB 6; Length 1425;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1355; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

DB 224 GGGCCCATCCCTGGGGAAGAAGCCCATCTTGTACCTCTCTGAACTACAGGATGTGCA 283  
QY 941 GTATTGGGGAAATGGGCTGGGAGCGCTCCACAAAATCTACGTGTGGCTTGACAC 1000  
DB 284 GTATTGGGGAAATGGGCTGGGAGCGCTCCACAAAATCTACGTGTGGCTTGACAC 343  
QY 1001 TGGCTCTCCCAATCTCTGGGTCCCGTCCAGAGATGCGACCTTCTTCACTGTGCGCTG 1060  
DB 344 TGGCTCTCCCAATCTCTGGGTCCCGTCCAGAGATGCGACCTTCTTCACTGTGCGCTG 403  
QY 1061 GTTACACACCGATTTGATTCACAAAGCTCTAGCTCTTCCAGGCGCAATGGAGCAAGTT 1120  
DB 404 GTTACACACCGATTTGATTCACAAAGCTCTAGCTCTTCCAGGCGCAATGGAGCAAGTT 463  
QY 1121 TGCCATTCATATGGAATGGGCGGAGTAGATGAATCTGACGAGCAAGTACTAT 1180  
DB 464 TGCCATTCATATGGAATGGGCGGAGTAGATGAATCTGACGAGCAAGTACTAT 523  
QY 1181 TGGTGGATCAAGGTTGATGATGATTTTGGGGAGGCTCTGTTGGAGCCAGCTGTGT 1240  
DB 524 TGGTGGATCAAGGTTGATGATGATTTTGGGGAGGCTCTGTTGGAGCCAGCTGTGT 583  
QY 1241 CTTGCGCTTTGCCATTTTGTATGGGATATGGGCTCGGTTTCCATTTCTGTGTGA 1300  
DB 584 CTTGCGCTTTGCCATTTTGTATGGGATATGGGCTCGGTTTCCATTTCTGTGTGA 643  
QY 1301 AGGAGTTGGGCGCCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1360  
DB 644 AGGAGTTGGGCGCCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 703  
QY 1361 CTCCTTTTACTCAACAGGAGCCCTGGAAGAGCTGTATGAGAGAGAGAGAGAGAGAGAG 1420  
DB 704 CTCCTTTTACTCAACAGGAGCCCTGGAAGAGCTGTATGAGAGAGAGAGAGAGAGAGAG 763  
QY 1421 CTCGAGCCCGGACACATCATCCACCCCTGACCTTCTGTCAGTACAGGCTCGGCTGA 1480  
DB 764 CTCGAGCCCGGACACATCATCCACCCCTGACCTTCTGTCAGTACAGGCTCGGCTGA 823  
QY 1481 CTGGAGATTCACATGAGAGCGTGTGTAAGTGGGCGGAGGCTGACTCTGTGCCAAGG 1540  
DB 824 CTGGAGATTCACATGAGAGCGTGTGTAAGTGGGCGGAGGCTGACTCTGTGCCAAGG 883  
QY 1541 CTGTCTCTCCATCTGTGATAGGGGACGTCCTCATACAGAGAGCCACTGAGAGAGATCG 1600  
DB 884 CTGTCTCTCCATCTGTGATAGGGGACGTCCTCATACAGAGAGCCACTGAGAGAGATCG 943  
QY 1601 GAGCCCTGATGAGGATTTGGGGGAATCCCTTGTGCTGGGAGTATCATATCATCTGTG 1660  
DB 944 GAGCCCTGATGAGGATTTGGGGGAATCCCTTGTGCTGGGAGTATCATATCATCTGTG 1003  
QY 1661 CTCGGAATATCCCAAGCTCCCGCAGTCTCTTCTTGGGGGGGTGTGTTAACT 1720  
DB 1004 CTCGGAATATCCCAAGCTCCCGCAGTCTCTTCTTGGGGGGGTGTGTTAACT 1063  
QY 1721 CAGGGCCCATGATTAGCATACGACATCGAATAAGGCGTCCGGCTTCGCTGTCGG 1780  
DB 1064 CAGGGCCCATGATTAGCATACGACATCGAATAAGGCGTCCGGCTTCGCTGTCGG 1123  
QY 1781 TTTCCAGGCGCTGATGTCTCCCTCCGCTGACAGGCGCTTCTGATCTCGGTGACGCTT 1840  
DB 1124 TTTCCAGGCGCTGATGTCTCCCTCCGCTGACAGGCGCTTCTGATCTCGGTGACGCTT 1183  
QY 1841 CTTGGGAGGATATGTGGCGCTTTCGACCGCGGGGACATGAAGACAGCGCGGGTGGG 1900  
DB 1184 CTTGGGAGGATATGTGGCGCTTTCGACCGCGGGGACATGAAGACAGCGCGGGTGGG 1243  
QY 1901 CTTGGGCGCGGCTCTCCACTCGCGGAGCGGACCTCGGATGGGAGAGACTGCGCAGGCGCA 1960  
DB 1244 CTTGGGCGCGGCTCTCCACTCGCGGAGCGGACCTCGGATGGGAGAGACTGCGCAGGCGCA 1303  
QY 1961 GTTCCCGGAGGAGCGGCAAGTGAAGCGATGCGAGGCGGTGTGGGGAGGTCTGCT 2020  
DB 1304 GTTCCCGGAGGAGCGGCAAGTGAAGCGATGCGAGGCGGTGTGGGGAGGTCTGCT 1363





|||||

DB 1321 GTAAATACTATTTCATTGAAAAA 1355

RESULT 8  
E33553  
LOCUS E33553 1519 bp DNA linear PAT 18-JUN-2001  
DEFINITION ASP.  
ACCESSION E33553  
VERSION E33553.1 GI:13026986  
KEYWORDS JP 199155583-A/2.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1519)  
AUTHORS David,J.P., John,K., Jeffrey,H. and Tudy,S.  
TITLE ASP5  
JOURNAL Patent: JP 199155583-A 2 15-JUN-1999;  
SMITHKLINE BEECHAM CORP  
OS Homo sapiens (human)  
PN JP 199155583-A/2  
PD 15-JUN-1999  
PE 21-AUG-1998 JP 1998236037  
PR 21-AUG-1997 US 60/056480,08-JUL-1998 US 09/111727 P1  
DAVID J POWER,JOHN KEI,JEFFREY HITL,TUDY SMITH PC  
C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61K45/00,A61K48/00,PC  
C07H16/18,  
PC C12N5/10,C12P21/02,G01N33/53,G01N33/566,C12N15/00,A61K37/02,  
PC C12N5/00  
CC  
FH Key Location/Qualifiers  
FT source 1.1519  
/organism='Homo sapiens (human)'.  
location/Qualifiers  
1.1519  
/organism='Homo sapiens'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:9606'  
BASE COUNT 304 a 446 c 436 g 331 t 2 others  
ORIGIN

Query Match 65.6%; Score 1350.4; DB 6; Length 1519;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1354; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

DB 701 GTCCACGAGATGTCACACACGCGTGTGCAACCCCTGTCGTCGTCCTGCT 760  
DB 109 GTCCACGAGATGTCACACACGCGTGTGCAACCCCTGTCGTCGTCCTGCT 168  
DB 761 GAATGTGAGAGCTTCCGGGGCCACACTGATCCGCAATCCCTTTCATCGAGTCAACCTGG 820  
DB 169 GAATGTGAGAGCTTCCGGGGCCACACTGATCCGCAATCCCTTTCATCGAGTCAACCTGG 228  
DB 821 ACGCAGGAGCCTGAACTTACTGAGGGATGAGAGACAGACAGAGCTCCCAAGTTGGG 880  
DB 229 ACGCAGGAGCCTGAACTTACTGAGGGATGAGAGACAGACAGAGCTCCCAAGTTGGG 288  
DB 881 GGGCCCATCCCTGGGGAGCAAGCCATCTTGTACTCTCTGAGACTACAGGATGTGCA 940  
DB 289 GGGCCCATCCCTGGGGAGCAAGCCATCTTGTACTCTCTGAGACTACAGGATGTGCA 348  
DB 941 GTATTTTGGGAAATTTGGGCTGGGAAGCGCTCCACAAAACCTTCACTGTTGCCCTTGACAC 1000  
DB 349 GTATTTTGGGAAATTTGGGCTGGGAAGCGCTCCACAAAACCTTCACTGTTGCCCTTGACAC 408  
DB 1001 TGGCTCTTCATCTCTGGGTCGGTCCAGAGATGCCATCTTTCATGAGTGCCTGCTG 1060  
DB 409 TGGCTCTTCATCTCTGGGTCGGTCCAGAGATGCCATCTTTCATGAGTGCCTGCTG 468  
DB 1061 GTTACACACAGGATTTGATCCCAAGCGCTTAGCTCTTCCAGGGCAATGGGACCAAGTT 1120  
DB 469 GTTACACACAGGATTTGATCCCAAGCGCTTAGCTCTTCCAGGGCAATGGGACCAAGTT 528

1121 TGCATTCATATGGAAGTGGCGGTAGATGGAATCTGACGAGACAGCAAGCTGACTAT 1180  
DB 529 TGCATTCATATGGAAGTGGCGGTAGATGGAATCTGACGAGACAGCAAGCTGACTAT 588  
DB 1181 TGGTGAATCAAGGGTGCATCATGATTTTCCGGGAGGCTCTCTGGGACCCAGCTGGT 1240  
DB 589 TGGTGAATCAAGGGTGCATCATGATTTTCCGGGAGGCTCTCTGGGACCCAGCTGGT 648  
DB 1241 CTTCGCTTTTGGCCATTTTGGATGGGATATTTGGGCGCGGTTTCCATCTCTGCTGGA 1300  
DB 649 CTTCGCTTTTGGCCATTTTGGATGGGATATTTGGGCGCGGTTTCCATCTCTGCTGGA 708  
DB 1301 AGAGATTGGCCCCCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1360  
DB 709 AGAGATTGGCCCCCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 768  
DB 1361 CTTCCTTTTACCTCAACAGGAGCCCTGMAAGAGCTGATGAGAGAGAGAGAGAGAG 1420  
DB 769 CTTCCTTTTACCTCAACAGGAGCCCTGMAAGAGCTGATGAGAGAGAGAGAGAGAG 828  
DB 1421 CTTCGACCGGACACTATACCCACCCCTCACTTCGTCGACAGTCAGGTCCTGCTCA 1480  
DB 829 CTTCGACCGGACACTATACCCACCCCTCACTTCGTCGACAGTCAGGTCCTGCTCA 888  
DB 1481 CTTCGACAGATCAATGAGAGCTGTGMAAGGTGGGCGGAGGCTGACTCTGTGCCAAGG 1540  
DB 889 CTTCGACAGATCAATGAGAGCTGTGMAAGGTGGGCGGAGGCTGACTCTGTGCCAAGG 948  
DB 1541 CTTCGCTGCTGATCTGATGATGAGGAGAGCTGCTCATACAGAGACCACTGAGAGATCCG 1600  
DB 949 CTTCGCTGCTGATCTGATGATGAGGAGAGCTGCTCATACAGAGACCACTGAGAGATCCG 1008  
DB 1601 GGGCCGTCATGAGAGCTTGGGGGAATCCCTTGTGCTGGGAGTATATATCTGCTGG 1660  
DB 1009 GGGCCGTCATGAGAGCTTGGGGGAATCCCTTGTGCTGGGAGTATATATCTGCTGG 1068  
DB 1661 CTTCGGAATCCCAAGAGCTCCCGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1720  
DB 1069 CTTCGGAATCCCAAGAGCTCCCGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1128  
DB 1721 CACGGCCATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1780  
DB 1129 CACGGCCATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1188  
DB 1781 TTTTCAGAGCCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1840  
DB 1189 TTTTCAGAGCCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1248  
DB 1841 CTTCGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1900  
DB 1249 CTTCGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1308  
DB 1901 CCTGGGCGCGCTCTGCACTTCGCGGAGGAGACCTCGATGGGAGAGACTGCGAGCGCA 1960  
DB 1309 CCTGGGCGCGCTCTGCACTTCGCGGAGGAGACCTCGATGGGAGAGACTGCGAGCGCA 1368  
DB 1961 GTTCCCGGGGTACGCGCCAAAGTGAAGCGGATGCGGAGGCGGAGGCTGCTGCT 2020  
DB 1369 GTTCCCGGGGTACGCGCCAAAGTGAAGCGGATGCGGAGGCGGAGGCTGCTGCTG 1428  
DB 2021 ACCCAGTAAATTCATATTTTCATTTGAAAAA 2060  
DB 1429 ACCCAGTAAATTCATATTTTCATTTGAAAAA 1468

RESULT 9  
E33552  
LOCUS E33552 1648 bp DNA linear PAT 18-JUN-2001  
DEFINITION ASP5.  
ACCESSION E33552  
VERSION E33552.1 GI:13026985  
KEYWORDS JP 199155583-A/1.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE 1 (bases 1 to 1648)  
JOURNAL David,J.P., John,K., Jeffrey,H. and Tudy,S.  
ASPS Patent: JP 1999155583-A 1 15-JUN-1999;  
COMMENT SMITHKLINE BEECHAM CORP  
OS Homo sapiens (human)  
PN JP 1999155583-A/1  
PD 15-JUN-1999  
PF 21-AUG-1998 JP 1998236037  
PR DAVID J POWERU,JOHN KEI,JEFFREY HILL,TUDY SMITH PC  
C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61K45/00,A61K48/00, PC  
C07K16/18,  
PC C12N5/10,C12P21/02,G01N33/53,G01N33/566,C12N15/00,A61K37/02,  
CC C12N5/00  
FH key Location/Qualifiers  
FT source Location/Qualifiers  
1.1648  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

BASE COUNT 343 a 492 c 459 g 354 t

ORIGIN

Query Match 65.6%; Score 1350.4; DB 6; Length 1648;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1354; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 701 GTCCCAAGCATGCTCCACACCGCTGCTGCAACCCCTGCTGCTGCTGCTGCT 760  
Db 238 GTCCCAAGCATGCTCCACACCGCTGCTGCAACCCCTGCTGCTGCTGCTGCT 297  
QY 761 GAATGAGAGCTTCCCGGGGCAACAGTATCCGATCCCTGCTGCTGCTGCTGCT 820  
Db 298 GAATGAGAGCTTCCCGGGGCAACAGTATCCGATCCCTGCTGCTGCTGCTGCT 357  
QY 821 ACGGAGACCTGTAACCTACTAGAGGGATGAGAGAACAGAGAGCTCCCAAGTGGG 880  
Db 358 ACGGAGATCTGTAACCTACTAGAGGGATGAGAGAACAGAGAGCTCCCAAGTGGG 417  
QY 881 GGGCCCATCCCTGGGAGCAAGCCCATCTGTAACCTCTGTAACCTAGAGAGATGCA 940  
Db 418 GGGCCCATCCCTGGGAGCAAGCCCATCTGTAACCTCTGTAACCTAGAGAGATGCA 477  
QY 941 GATATTTGGGGAATTTGGGAGGAGCCCTCCCAAAACTTCACTTTGCTTTGACAC 1000  
Db 478 GATATTTGGGGAATTTGGGAGGAGCCCTCCCAAAACTTCACTTTGCTTTGACAC 537  
QY 1001 TGGCTCTCCAACTCTGAGGCTCCGCTCCAGAGATGCCATCTGAGTGGCTGCTG 1060  
Db 538 TGGCTCTCCAACTCTGAGGCTCCGCTCCAGAGATGCCATCTGAGTGGCTGCTG 597  
QY 1061 GTTACACCAACGATTTGATCCCAAGGCTTACTCTTCCAGAGCAATGGAACCAATT 1120  
Db 598 GTTACACCAACGATTTGATCCCAAGGCTTACTCTTCCAGAGCAATGGAACCAATT 657  
QY 1121 TGGCATTCATATGGAAGTGGGGGATGATGGAATCCTAGAGAGAGCAAGCTGACTAT 1180  
Db 658 TGGCATTCATATGGAAGTGGGGGATGATGGAATCCTAGAGAGAGCAAGCTGACTAT 1180  
QY 1181 TGGTGAATCAAGGATGATGATTTTGGGAGGCTCTGTTGGAGCCAGCTGCTG 1240  
Db 718 TGGTGAATCAAGGATGATGATTTTGGGAGGCTCTGTTGGAGCCAGCTGCTG 777  
QY 1241 CTTCGCTTTTGGCATTTTGAATGAGATTTGGGCTCGGTTTCCATCTGCTGTGA 1300  
Db 1300 CTTCGCTTTTGGCATTTTGAATGAGATTTGGGCTCGGTTTCCATCTGCTGTGA 1300

Db 778 CTTCGCTTTTGGCATTTTGAATGAGATTTGGGCTCGGTTTCCATCTGCTGTGA 837  
QY 1301 AGGATTCGCCCCCGATGATGATGATGATGATGATGATGATGATGATGATGAT 1360  
Db 838 AGGATTCGCCCCCGATGATGATGATGATGATGATGATGATGATGATGATGAT 897  
QY 1361 CTTCGCTTTTGGCATTTTGAATGAGATTTGGGCTCGGTTTCCATCTGCTGTGA 1420  
Db 898 CTTCGCTTTTGGCATTTTGAATGAGATTTGGGCTCGGTTTCCATCTGCTGTGA 957  
QY 1421 CTTCGCTTTTGGCATTTTGAATGAGATTTGGGCTCGGTTTCCATCTGCTGTGA 1480  
Db 958 CTTCGCTTTTGGCATTTTGAATGAGATTTGGGCTCGGTTTCCATCTGCTGTGA 1017  
QY 1481 CTTCGCTTTTGGCATTTTGAATGAGATTTGGGCTCGGTTTCCATCTGCTGTGA 1540  
Db 1018 CTTCGCTTTTGGCATTTTGAATGAGATTTGGGCTCGGTTTCCATCTGCTGTGA 1077  
QY 1541 CTTCGCTTTTGGCATTTTGAATGAGATTTGGGCTCGGTTTCCATCTGCTGTGA 1600  
Db 1078 CTTCGCTTTTGGCATTTTGAATGAGATTTGGGCTCGGTTTCCATCTGCTGTGA 1137  
QY 1601 GGGCTTCATGACAGCATTTGGGGGAATCCCTTGTGCTGCTGCTGCTGCTGCTG 1660  
Db 1138 GGGCTTCATGACAGCATTTGGGGGAATCCCTTGTGCTGCTGCTGCTGCTGCTG 1197  
QY 1661 CTTCGCTTTTGGCATTTTGAATGAGATTTGGGCTCGGTTTCCATCTGCTGTGA 1720  
Db 1198 CTTCGCTTTTGGCATTTTGAATGAGATTTGGGCTCGGTTTCCATCTGCTGTGA 1257  
QY 1721 CACGGCCCATGATTTAGCTATCCAGACTATCCAGACTATCCAGACTATCCAGACT 1780  
Db 1258 CACGGCCCATGATTTAGCTATCCAGACTATCCAGACTATCCAGACTATCCAGACT 1317  
QY 1781 TTTTCCAGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1840  
Db 1318 TTTTCCAGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1377  
QY 1841 CTTCGCTTTTGGCATTTTGAATGAGATTTGGGCTCGGTTTCCATCTGCTGTGA 1900  
Db 1378 CTTCGCTTTTGGCATTTTGAATGAGATTTGGGCTCGGTTTCCATCTGCTGTGA 1437  
QY 1901 CTTCGCTTTTGGCATTTTGAATGAGATTTGGGCTCGGTTTCCATCTGCTGTGA 1960  
Db 1438 CTTCGCTTTTGGCATTTTGAATGAGATTTGGGCTCGGTTTCCATCTGCTGTGA 1497  
QY 1961 GTTCGCTTTTGGCATTTTGAATGAGATTTGGGCTCGGTTTCCATCTGCTGTGA 2020  
Db 1498 GTTCGCTTTTGGCATTTTGAATGAGATTTGGGCTCGGTTTCCATCTGCTGTGA 1557  
QY 2021 ACCGAGTAAATTCATTTTCCATTTGAAAAA 2060  
Db 1558 ACCGAGTAAATTCATTTTCCATTTGAAAAA 1597

RESULT 10  
AF090386 1365 bp mRNA linear PRI 14-JAN-1999  
LOCUS Homo sapiens napsin A mRNA, complete cds.  
DEFINITION AF090386  
ACCESSION AF090386.1 GI:4154286  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLE 1 (bases 1 to 1365)  
JOURNAL Tattelli,P.J., Powell,D.J., Hill,J., Smith,T.S., Tew,D.G. and Kay,J.  
Napsins: new human aspartic proteinases. Distinction between two  
closely related genes  
FEBS Lett. 441 (1), 43-48 (1998)  
MEDLINE 99092989  
PUBMED 9877162





1057 GCTGTGACACACCGATTGATCCCAAGCCTTACTCTTCCAGGCCAATGGACCA 1116  
1117 AGTTGGCATTCATATGAACTGGGGGTAGATGGAATCCTGAGGAGACAAAGTGA 1176  
423 AGTTGGCATTCATATGAACTGGGGGTAGATGGAATCCTGAGGAGACAAAGTGA 482  
1177 CTATTTGGTGAATCAAGGATGATCACTGATTTTTCGGGAGGCTCTCTGGAGCCAGCC 1236  
483 CTATTTGGTGAATCAAGGATGATCACTGATTTTTCGGGAGGCTCTCTGGAGCCAGCC 542  
1237 TGGTCTTCGCTTTTGGCCATTTTGAATGGAATTTGGGCTCGGTTTCCATTCCTGTG 1296  
543 TGGATCTTCGCTTTTGGCCATTTTGAATGGAATTTGGGCTCGGTTTCCATTCCTGTG 602  
1297 TGGAGAGATTCGGCCCGCATGGATGATGATGATGATGATGATGATGATGATGATGATG 1356  
603 TGGAGAGATTCGGCCCGCATGGATGATGATGATGATGATGATGATGATGATGATGATG 662  
1357 TCTTCTCTCTTTTACCTTCACAGGAGACCTTGAAGAGCTGATGAGAGAGAGAGAGAGAG 1416  
663 TCTTCTCTCTTTTACCTTCACAGGAGACCTTGAAGAGCTGATGAGAGAGAGAGAGAGAG 722  
1417 GGGGCTCGAACCGGACACTACATCCACCCCTCACCTTCGTCCAGTACAGGTCCTG 1476  
723 GGGGCTCGAACCGGACACTACATCCACCCCTCACCTTCGTCCAGTACAGGTCCTG 782  
1477 CCTACTGGAGATCCATGAGAGGTGTAAGGTGGGGGCGGAGGCTGATCTCTGTGCA 1536  
783 CCTACTGGAGATCCATGAGAGGTGTAAGGTGGGGGCGGAGGCTGATCTCTGTGCA 842  
1537 AGGAGCTGTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1596  
843 AGGAGCTGTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 902  
1597 TCGGGGCTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1656  
903 TCGGGGCTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 962  
1657 TGTGCTGGAATTCACCAAGCTCCCGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1716  
963 TGTGCTGGAATTCACCAAGCTCCCGGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1022  
1717 ACCTCAGGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1776  
1023 ACCTCAGGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1062  
1777 CCGGTTTCCAGGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1836  
1063 -----TGACG-----TGACG-----TGACG-----TGACG-----TGACG-----TGACG 1067  
1837 TCTTCTGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1896  
1068 TCTTCTGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1127  
1897 TGGGCTCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1956  
1128 TGGGCTCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1187  
1957 CGGAGTTCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2016  
1188 CGGAGTTCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1247  
2017 TGGTACCCAGTAAATTCACATTTTTCATTTGAAAAA 2060  
1248 TGGTACCCAGTAAATTCACATTTTTCATTTGAAAAA 1291

RESULT 13  
AR242712 1299 bp mRNA linear PAT 20-DEC-2002  
LOCUS AR242712  
DEFINITION Sequence 4 from patent US 6475485.

ACCESSION AR242712  
VERSION AR242712.1 GI:27289214  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 1299)  
AUTHORS Bandman, O. and Coleman, R.  
TITLE Two novel human cathepsin proteins  
JOURNAL Patent: US 6475485-A 4 05-NOV-2002;  
FEATURES  
source location/Qualifiers  
BASE COUNT 258 a 385 c 373 g 283 t  
ORIGIN  
Query Match 58.28; Score 1199.2; DB 6; Length 1299;  
Best Local Similarity 94.38; Pred. No. 2e-304;  
Matches 1286; Conservative 0; Mismatches 3; Indels 75; Gaps 1;  
697 ACAGGCTCCGAGGATGCTTCACACGCGTGGCAACCCGCTGCTGCTGCTGCTGCTGCTGCTG 756  
3 ACAGGCTCCGAGGATGCTTCACACGCGTGGCAACCCGCTGCTGCTGCTGCTGCTGCTGCTG 62  
757 TGTGAATGTGAGACCTTCGCGGCGCACACTGATCCGATCCCTCTTCATGAGTCCAC 816  
63 TGTGAATGTGAGACCTTCGCGGCGCACACTGATCCGATCCCTCTTCATGAGTCCAC 122  
817 CTGAGACGAGACCTTCACACTGATGAGGATGAGAGAACAGACAGAGCTCCCAAGT 876  
123 CTGAGACGAGACCTTCACACTGATGAGGATGAGAGAACAGACAGAGCTCCCAAGT 182  
877 TGGGGGCGCCATCCCTCGGGGACAAAGCCATCTTCGTACCTCTGCACTACAGGATG 936  
183 TGGGGGCGCCATCCCTCGGGGACAAAGCCATCTTCGTACCTCTGCACTACAGGATG 242  
937 TGCAGTATTTTGGGGAATTTGGGCTGGGAAAGCCCTCCACAAATTCATCTGTCCTTG 996  
243 TGCAGTATTTTGGGGAATTTGGGCTGGGAAAGCCCTCCACAAATTCATCTGTCCTTG 302  
997 ACAGTGGCTCTCCCAATCTGCGGTCCCGTCCAGAGATGCACTTCTTCAATGATGCTCT 1056  
303 ACAGTGGCTCTCCCAATCTGCGGTCCCGTCCAGAGATGCACTTCTTCAATGATGCTCT 362  
1057 GCTGTGACACACCGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1116  
363 GCTGTGACACACCGATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 422  
1117 AGTTGGCATTCATATGAACTGGGGGTAGATGGAATCCTGAGGAGACAAAGTGA 1176  
423 AGTTGGCATTCATATGAACTGGGGGTAGATGGAATCCTGAGGAGACAAAGTGA 482  
1177 CTATTTGGTGAATCAAGGATGATCACTGATTTTTCGGGAGGCTCTCTGGAGCCAGCC 1236  
483 CTATTTGGTGAATCAAGGATGATCACTGATTTTTCGGGAGGCTCTCTGGAGCCAGCC 542  
1237 TGGTCTTCGCTTTTGGCCATTTTGAATGGAATTTGGGCTCGGTTTCCATTCCTGTG 1296  
543 TGGTCTTCGCTTTTGGCCATTTTGAATGGAATTTGGGCTCGGTTTCCATTCCTGTG 602  
1297 TGGAGAGATTCGGCCCGCATGGATGATGATGATGATGATGATGATGATGATGATGATG 1356  
603 TGGAGAGATTCGGCCCGCATGGATGATGATGATGATGATGATGATGATGATGATGATG 662  
1357 TCTTCTCTCTTTTACCTTCACAGGAGACCTTGAAGAGCTGATGAGAGAGAGAGAGAGAG 1416  
663 TCTTCTCTCTTTTACCTTCACAGGAGACCTTGAAGAGCTGATGAGAGAGAGAGAGAGAG 722  
1417 GGGGCTCGAACCGGACACTACATCCACCCCTCACCTTCGTCCAGTACAGGTCCTG 1476  
723 GGGGCTCGAACCGGACACTACATCCACCCCTCACCTTCGTCCAGTACAGGTCCTG 782  
1477 CCTACTGGAGATCCATGAGAGGTGTAAGGTGGGCGGAGGCTGATCTCTGTGCA 1536



Db	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
Db	BD082059	Two human cathepsin proteins.,	BD082059	1	GI:22627669		
QY	1537	AGGGCTGTCGTCACATCCATGAGAGCTGTGAAGGTGGGCCACAGGGCTGACTCTGTGGCA					842
Db	843	AGGGCTGTGCTCCCACTCTGGATACGGGACGTCCTTCATACAGAGACCCACTGTAGGAGA					902
QY	1597	TCGGGGCCCTGCATCAGCCATTTGGGGGAATCCCTTCCTGGCTGGGAGTACATATCC					1656
Db	903	TCGGGGCCCTGCATCAGCCATTTGGGGGAATCCCTTCCTGGCTGGGAGTACATATCC					962
QY	1657	TGTGCTGGAAATCCCAAAAGCTCCCGCAGTCTCTCTCTTGGGGGGGTCTGTGTTA					1716
Db	963	TGTGCTCGGAAATCCCAAAAGCTCCCGCAGTCTCTCTCTTGGGGGGGTCTGTGTTA					1022
QY	1717	ACCTACAGGCCCATGATTACGCATCCAGACACTCCGAAATGGGCTCCGCTCTGCTTGT					1778
Db	1023	ACCTACAGGCCCATGATTACGCATCCAGACACTCCGAAATGGGCTCCGCTCTGCTTGT					1063
QY	1777	CCGGTTTCCAGAGCCCTGTGATGTCCCTCCGCTCCAGGGCCCTTCTGATCCTCGGTGACG					1836
Db	1063	-----TGACG					1066
QY	1837	TCTTCTTGGGAGCATATGTGGCCGCTTTCGACCCGGGGGACATGAAAGACAGCCGCCGG					1896
Db	1068	TCTTCTTGGGAGCATATGTGGCCGCTTTCGACCCGGGGGACATGAAAGACAGCCGCCGG					1127
QY	1897	TGGGCGTGGCGGGCGCTGCGACATCGCGGAGGGAGCCTCGAATGGGGAAGAACTGGCGAGG					1956
Db	1128	TGGGCGTGGCGGGCGCTGCGACATCGCGGAGGGAGCCTCGAATGGGGAAGAACTGGCGAGG					1187
QY	1957	CGCAATTCCCGGGGTGACGCCCAAGTGAAGCGCATGCAGCGGGTGTCTCCGGAGTCC					2018
Db	1188	CGCAATTCCCGGGGTGACGCCCAAGTGAAGCGCATGCAGCGGGTGTCTCCGGAGTCC					1247
QY	2017	TGCTACCCAGTAAAAATCCACTATTTCATTTGAAAAA					2060
Db	1248	TGCTACCCAGTAAAAATCCACTATTTCATTTGAAAAA					1291
RESULT 14	BD082059	1299 bp	DNA	linear	PAT 27-AUG-2002		
LOCUS	BD082059	Two human cathepsin proteins.,					
DEFINITION	BD082059	1	GI:22627669				
ACCESSION	BD082059						
VERSION	1						
KEYWORDS	JP 2001523943-A/2.						
SOURCE	Zea mays						
ORGANISM	Zea mays						
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;						
AUTHORS	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD						
TITLE	1 (bases 1 to 1299)						
JOURNAL	Bandman, O. and Coleman, R.						
	Patent: JP 2001523943-A 2 27-NOV-2001;						
	INCYTE PHARMACEUTICALS INC						
COMMENT	PN JP 2001523943-A/2						
	PD 27-NOV-2001						
	PF 25-SEP-1997 JP 1998515887						
	PR 26-SEP-1996 US 08/722938						
	PI OLGA BANDMAN, ROGER COLEMAN						
	PC C12N9/64, C12N15/09, C12N15/57, C07K16/40, C07K16/18, A61K38/48, PC						
	A61K39/395						

FEATURES	FH	Key	Location/Qualifiers
source			Location/Qualifiers
		1..1299	
		/organism="zeae_mays"	
		/mol_type="genomic DNA"	
		/db_xref="taxon:4577"	
BASE COUNT		385 c	373 g
ORIGIN		258 a	283 t

[illegible]



QY 1717 ACCTCAGCGCCATGATATACATCATCAGACTACTGGAATGCGCTCCGCTTGTCT 1776  
|||||  
Db 1023 ACCTCAGCGCCATGATATACATCATCAGACTACTGGAATGCGCTCCGCTTGTCT 1062  
QY 1777 CCGGTTTCCAGGCGCTGGAATGTCCTCCGCGCTCAGAGGCGCTTCTGGATCTCGGTGAGC 1836  
Db 1063 -----TGACG 1067  
QY 1837 TCTTCTGGGAGAGTATGTGCGCTCTGCGACCGCGGGACATGAAAGAGCGCCGG 1896  
|||||  
Db 1068 TCTTCTGGGAGAGTATGTGCGCTCTGCGACCGCGGGACATGAAAGAGCGCCGG 1127  
QY 1897 TGGGCTGGCGCGCTCGACCTCGCGAGCGGACCTCGGATGGGAGAGACTGCGCAGG 1956  
Db 1128 TGGGCTGGCGCGCTCGACCTCGCGAGCGGACCTCGGATGGGAGAGACTGCGCAGG 1187  
QY 1957 CGGAGTCCCGGGGTAGCGCCCAAGTGAAGCGCATGCGCGGGGTGGTGGCGGAGGTCC 2016  
|||||  
Db 1188 CGGAGTCCCGGGGTAGCGCCCAAGTGAAGCGCATGCGCGGGGTGGTGGCGGAGGTCC 1247  
QY 2017 TGGTACCCAGTAAATTCACATTTTCATTTGAAAAA 2060  
|||||  
Db 1248 TGGTACCCAGTAAATTCACATTTTCATTTGAAAAA 1291

## RESULT 15

A70198 1375 bp DNA linear PAT 07-MAY-1999  
LOCUS A70198  
DEFINITION Sequence 2 from Patent WO9811236.  
ACCESSION A70198  
VERSION A70198.1 GI:4774612  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.

REFERENCE 1 (bases 1 to 1375)  
AUTHORS Hill,J., Kay,J. and Powell,D.  
TITLE ASPARTIC PROTEASE  
JOURNAL Patent: WO 9811236-A 2 19-MAR-1998;  
HILL JEFFREY (GB)

FEATURES  
source location/Qualifiers  
1..1375

BASE COUNT 255 a 419 c 396 g 305 t  
ORIGIN  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

Query Match 55.98; Score 1151.8; DB 6; Length 1375;  
Best Local Similarity 90.8%; Pred. No. 6.1e-292;  
Matches 1238; Conservative 0; Mismatches 122; Indels 3; Gaps 1;

QY 698 CGGCTCCCAAGCATGTCCTCACACCGGCTGTGCAACCGCTGCTGCTGCTGCTGCT 757  
Db 13 CGGCTCCCAAGCATGTCCTCACACCGGCTGTGCAACCGCTGCTGCTGCTGCTGCT 72  
QY 758 GCTGAATGTGAGCTTCGCGGCGCAACATGATCCGATCCCTTCATCGAGTCCAAAC 817  
Db 73 GCTGAATGTGAGCTTCGCGGCGCAACATGATCCGATCCCTTCATCGAGTCCAAAC 132  
QY 818 TGAACGAGGACCTGTAACCTATGAGGGATGAGAGAACAGCAGAGCTCCCAAGTT 877  
Db 133 TGAACGAGGACCTGTAACCTATGAGGGATGAGAGAACAGCAGAGCTCCCAAGTT 192  
QY 878 GGGGGGCCATCCCTGGGGACAAGCCATCTTCATCTCTGCAACAGAGGATGT 937  
Db 193 GGGGGGCCATCCCTGGGGACAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 252  
QY 938 GCAGATTTTGGGAAATGGGCTGGGAAAGCCTCCACAAATCTGCTGCTGCTGCTGCT 997  
Db 253 GCAGATTTTGGGAAATGGGCTGGGAAAGCCTCCACAAATCTGCTGCTGCTGCTGCT 312  
QY 998 CACTGCTCTCTCCAAATCTCTGGGTCCCGCTCCAGAGATGCCACTTCTTCAGTGTGCC 1057

|||||  
Db 313 CACTGCTCTCTCCAAATCTCTGGGTCCCGCTCCAGAGATGCCACTTCTTCAGTGTGCC 372  
QY 1058 CTGGTTACACACACGATTTGATCCCAAAGCCTTACCTCTCCAGGCGCAATGGGACCA 1117  
Db 373 CTGGTTACACACACGATTTGATCCCAAAGCCTTACCTCTCCAGGCGCAATGGGACCA 432  
QY 1118 GTTGGCATTCATATGGAAGTGGGCGGTGAGATGGAATCTTACGAGGAGCAAGCTGAC 1177  
Db 433 GTTGGCATTCATATGGAAGTGGGCGGTGAGATGGAATCTTACGAGGAGCAAGCTGAC 492  
QY 1178 TATTTGGTGAATCAAGGGTCAATCAATGATTTTTCGGGAGCTCTGGAGCCACCT 1237  
Db 493 TATTTGGTGAATCAAGGGTCAATCAATGATTTTTCGGGAGCTCTGGAGCCACCT 552  
QY 1238 GGTCTTCGCTTTTGGCCATTTGATGGGATGATGGGCTGGGTTTCCATCTGCTGT 1297  
Db 553 GGTCTTCGCTTTTGGCCATTTGATGGGATGATGGGCTGGGTTTCCATCTGCTGT 612  
QY 1298 GGAAGGATTCGGCCCGCATGATGATGATGATGATGATGATGATGATGATGATGAT 1357  
Db 613 GGAAGGATTCGGCCCGCATGATGATGATGATGATGATGATGATGATGATGATGAT 672  
QY 1358 CTCTCTCTTTTACTCAACAGGACCTGTAAGACCTGATGAGAGAGCTGCTGTGG 1417  
Db 673 CTCTCTCTTTTACTCAACAGGACCTGTAAGAGCTGATGAGAGAGCTGCTGTGG 732  
QY 1418 GGGCTGGAGCCGCGACATCATATCCACCCCTACCTTGTGCGACGAGCCCTGTC 1477  
Db 733 GGGCTGGAGCCGCGACATCATATCCACCCCTACCTTGTGCGACGAGCCCTGTC 792  
QY 1478 CTACTGGCAGATCCATGAGAGCTGTGAAGGTGGGCCAGGCTGACTCTGTGTGCA 1537  
Db 793 CTACTGGCAGATCCATGAGAGCTGTGAAGGTGGGCCAGGCTGACTCTGTGTGCA 852  
QY 1538 GGGCTGTGCTCCATCTGTGATGAGGCGACGCTCTCATACAGAGCCACTGAGAGAT 1597  
Db 853 GGGCTGTGCTCCATCTGTGATGAGGCGACGCTCTCATACAGAGCCACTGAGAGAT 912  
QY 1598 CCGGGCCCTGATGAGAGCAATTTGGGGAATCCCTTCTGCTGGGAGATGATCATCT 1657  
Db 913 CCGGGCCCTGATGAGAGCAATTTGGGGAATCCCTTCTGCTGGGAGATGATCATCT 972  
QY 1658 GTGCTCGGAATCCCAAGCTCCCGCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1717  
Db 973 GTGCTCGGAATCCCAAGCTCCCGCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1032  
QY 1718 CTTACGCGCCCATGATTTAGCTCATCGACACTCTCGAAATGGGCTCCGCTGTGTGC 1777  
Db 1033 CTTACGCGCCCATGATTTAGCTCATCGACACTCTCGAAATGGGCTCCGCTGTGTGC 1092  
QY 1778 CGGTTTCAGGCGCTGATGTCCTCGGCGGAGGCGCTTCTGGAATGCTCGGTGAGT 1837  
Db 1093 CGGTTTCAGGCGCTGATGTCCTCGGCGGAGGCGCTTCTGGAATGCTCGGTGAGT 1152  
QY 1838 CTTCTTGGGAGCATGATGTGGCCGCTTTCGACCGCGGGGACATGAAGACAGCGCGGT 1897  
Db 1153 CTTCTTGGGAGCATGATGTGGCCGCTTTCGACCGCGGGGACATGAAGACAGCGAGT 1212  
QY 1898 GGGCTGTGGCGCGCTTGCACCTGCGGAGCGGACCTGGAATGGGAGAGACTGCGAGGC 1957  
Db 1213 GGGCTGTGGCGCGCGCTTGCACCTGCGGAGCGGACCTGGAATGGGAGAGACTGCGAGGC 1272  
QY 1958 GCAATTCGCGGGGAGCGCCCAAGTGAAGGCAATGCGGACGAGGAGGTGCTCCGAGGTCT 2017  
Db 1273 GCAATTCGCGGGGAGCGCCCAAGTGAAGGCAATGCGGACGAGGAGGTGCTCCGAGGTCT 1329  
QY 2018 GCTACCCAGTAAATTCATATTTTCATTTGAAAAA 2060  
Db 1330 GCTACCCAGTAAATTCATATTTTCATTTGAAAAA 1372

Search completed: October 9, 2003, 19:48:12

Fri Oct 10 09:35:40 2003

us-09-700-770-3.rge

Page 16

Job time : 7938.98 secs

---

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2003, 12:42:26 ; Search time 6467.98 Seconds  
(without alignments)  
10625.902 Million cell updates/sec

Title: US-09-700-770-2

Perfect score: 1680

Sequence: 1 ggtgtgcagataaagtt.....tcaataacactgtcctgtg 1680

Scoring table: IDENTITY\_NTC  
Gapop 10.0, Gapext 1.0

Searched: 2886711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.\*  
1: gb\_da.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pi.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*  
15: em\_da.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_om.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pat.\*  
24: em\_ph.\*  
25: em\_pi.\*  
26: em\_ro.\*  
27: em\_sts.\*  
28: em\_un.\*  
29: em\_vi.\*  
30: em\_htg\_hum.\*  
31: em\_htg\_in.\*  
32: em\_htg\_inv.\*  
33: em\_htg\_mus.\*  
34: em\_htg\_pln.\*  
35: em\_htg\_rod.\*  
36: em\_htg\_man.\*  
37: em\_htg\_vrt.\*  
38: em\_sy.\*  
39: em\_htg\_hum.\*  
40: em\_htg\_mus.\*  
41: em\_htg\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1679.2	100.0	1680	6 AX224643	AX224643 Sequence
2	1656.2	98.6	2036	6 AX224647	AX224647 Sequence
3	1631.6	97.1	1646	9 AF364078	AF364078 Homo sapi
4	1617	96.2	1636	6 AX092346	AX092346 Sequence
5	1617	96.2	1636	6 AX376212	AX376212 Sequence
6	1617	96.2	1636	6 AX697059	AX697059 Sequence
7	1615.8	96.2	1684	9 BC008429	BC008429 Homo sapi
8	873	52.0	1624	4 AF488705	AF488705 Bos tauri
9	830.4	49.4	1654	10 MM046068	MM046068 Mus muscu
10	806	48.0	1035	6 AX301908	AX301908 Sequence
11	724.2	43.1	963	6 AX301906	AX301906 Sequence
12	641	38.2	1172	6 AR243136	AR243136 Sequence
13	634.8	37.8	1175	6 AR243045	AR243045 Sequence
14	382	22.7	382	6 AR273207	AR273207 Sequence
15	382	22.7	382	6 AR276788	AR276788 Sequence
16	382	22.7	382	6 AX368240	AX368240 Sequence
17	181.4	10.8	159440	9 HSB049G10	AL355392 Human DNA
18	161	9.6	161593	2 AC137726	AL121901 Human DNA
19	155.4	9.2	62861	3 AC137726	AL137726 Homo sapi
20	94	5.6	192944	10 AL732601	AL732601 Mouse DNA
21	94	5.6	246577	2 AC107771	AC107771 Mus muscu
22	89.8	5.3	220161	2 AC094188	AC094188 Rattus no
23	83.6	5.0	62861	2 AC137726	AC137726 Homo sapi
24	67	4.0	1049	4 AF488706	AF488706 Bos tauri
25	61.8	3.7	2000	6 AX655393	AX655393 Sequence
26	58.8	3.5	125020	6 AF429315	AF429315 Homo sapi
27	54.6	3.2	999	4 BT079413	BT079413 Bos tauri
28	50.4	3.0	1011	9 AF172993	AF172993 Homo sapi
29	50	3.0	298550	1 AP005047	AP005047 Streptomy
30	48.8	2.9	768	6 E53840	E53840 LUNX gene a
31	48.8	2.9	1009	6 BD093486	BD093486 Reagents
32	48.8	2.9	1015	6 E53841	E53841 LUNX gene a
33	48.8	2.9	1015	6 AB024937	AB024937 Homo sapi
34	48.8	2.9	1017	6 BD093487	BD093487 Reagents
35	48.8	2.9	1021	6 AX376306	AX376306 Sequence
36	48.8	2.9	1035	6 AF417256	AF417256 Homo sapi
37	48.8	2.9	1053	9 BC012549	BC012549 Homo sapi
38	48.8	2.9	1074	9 AF439448	AF439448 Homo sapi
39	48.8	2.9	1084	9 AF158745	AF158745 Homo sapi
40	48.8	2.9	1090	9 AF417257	AF417257 Homo sapi
41	48	2.9	2000	6 AX655393	AX655393 Sequence
42	47.8	2.8	146500	2 AC119500	AC119500 Tetrahym
43	47.8	2.8	303550	1 SC0939131	AL939131 Streptomy
44	47	2.8	3222	6 AX695979	AX695979 Sequence
45	47	2.8	4860	9 AB033050	AB033050 Homo sapi

#### ALIGNMENTS

RESULT 1  
AX224643  
LOCUS AX224643 1680 bp DNA linear PAT 10-SEP-2001  
DEFINITION Sequence 1 from Patent WO0161055.  
ACCESSION AX224643  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Chen, S.Y., Sun, Y. and Macina, R.A.  
TITLE Methods for diagnosing, monitoring, staging, imaging and treating lung cancer via lung cancer specific genes



/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 477 a 586 c 528 g 444 t 1 others  
ORIGIN

Query Match 98.6%; Score 1656.2; DB 6; Length 2036;  
Best local Similarity 99.7%; Pred. No. 0;  
Matches 1678; Conservative 2; Mismatches 0; Indels 3; Gaps 2;

```

OY 1 GGTGGCAGGATATTAAGGTTGGACTTCCAGACCCACTGCCCGGAGAG--GAGRGAGG 58
    |||||||
Db 38 GGTGGCAGGATATTAAGGTTGGACTTCCAGACCCACTGCCCGGAGAGAGAGAGG 97
OY 59 GGCAGGAGACTCCAGAGCTGAGGCTGCTGGATCCGACTTGTGCTGCTGACACCTG 118
    |||||||
Db 98 GGCAGGAGACTCCAGAGCTGAGGCTGCTGGATCCGACTTGTGCTGCTGACACCTG 157
OY 119 GGAAGATGGCGGCGCCGCTGGACCTTACCCCTCTGTGTGTGGTGGACCCACCTTGA 178
    |||||||
Db 158 GGAAGATGGCGGCGCCGCTGGACCTTACCCCTCTGTGTGTGGTGGACCCACCTTGA 217
OY 179 TCCAGGCAACCCCTGATCCCACTGATCTCATCTCTGCGCCCAAAAGTCATCAAGAA 238
    |||||||
Db 218 TCCAGGCAACCCCTGATCCCACTGATCTCATCTCTGCGCCCAAAAGTCATCAAGAA 277
OY 239 ACCTGACACAGAGAGTGAAGAGACCAACAGCCACAGATCCTGACAGCTGCCGCTGC 298
    |||||||
Db 278 ACCTGACACAGAGAGTGAAGAGACCAACAGCCACAGATCCTGACAGAGCTGCCGCTGC 337
OY 299 TGAAGTCCATGCGGGGAAAAAGCCAGCGGAG--ATCCCTGTGCTGGGACCTGTGTGACA 357
    |||||||
Db 338 TGAAGTCCATGCGGGGAAAAAGCCAGCGGAGATCCTGCTGTGGGCAACCTGTGTGACA 397
OY 358 CCGTCCGTAAGACATCATCTGGCTGAAGATCATCAACAGCTAACAATCCCTCCAGCTCAGG 417
    |||||||
Db 398 CCGTCCGTAAGACATCATCTGGCTGAAGATCATCAACAGCTAACAATCCCTCCAGCTCAGG 457
OY 418 TGAAGCCCTCGGCCATGACACAGAGCTCTAGTCAAGATCCCTCGACATGCTGGCTG 477
    |||||||
Db 458 TGAAGCCCTCGGCCATGACACAGAGCTCTAGTCAAGATCCCTCGACATGCTGGCTG 517
OY 478 GATTCAACACGCGCCCTGGTCAAGACCATCTGTGAGAGTCCACATGACAGTGAAGCCCAAG 537
    |||||||
Db 518 GATTCAACACGCGCCCTGGTCAAGACCATCTGTGAGAGTCCACATGACAGTGAAGCCCAAG 577
OY 538 CCACCATCCGAGTGAACACAGTGAAGTGGCCCAACCCGCTGCTCCACAGTGAAGTGG 597
    |||||||
Db 578 CCACCATCCGAGTGAACACAGTGAAGTGGCCCAACCCGCTGCTCCACAGTGAAGTGG 637
OY 598 CCACCATCCGAGTGAAGTGGCCCAACAGTGAAGTGGCCCAACCTCTCTCTGCTGAGG 657
    |||||||
Db 638 CCACCATCCGAGTGAAGTGGCCCAACAGTGAAGTGGCCCAACCTCTCTCTGCTGAGG 697
OY 658 CCTTACGTAAGCAGTGAAGTGAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 717
    |||||||
Db 698 CCTTACGTAAGCAGTGAAGTGAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 757
OY 718 ACCTGTGCTCGGTGATCGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 777
    |||||||
Db 758 ACCTGTGCTCGGTGATCGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 817
OY 778 TGAAGGTGCCCATTTTCCCTCAGCATTTGACCTGTGAGTTTGAACCTTCTGTATCCGCA 837
    |||||||
Db 818 TGAAGGTGCCCATTTTCCCTCAGCATTTGACCTGTGAGTTTGAACCTTCTGTATCCGCA 877
OY 838 TCAAGGGTGAACCATTTCACTCTACCTGAGGAGGCAAGTTGTTGGAAGTCAAGGAAAG 897
    |||||||
Db 878 TCAAGGGTGAACCATTTCACTCTACCTGAGGAGGCAAGTTGTTGGAAGTCAAGGAAAG 937
OY 898 TGAACCAAGGTGTTCAATCTCTGACAGCTTCCCTGACAAATGCCACCTGAGACATCC 957
    |||||||
Db 938 TGAACCAAGGTGTTCAATCTCTGACAGCTTCCCTGACAAATGCCACCTGAGACATCC 997

```

```

OY 958 CATTACGCTCATTCGTGAGTCAAGAGAGCTGATGAAAGCTCAGTGGCTGTCTCTCTC 1017
    |||||||
Db 998 CATTACGCTCATTCGTGAGTCAAGAGAGCTGATGAAAGCTCAGTGGCTGTCTCTCTC 1057
OY 1018 CAGAAGAAATTCATGCTCTGTTGGAGTCTGTGCTCTCTGAGAGTGGCCATCGGCTGAAGT 1077
    |||||||
Db 1058 CAGAAGAAATTCATGCTCTGTTGGAGTCTGTGCTCTCTGAGAGTGGCCATCGGCTGAAGT 1117
OY 1078 CAAGCATGGGCTGATCATTAAGAAAGCTGCAATTAAGCTGGATCTACCCAGATGTGA 1137
    |||||||
Db 1118 CAAGCATGGGCTGATCATTAAGAAAGCTGCAATTAAGCTGGATCTACCCAGATGTGA 1177
OY 1138 ACATCTTAATCAAGAGACACTCCGAGATTTTATAGACCAAGGCAATGCAAGTGGGCC 1197
    |||||||
Db 1178 ACATCTTAATCAAGAGACACTCCGAGATTTTATAGACCAAGGCAATGCAAGTGGGCC 1237
OY 1198 AACCTGATGCTGTGAAGTGTTCCTCTGACAGTGAAGCCCTCGCCCTTGTTCACCCCTG 1257
    |||||||
Db 1238 AACCTGATGCTGTGAAGTGTTCCTCTGACAGTGAAGCCCTCGCCCTTGTTCACCCCTG 1297
OY 1258 GCATGGAAGCAGCTGGAAGTCTGATTTTATACCAAGGTGACCAACTTATCTCACT 1317
    |||||||
Db 1298 GCATGGAAGCAGCTGGAAGTCTGATTTTATACCAAGGTGACCAACTTATCTCACT 1357
OY 1318 TGAATTAACATCAGCTCTGATCCGATCCAGCTGATGAATCTGAGATTTGGCTGCTCAAC 1377
    |||||||
Db 1358 TGAATTAACATCAGCTCTGATCCGATCCAGCTGATGAATCTGAGATTTGGCTGCTCAAC 1417
OY 1378 CTGATGTTGTGAAAAATCATCATCTGATGATCCATCTGCTGCTGCGCAACCA 1437
    |||||||
Db 1418 CTGATGTTGTGAAAAATCATCATCTGATGATCCATCTGCTGCTGCGCAACCA 1477
OY 1438 ATGGCAAAATTAAGATCTGGGGTCCAGTGTCAATTTGGTGAAGGCTTGGATCGAGGCA 1497
    |||||||
Db 1478 ATGGCAAAATTAAGATCTGGGGTCCAGTGTCAATTTGGTGAAGGCTTGGATCGAGGCA 1537
OY 1498 CTGATGCTCTACAGTCAAGAGATGCTTGTGCTGCTCTCTCTCTCTCTCTCTCTCTCT 1557
    |||||||
Db 1538 CTGATGCTCTACAGTCAAGAGATGCTTGTGCTGCTCTCTCTCTCTCTCTCTCTCTCT 1597
OY 1558 GCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1617
    |||||||
Db 1598 GCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1657
OY 1618 TGGGATATGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1677
    |||||||
Db 1658 TGGGATATGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1717
OY 1678 GTG 1680
    |||
Db 1718 GTG 1720

```

RESULT 3  
AF364078  
LOCUS AF364078 Homo sapiens von Ebner minor protein mRNA, complete cds.  
DEFINITION AF364078  
ACCESSION AF364078.1 GI:19880273  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
AUTHORS 1 (bases 1 to 1646)  
TITLE Human von Ebner minor protein: a Plunc-related protein expressed in  
the upper airways and nasopharyngeal epithelium  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1646)  
AUTHORS Bingle, C.D.  
TITLE Direct Submission



LOCUS	AX092346	1636 bp	DNA	linear	PAT 21-MAR-2001
DEFINITION	Sequence 77 from Patent WO0116318.				
ACCESSION	AX092346				
VERSION	AX092346.1	GI:13444487			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS	1. Eaton,D.T., Filvaroff,E., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Matanabe,C.K. and Wood,W.I.				
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same				
JOURNAL	Patent: WO 0116318-A 77 08-MAR-2001;				
FEATURES	Genentech, Inc. (US)				
source	Location/Qualifiers				
	1..1636				
	/organism="Homo sapiens"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:9606"				
BASE COUNT	374 a 492 c 411 g 359 t				
ORIGIN					
Query Match	96.2%; Score 1617; DB 6; Length 1636;				
Best Local Similarity	99.8%; Pred. No. 0;				
Matches 1628; Conservative	1; Mismatches 1; Indels 1; Gaps 1;				
OY	51 GRGAGCGGGCGAGGACTCCAGCGTGGCCAGCTCTGGACATCTGCACCTGCTGCTCT	110			
DB	1 GAGGAGCGGGCGAGGACTCCAGCGTGGCCAGCTCTGGACATCTGCACCTGCTGCTCT	60			
OY	111 GACACCTGGGAAGATGGCGGGCCGCTGGACCTTCAACCTTCTCTGTGTTGCTGCAGC	170			
DB	61 GACACCTGGGAAGATGGCGGGCCGCTGGACCTTCAACCTTCTCTGTGTTGCTGCAGC	120			
OY	171 CACCTGTATCCAAAGCACCTCAGTCCAGTGCAGTTCATTCCTCGGCCCAAAAGTAT	230			
DB	121 CACCTGTATCCAAAGCACCTCAGTCCAGTGCAGTTCATTCCTCGGCCCAAAAGTAT	180			
OY	231 CAAAGAAAGTGACACAGAGAGCTGAAGAGCACAAAGCCCAAGACATCTGCAGACCT	290			
DB	181 CAAAGAAAGTGACACAGAGAGCTGAAGAGCACAAAGCCCAAGACATCTGCAGACCT	240			
OY	291 GCCCGTGTCTAGTGGCATGCGGGAAACCCAGCGGAGG -ATCCTGTGCTGGGAGCCT	349			
DB	241 GCCCGTGTCTAGTGGCATGCGGGAAACCCAGCGGAGGATCCTGTGCTGGGAGCCT	300			
OY	350 GGTGAACACCGCTCCGAAGCAGCATCATCTGGCTGAAGGTCATACAGCTAACATCTCCA	409			
DB	301 GGTGAACACCGCTCCGAAGCAGCATCATCTGGCTGAAGGTCATACAGCTAACATCTCCA	360			
OY	410 GCTGAGGTGAAGCCCTTGCCCAATGACACAGAGAGCTGTAGTCAAGATCCCCTGGACAT	469			
DB	361 GCTGAGGTGAAGCCCTTGCCCAATGACACAGAGAGCTGTAGTCAAGATCCCCTGGACAT	420			
OY	470 GGTGCTGTGATTCACAGCAGCCCGCTGGTCAAGCAATCTGTGAGTCCACATGACAGCA	529			
DB	421 GGTGCTGTGATTCACAGCAGCCCGCTGGTCAAGCAATCTGTGAGTCCACATGACAGCA	480			
OY	530 GGCCCAAGCCACATCCGATGGAAGCAGTGAAGTGGCCCAAGCCCGCTGGTCTTAG	589			
DB	481 GGCCCAAGCCACATCCGATGGAAGCAGTGAAGTGGCCCAAGCCCGCTGGTCTTAG	540			
OY	550 TGACTGTGACACAGCCATGGGAGCTTGCGCATCCACTGCTGCAATTAAGTCTCTCTCT	649			
DB	541 TGACTGTGACACAGCCATGGGAGCTTGCGCATCCACTGCTGCAATTAAGTCTCTCTCT	600			
OY	650 GGTGAAGCGCTTAGTAAAGCAGGTATGAACCTCTAGGCCATCCCGCCCAATCTAGT	709			
DB	601 GGTGAAGCGCTTAGTAAAGCAGGTATGAACCTCTAGGCCATCCCGCCCAATCTAGT	660			

QY	710	GAANAACAGCTGTGTGTCCTCCCGATCGAGGCTCTCTTCAATGGCATGTATGAGACCTCCT	765
Db	661	GAANAACAGCTGTGTGTCCTCCCGATCGAGGCTCTCTTCAATGGCATGTATGAGACCTCCT	720
QY	770	GCACCTGGTGAAGGTGGCCATTTTCCCTCAGCATTTGACCGTGTGAGTTTGAACCTTCGTA	829
Db	721	GCACCTGGTGAAGGTGGCCATTTTCCCTCAGCATTTGACCGTGTGAGTTTGAACCTTCGTA	780
QY	830	TCCTGCCATCAAGGGGTGACACCAATTCAGCTTACCTGGGGGCCAAGTGTGTGACATCACA	889
Db	781	TCCTGCCATCAAGGGGTGACACCAATTCAGCTTACCTGGGGGCCAAGTGTGTGACATCACA	840
QY	890	GGGAAAGGTGACCAAGTGTGTCATTAATCTGTGACAGCTTCCTTGACATAGCCACCCTGGA	949
Db	841	GGGAAAGGTGACCAAGTGTGTCATTAATCTGTGACAGCTTCCTTGACATAGCCACCCTGGA	900
QY	950	CAACATCCCGTTCAGGCTCATCGAGTCAGAGAGTGTGAAGCTGCAGTGGCGTGT	1009
Db	901	CAACATCCCGTTCAGGCTCATCGAGTCAGAGAGTGTGAAGCTGCAGTGGCGTGT	960
QY	1010	GCTCTCTTCAGAGAATTCATGTCGTCCGTGTTGAGCTGTGCTTCCTGAGATGGCCATCG	1065
Db	961	GCTCTCTTCAGAGAATTCATGTCGTCCGTGTTGAGCTGTGCTTCCTGAGATGGCCATCG	1020
QY	1070	GCTGAAGTCAGACATCGGGCTGTATCATTAAGAAAGGCTCAGATTAAGCTGGATCTACCA	1129
Db	1021	GCTGAAGTCAGACATCGGGCTGTATCATTAAGAAAGGCTCAGATTAAGCTGGATCTACCA	1080
QY	1130	GATCGTGAAGATCCTTAATCTAGAGACATCCCGAGTTTATTTATAGACCAAGGCAATGCCAA	1189
Db	1081	GATCGTGAAGATCCTTAATCTAGAGACATCCCGAGTTTATTTATAGACCAAGGCAATGCCAA	1140
QY	1190	GGTGGCCCAACTGATCGTGTGGAAGTGTTCCTTCACAGTGAAGCCCTCCGCCCTTGT	1249
Db	1141	GGTGGCCCAACTGATCGTGTGGAAGTGTTCCTTCACAGTGAAGCCCTCCGCCCTTGT	1200
QY	1250	CACCTGGGCGATCGAAGCCAGCTGCGAAGCTCAGTTTACACCAAGGTGACCAATTTAT	1309
Db	1201	CACCTGGGCGATCGAAGCCAGCTGCGAAGCTCAGTTTACACCAAGGTGACCAATTTAT	1260
QY	1310	ACTCAACTGGATTAACATCAGCTGTGATCGGATGCCAGTGCATGTAATCTGGGATGGCTG	1365
Db	1261	ACTCAACTGGATTAACATCAGCTGTGATCGGATGCCAGTGCATGTAATCTGGGATGGCTG	1320
QY	1370	GTTCCAACCTGATGTTCTGAAGAAACATCATCAGTGAATCATCCACTCATCTGCTGCC	1429
Db	1321	GTTCCAACCTGATGTTCTGAAGAAACATCATCAGTGAATCATCCACTCATCTGCTGCC	1380
QY	1430	GAACCCAGATGGCAAAATTAAGATCTGGGGTCCCACTGTCAATTTGGTGAAGGCTTGGGATT	1489
Db	1381	GAACCCAGATGGCAAAATTAAGATCTGGGGTCCCACTGTCAATTTGGTGAAGGCTTGGGATT	1440
QY	1490	CGAGGCACTGAGTGTCTCAGTACCAAGATGCCCTTGCTGTTACTCCAGCTCCTTGAG	1549
Db	1441	CGAGGCACTGAGTGTCTCAGTACCAAGATGCCCTTGCTGTTACTCCAGCTCCTTGAG	1500
QY	1550	GAAGCCAGCTCTCCTGTCTCCCACTGAAGACTTGGATGGCAGCCATCAGGAAGGCTGG	1609
Db	1501	GAAGCCAGCTCTCCTGTCTCCCACTGAAGACTTGGATGGCAGCCATCAGGAAGGCTGG	1560
QY	1610	GTCCCAAGTGGGAGTAGTGGGTGAGCTCTATAGACCAATCCCTCTCTGCAATCAATTAAC	1665
Db	1561	GTCCCAAGTGGGAGTAGTGGGTGAGCTCTATAGACCAATCCCTCTCTGCAATCAATTAAC	1620
QY	1670	ACTTGGCTGTG 1680	
Db	1621	ACTTGGCTGTG 1631	
RESULT 5			
LOCUS	AX376212	1636 bp	DNA linear PAT 01-MAR-2002
DEFINITION	Sequence 279 from Patent WO0168848.		



```

ACCESSION   AX376212
VERSION     AX376212.1  GI:19170497
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE   1
AUTHORS     Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.,
            Gurney,A.L., Pan,J., Smith,Y., Watanabe,C.K., Wood,W.I. and
            Zhang,Z.
TITLE       Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
JOURNAL     Patent: WO 0168848-A 279 20-SEP-2001;
            Genentech, Inc. (US)
FEATURES
            source          1..1636
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"
BASE COUNT   374 a 492 c 411 g 359 t
ORIGIN
Query Match      96.2%; Score 1617; DB 6; Length 1636;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1628; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

```

```

Db 661 GAAAAACAGCTGTGTCGCCGTGATGAGGCTTCCTCAATGAGCATGTATGACAGCTCCCT 720
OY GCAGCTGTGTAAGGTGGCCATTTCCTCAGCATTTGACCCGCTGGAGTTGACCTTCGTA 829
Db 721 GCAGCTGTGTAAGGTGGCCATTTCCTCAGCATTTGACCCGCTGGAGTTGACCTTCGTA 780
OY 830 TCCCTGCATCAAGGGTGTGACACATTCAGCTCTACCTGCGGGGCCAAGTTGTTGACAC 889
Db 781 TCCCTGCATCAAGGGTGTGACACATTCAGCTCTACCTGCGGGGCCAAGTTGTTGACAC 840
OY 890 GGGAAAGGTGACCAATGTGTTCAATTAATCTGACAGCTTCCTTACAAATGCCACCTGGA 949
Db 841 GGGAAAGGTGACCAATGTGTTCAATTAATCTGACAGCTTCCTTACAAATGCCACCTGGA 900
OY 950 CAACATCCGTTTACGCTCATGCTGATGATGAGACGCTGGTGAAGTGCAGTGGCTGCTG 1009
Db 901 CAACATCCGTTTACGCTCATGCTGATGATGAGACGCTGGTGAAGTGCAGTGGCTGCTG 960
OY 1010 GCTCTCTCAGAAATTCATGCTGCTGTTGACCTCTGCTCTCTGAGAGTCCCATCG 1069
Db 961 GCTCTCTCAGAAATTCATGCTGCTGTTGACCTCTGCTCTCTGAGAGTCCCATCG 1020
OY 1070 GCTGAAGTCAAGCATGGGCTGATCAATGAAAAGCTGCAGATTAAGTGGATCTACCA 1129
Db 1021 GCTGAAGTCAAGCATGGGCTGATCAATGAAAAGCTGCAGATTAAGTGGATCTACCA 1080
OY 1130 GATCGTGAAGATCTTAATCTAGACACTCCCGAGTTTATATGACCAAGGCCATGCCAA 1189
Db 1081 GATCGTGAAGATCTTAATCTAGACACTCCCGAGTTTATATGACCAAGGCCATGCCAA 1140
OY 1190 GTGGGCCCAACTGATGCTGTGGAAGTGTTCCTCCAGTGAAGCCCTCGCCCTTGT 1249
Db 1141 GTGGGCCCAACTGATGCTGTGGAAGTGTTCCTCCAGTGAAGCCCTCGCCCTTGT 1200
OY 1250 CACCTGGGATGGAAGCCAGCTCGGAAGTCACTTTACCAAGGTGACCAACTTAA 1309
Db 1201 CACCTGGGATGGAAGCCAGCTCGGAAGTCACTTTACCAAGGTGACCAACTTAA 1260
OY 1310 ACTCAACTGAAATTAATCATGATCTGATGATGATGATGATGATGATGATGATGATG 1369
Db 1261 ACTCAACTGAAATTAATCATGATCTGATGATGATGATGATGATGATGATGATGATG 1320
OY 1370 GTTCCAACTGATGTTCTGAAAAAATCATCATGATGATGATGATGATGATGATGATG 1429
Db 1321 GTTCCAACTGATGTTCTGAAAAAATCATCATGATGATGATGATGATGATGATGATG 1380
OY 1430 GAACAGAAATGGCAATTAAGATCTGGGGGCCAGTGAATGTTGAAGGCTTGGGATT 1489
Db 1381 GAACAGAAATGGCAATTAAGATCTGGGGGCCAGTGAATGTTGAAGGCTTGGGATT 1440
OY 1490 CGAGGAGCTGAGTCTCTACTGACCAAGATGCTTGTGCTTACTCCAGCCTCTTGTG 1549
Db 1441 CGAGGAGCTGAGTCTCTACTGACCAAGATGCTTGTGCTTACTCCAGCCTCTTGTG 1500
OY 1550 GAAACCCAGCTCTCTCTCTCTCCAGTGAAGACTTGGATGGACCAATCAGGGAAGCTGG 1609
Db 1501 GAAACCCAGCTCTCTCTCTCTCTCCAGTGAAGACTTGGATGGACCAATCAGGGAAGCTGG 1560
OY 1610 GTCCAGCTGGGATGTTGGGTGAGCTCTATTAAGACATCCCTCTGCAATCAATAAAC 1669
Db 1561 GTCCAGCTGGGATGTTGGGTGAGCTCTATTAAGACATCCCTCTGCAATCAATAAAC 1620
OY 1670 ACTTGCTGTG 1680
Db 1621 ACTTGCTGTG 1631

```

```

RESULT 6
AX697059 1636 bp DNA linear PAT 02-APR-2003
LOCUS Sequence 127 from Patent W00078961.
DEFINITION
ACCESSION AX697059
VERSION AX697059.1 GI:29498039

```

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Ferrara, N., Stewart, T. A., Williams, P. M., Baker, K. P., Desnoyers, L., Eaton, D. L., Gao, W. Q., Pan, J., Bolstein, D., Pong, S., Goddard, A., Godowski, P. J., Gurney, A. L., Smith, V., Tumas, D., Wood, W. I., Grimaldi, C. J., Hillan, K. J., Paoni, N. F., Roy, M. A., and Mataranbe, C. K.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same  
JOURNAL Patent: WO 0078961-A 127 28-DEC-2000;  
Genentech Inc. (US)  
FEATURES  
source location/Qualifiers  
1. 1636  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 374 a 492 c 411 g 359 t  
ORIGIN  
Query Match 96.28; Score 1617; DB 6; Length 1636;  
Best Local Similarity 99.88; Pred. No. 0;  
Matches 1628; Conservative 1; Mismatches 1; Indels 1; Gaps 1;  
QY 51 GRGAGGCGGCGGAGACTCCAGCTGCGCCAGCTGCGCATCCGCACTTGTGCTCCCT 110  
DB 1 GAGGAGCGGCGGAGACTCCAGCTGCGCCAGCTGCGCATCCGCACTTGTGCTCCCT 60  
QY 111 GACACCTGGGAGATGGCGCGCGCGCTGACCTTCTCTGTGTGTTGCTGCGAC 170  
DB 61 GACACCTGGGAGATGGCGCGCGCGCTGACCTTCTCTGTGTGTTGCTGCGAC 120  
QY 171 CACCTTATCCAAAGCCACCTCAGTCCAGTTCATCTCATCTCGGCCCAAAAGTCAT 230  
DB 121 CACCTTATCCAAAGCCACCTCAGTCCAGTTCATCTCATCTCGGCCCAAAAGTCAT 180  
QY 231 CAAAGAAAAGCTGACACAGAGCTGAGAGACCAACAGCCACAGCATCTCGACAGCT 290  
DB 181 CAAAGAAAAGCTGACACAGAGCTGAGAGACCAACAGCCACAGCATCTCGACAGCT 240  
QY 291 GCGGCTCTCAGTCCAGTGGCGGAAAAGCCAGCGGAGG-ATCCCTGTGCTGGCAGCT 349  
DB 241 GCGGCTCTCAGTCCAGTGGCGGAAAAGCCAGCGGAGGATCCCTGTGCTGGCAGCT 300  
QY 350 GGTGAACACCGCTCGAAGACATCATCTGCTGAAGGTATCATCAGCTAAACATCTCCA 409  
DB 301 GGTGAACACCGCTCGAAGACATCATCTGCTGAAGGTATCATCAGCTAAACATCTCCA 360  
QY 410 GCTGACAGTGAAGCCCTCGGCCAATGACAGAGAGCTCTAGTCAAGATCCCTCGACAT 469  
DB 361 GCTGACAGTGAAGCCCTCGGCCAATGACAGAGAGCTCTAGTCAAGATCCCTCGACAT 420  
QY 470 GGTGGCTGGATTCAACACGCGCGCTGGTCAAGACCATGTGGAGTTCCACATGACGACTGA 529  
DB 421 GGTGGCTGGATTCAACACGCGCGCTGGTCAAGACCATGTGGAGTTCCACATGACGACTGA 480  
QY 530 GGGCCAAAGCCACCTCGGATGGACACAGTGAAGTGGGCCCGCCGCGCTGGCTCAG 589  
DB 481 GGGCCAAAGCCACCTCGGATGGACACAGTGAAGTGGGCCCGCCGCGCTGGCTCAG 540  
QY 590 TGACTGTGCACAGCAGCCATGGAGCCCTGCGCATCCAAGTGTGATTAAGCTCTCTCTCT 649  
DB 541 TGACTGTGCACAGCAGCCATGGAGCCCTGCGCATCCAAGTGTGATTAAGCTCTCTCTCT 600  
QY 650 GGTGAAGCCCTTGAAGCTAAGAGTGAAGCTCTTGTGCTGCTGCTGCTGCTGCTGCT 709  
DB 601 GGTGAAGCCCTTGAAGCTAAGAGTGAAGCTCTTGTGCTGCTGCTGCTGCTGCTGCT 660  
QY 710 GAAAAACACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 769  
DB 661 GAAAAACACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720

QY 770 GCACCTGTGTAAGGTGCCATTTCCTCAGACATGACCGTGTGAGTTGACCTTCTGTA 829  
DB 721 GCACCTGTGTAAGGTGCCATTTCCTCAGACATGACCGTGTGAGTTGACCTTCTGTA 780  
QY 830 TCCGTCATCAAGGTGACACCATTCAGCTCTACCTGGGGCCAAAGTTGTTGACTACA 889  
DB 781 TCCGTCATCAAGGTGACACCATTCAGCTCTACCTGGGGCCAAAGTTGTTGACTACA 840  
QY 890 GGGAAAGGTGCAAGGTGTTCAATCTGCGAGCTTCCCTGCAATGCCACCTCGGA 949  
DB 841 GGGAAAGGTGCAAGGTGTTCAATCTGCGAGCTTCCCTGCAATGCCACCTCGGA 900  
QY 950 CAACATCCCGTTACGCTCATCTGAGTCAAGAGAGTGGTGAAGCTCAGTGGCTGCTGT 1009  
DB 901 CAACATCCCGTTACGCTCATCTGAGTCAAGAGAGTGGTGAAGCTCAGTGGCTGCTGT 960  
QY 1010 GCTCTCTCCAGAGAAATTCATGTCGTCTGTTGAGACTGTGTGCTTCTGAGAGTCCCATCG 1069  
DB 961 GCTCTCTCCAGAGAAATTCATGTCGTCTGTTGAGACTGTGTGCTTCTGAGAGTCCCATCG 1020  
QY 1070 GCTGAAGTCAAGCATCGGGGTCATCATGAAGAGGTGCAAGATGAGTGGATCTACCA 1129  
DB 1021 GCTGAAGTCAAGCATCGGGGTCATCATGAAGAGGTGCAAGATGAGTGGATCTACCA 1080  
QY 1130 GATCGTAAGATCCCTAATCTCAGACACTCCGAGTTTATAGACCAAGGCAATGCA 1189  
DB 1081 GATCGTAAGATCCCTAATCTCAGACACTCCGAGTTTATAGACCAAGGCAATGCA 1140  
QY 1190 GGTGGCCCAACTGATGCTGTGGAAGTGTTCCTCCAGTGAAGCCCTCGCCCTTGT 1249  
DB 1141 GGTGGCCCAACTGATGCTGTGGAAGTGTTCCTCCAGTGAAGCCCTCGCCCTTGT 1200  
QY 1250 CACCTTGGGATGCAAGACAGCTGGAAGTCACTTTTACCAAGGTGACCAACTAT 1309  
DB 1201 CACCTTGGGATGCAAGACAGCTGGAAGTCACTTTTACCAAGGTGACCAACTAT 1260  
QY 1310 ACTCAACTTGAATTAATCAATCAAGCTCTGATCGATCAGCTGATGAAGTCTGGGATG 1369  
DB 1261 ACTCAACTTGAATTAATCAATCAAGCTCTGATCGATCAGCTGATGAAGTCTGGGATG 1320  
QY 1370 GTTCAACCTGATGTTTGTGAAAAATCATCATCTGATCATCATCATCATCATCAT 1429  
DB 1321 GTTCAACCTGATGTTTGTGAAAAATCATCATCTGATCATCATCATCATCATCAT 1380  
QY 1430 GAACCAAGATGGCAATTAAGATCTGGGGTCCAGTGTCAATGGTGAAGGCTGGGATT 1489  
DB 1381 GAACCAAGATGGCAATTAAGATCTGGGGTCCAGTGTCAATGGTGAAGGCTGGGATT 1440  
QY 1490 CGAGGAGCTGAGTCTCAGTCACTGACCAAGAGATGCCCTTGTGCTTACTCAGCTCTGTG 1549  
DB 1441 CGAGGAGCTGAGTCTCAGTCACTGACCAAGAGATGCCCTTGTGCTTACTCAGCTCTGTG 1500  
QY 1550 GAAACCCAGCTCTCTCTGCTCCAGTGAAGACTTGAATGGACCATCAGGAAAGGCTGG 1609  
DB 1501 GAAACCCAGCTCTCTCTGCTCCAGTGAAGACTTGAATGGACCATCAGGAAAGGCTGG 1560  
QY 1610 GTCCACAGTGGAGTATGGGTTGAGGCTTATAGCATCCCTCTGCAATCAATTAAC 1669  
DB 1561 GTCCACAGTGGAGTATGGGTTGAGGCTTATAGCATCCCTCTGCAATCAATTAAC 1620  
QY 1670 ACTTGCTGTG 1680  
DB 1621 ACTTGCTGTG 1631  
RESULT 7  
BC008429  
LOCUS BC008429 1684 bp mRNA linear PRI 12-JUL-2001  
DEFINITION Homo sapiens, similar to DNA segment, Chr 2, Massachusetts  
Institute of Technology 19, clone MGC:14597 IMAGE:4291561, mRNA,  
complete cds.  
ACCESSION BC008429

VERSION BC008429.1 GI:14250057  
 KEYWORDS MGC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 1 (bases 1 to 1684)  
 AUTHORS Strausberg, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgabs-rc@mail.nih.gov](mailto:cgabs-rc@mail.nih.gov)  
 Tissue Procurement: CLONTECH  
 DNA Library Preparation: CLONTECH Laboratories, Inc.  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LNL),  
 Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www.smgc.stanford.edu>  
 Contact: (Dickson, Mark) [medpaxil.stanford.edu](mailto:medpaxil.stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

FEATURES  
 source  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
 Series: IRAL Plate: 21 Row: J Column: 12  
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, similarity but not identity to protein.

location/Qualifiers  
 1..1684  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="MGC:14597 IMAGE:4291561"  
 /tissue\_type="Skeletal Muscle"  
 /clone\_lib="NIH\_MGC\_81"  
 /lab\_host="DH10B"  
 /note="Vector: pDNR-LIB"  
 77..1531  
 /codon\_start=1  
 /product="Similar to DNA segment, Chr 2, Massachusetts Institute of Technology 19"  
 /protein\_id="AA08429.1"  
 /db\_xref="GI:14250058"  
 /translation="MAGPWTFTLLGLAATLIQATLIPTAVILIPYIKRKLDEL KDNASTILQOLPILSAMREKPAIGISLVTVLKVTIWLKVTITLLOLVKPS ANDDELIVKTPIDMTVAGRTPLVKTIVEHMTTEAQTITMDTASGPTRIYLSOCAT SHGSLRQLHLKLSFLVNALAKQVNLVPPSLPNVKQLCPVIEASFGMTADLLOL VVPSILSIDRLEFDLIPAIKGTIOIYLGAKLDSOGKVTKFNNSAASITMPLD NIPFSLIVSDVVAKAVAIVLSEPFVILDLPSASARLKSSIGLITNEKADDTGK TQIVKILQODPEEPIDOGHAKVAOLIVLEVPSEBALRPLITLIEASSPEAQFTTKG DQLIINNNISSDRLOIWNISGTIGWFOPIVKITITIEIHSILPLPONGKLSGVPVSL VKALFEAASESLSDALVLTPLASLMKPTSPVSO"

BASE COUNT 419 a 493 c 414 g 358 t

Query Match 96.2%; Score 1615.8; DB 9; Length 1684;  
 Best local similarity 99.7%; Pred. No. 0;  
 Matches 1628; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 49 GAGRGAGCGGGCGGAGAGCTCCAGCGTGGCCAGGTCTGGACCTTGTGCGCCT 108  
 DB 2 GAGAGAGCGGGCGGAGAGCTCCAGCGTGGCCAGGTCTGGACCTTGTGCGCCT 61  
 QY 109 CTGACACCTGGGGAATGATGCGCGCGCGTGGAGACTTCCACCTTCTGTGTGTTGCTGGCA 168  
 DB 62 CTGACACCTGGGGAATGATGCGCGCGCGTGGAGACTTCCACCTTCTGTGTGTTGCTGGCA 121  
 QY 169 GCCACCTTGATCAGCAACCTCAGTCCCACTGACGTTCATCCTCGGCCCAAAAGTC 228

DB 122 GCCACCTTGATCAGCAACCTCAGTCCCACTGACGTTCATCCTCGGCCCAAAAGTC 181  
 QY 229 ATCAAGAAAAAGCTGACAGAGAGCTGAAGAGACACAGCCACAGATCTCTGACGAG 288  
 DB 182 ATCAAGAAAAAGCTGACAGAGAGCTGAAGAGACACAGCCACAGATCTCTGACGAG 241  
 QY 289 CTGGCCCTGCTCACTGTCATGCGCGGAAAAAGCCGCGGAGG -ATCCCTGTCTGGGCGAC 347  
 DB 242 CTGGCCCTGCTCACTGTCATGCGCGGAAAAAGCCGCGGAGGATCCCTGTCTGGGCGAC 301  
 QY 348 CTGGTGAACACCTCTCTGAAGACATCTGTGGCTGAAGTCAATCAGCTAAATCTTC 407  
 DB 302 CTGGTGAACACCTCTCTGAAGACATCTGTGGCTGAAGTCAATCAGCTAAATCTTC 361  
 QY 408 CAGCTCAGAGTGAAGCCCTCGGCCAATGACAGAGAGCTCTAGTCAAGATCCCGCTGAC 467  
 DB 362 CAGCTCAGAGTGAAGCCCTCGGCCAATGACAGAGAGCTCTAGTCAAGATCCCGCTGAC 421  
 QY 468 ATGGTGGCTGAATCAACAGCGCCCTGGTCAAGACACCATCTGTGAGTTCACATGACGACT 527  
 DB 422 ATGGTGGCTGAATCAACAGCGCCCTGGTCAAGACACCATCTGTGAGTTCACATGACGACT 481  
 QY 528 GAGGCCAAGCCACCATCCGATGACACAGCTGCAAGTGGCCCGCCCGCTGGTCTTC 587  
 DB 482 GAGGCCAAGCCACCATCCGATGACACAGCTGCAAGTGGCCCGCCCGCTGGTCTTC 541  
 QY 588 ATGATCTGTCACACAGACCATATGAGAGCTGCGCATTCACATCTCTGATTAAGCTCTCTC 647  
 DB 542 ATGATCTGTCACACAGACCATATGAGAGCTGCGCATTCACATCTCTGATTAAGCTCTCTC 601  
 QY 648 CTGGTGAACGCTTACCTGATGACAGCTGATCAACCTCTGATGACCTTCCATCCCTGCGCAATCA 707  
 DB 602 CTGGTGAACGCTTACCTGATGACAGCTGATCAACCTCTGATGACCTTCCATCCCTGCGCAATCA 661  
 QY 708 GTGAAAAACCACTGTGTCCCTGATTCGAGGCTTCTTCAATGAGCATGTATGACAGCTTC 767  
 DB 662 GTGAAAAACCACTGTGTCCCTGATTCGAGGCTTCTTCAATGAGCATGTATGACAGCTTC 721  
 QY 768 CTGGAGCTGGTGAAGTGGCCCAATTCCTCCAGACATGACCTGCTGAGATTGACCTTTCG 827  
 DB 722 CTGGAGCTGGTGAAGTGGCCCAATTCCTCCAGACATGACCTGCTGAGATTGACCTTTCG 781  
 QY 828 TATCTGCCATCAAGGGTGACACCATTCAGCTCTACCTGCGGGGCCAAGTGTGGAGCTCA 887  
 DB 782 TATCTGCCATCAAGGGTGACACCATTCAGCTCTACCTGCGGGGCCAAGTGTGGAGCTCA 841  
 QY 888 CAGGGAAGAGTGACCAAGTGTTCATTAATCTGACGCTTCCCTGACCAATGCCACCCCTG 947  
 DB 842 CAGGGAAGAGTGACCAAGTGTTCATTAATCTGACGCTTCCCTGACCAATGCCACCCCTG 901  
 QY 948 GACCAACATCCGTTGAGCTCATCTGTGATGAGAGCGTGGTGAAGAGCTGACAGTGGCTCT 1007  
 DB 902 GACCAACATCCGTTGAGCTCATCTGTGATGAGAGCGTGGTGAAGAGCTGACAGTGGCTCT 961  
 QY 1008 GTGCTCTCTCAGAGAATTCATGTGCTGTGGACTGTGCTGTCTCTGAGAGAGGCCAT 1067  
 DB 962 GTGCTCTCTCAGAGAATTCATGTGCTGTGGACTGTGCTGTCTCTGAGAGAGGCCAT 1021  
 QY 1068 CGGCTGAAGTCAAGCATGGGCTGTATCAATGAAGAGCTGAGATTAAGCTGGATTTAC 1127  
 DB 1022 CGGCTGAAGTCAAGCATGGGCTGTATCAATGAAGAGCTGAGATTAAGCTGGATTTAC 1081  
 QY 1128 CAGATCGTGAAGATCTTAATCAGAGACATCCCGCAAGTTTTTATATAGCAAGGCCATGCC 1187  
 DB 1082 CAGATCGTGAAGATCTTAATCAGAGACATCCCGCAAGTTTTTATATAGCAAGGCCATGCC 1141  
 QY 1188 AAGTGCCCAACATGATCTGTGAGAGTCTTCTCTCAATGAAGCCCTCGCCCTTTG 1247  
 DB 1142 AAGTGCCCAACATGATCTGTGAGAGTCTTCTCTCAATGAAGCCCTCGCCCTTTG 1201  
 QY 1248 TTCAACCTGGGCAATCGAAGCAGCTCGGAAGCTCAGTTTATACCAAGAGTGACCAACTT 1307



```

Db      840 GGAATCCCGGATATGCCCCACCCCTGACCCAGACACCCCTTACAGGCTCACCCTGAGAGAAGA 899
QY      983 CGTGGTGAAGGTGAGTGGCTGCTGCTCTCCAGAAAGATTCAGTCTCTTGA 1042
Db      900 TGTGGTGGTGGTATCATATGCTGCTTCCATTCATTCAGGAAACATCACAGTCTGTGGA 959
QY      1043 CTCTGCTGCTGCTGAGAGTGGCCATCGGCTGAAATCAAGCATCGGGCTGATCAATGAAGA 1102
Db      960 CTATGCTGCTGCTGAGTAGCCCGGCTGAGTGAAGCATCAAGTGTATGAGAAAC 1019
QY      1103 GGTCTGAGATTAAGTGGATCTTACCCAGATGCTGAAGATCTTACTCAGAGACATCCCGA 1162
Db      1020 GGCACACAGCGAGCTGGGGCCACACAGATCTGAAATCATGAGTCAAGACAGCCCAAT 1079
QY      1163 GTTTTATTAAGACCAAGGCAAGTGGCCCACTGATGCTGAGTGGTGGTTC 1222
Db      1080 GCTCATTTCTGGACAGGGGCAATGCCAAGGTGGCCCACTGATCTGTGGAATATTCGC 1139
QY      1223 CTCCAGTGAAGCCCTCCGCCCTTTGTTGCAACCTGGGCAATCGAAGCAGCTCGGAAGTCA 1282
Db      1140 CACGATTAAGACAGACCGGCCCTCTTCACTGGGCAATCGAAGCTCTCTGGACATTTCA 1199
QY      1283 GTTTTACACCAAGGTGACCAATTAATCACTTGAATTAATCACTGATCTGATCGAT 1342
Db      1200 GTTTTACGTCGAAGATGGCTCTGTTGTTACGTTTAAAGAAATCAGAGTGTATCGAT 1259
QY      1343 CCAGTGTATGAACCTGGGATGGCTGTGTTCAACCTGATGTTTGAAGAAATCATATCAG 1402
Db      1260 CCATCTGTGAACCTGACATGAGTGGTGTGTTCAACCTTAACTTGAACATCAATCACAC 1319
QY      1403 TGAGATCATCCACATCTGCTGCTGCGAACCAGATGGCAATTAAGATCTGGGGTCCC 1462
Db      1320 CAAGATCTCATCTCATCTCTGCTGCAAGAGATGCAATTAAGATCTGGGATCCC 1379
QY      1463 AGTGTCAATGGTGAAGAACTTGGGATTAAGTCGATTTCACTGTCTGACCAAGGAAC 1439
Db      1380 AGTGTCAATGGTGAAGAACTTGGGATTAAGTCGATTTCACTGTCTGACCAAGGAAC 1439
QY      1523 CTTTGTGCTACTCAGGCTCTCTTGTGAAACCCAG---CTCTGCTGCTGCCAGTGA 1578
Db      1440 CTTTGTGCTACTCAGGCTCTCTTGTGAAACCCAGCTCTCTCTCTCTGCCAGTGA 1499
QY      1579 GACTTGTGATGAGCAGCATCGAGGAAGCTGGGTCCAGCTGGGATGATGATGAGCTC 1638
Db      1500 GACTTGTGATGAGCAGCATCGAGGAAGCTGGGTCCAGCTGGGATGATGATGAGCTC 1559
QY      1639 TATAGACCATCCCTCTCTGCAATCAATTAAC 1669
Db      1560 TGTATCTGTGCTCTCTCTCAATTAATTAAC 1590

RESULT 9
LOCUS   MMU46068 1654 bp mRNA linear ROD 26-SEP-2002
DEFINITION Mus musculus von Ebner minor salivary gland protein mRNA, complete cds.
ACCESSION U46068
VERSION  U46068.3 GI:23327116
KEYWORDS
SOURCE  Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1654)
AUTHORS  Snead,M.L., Villanueva,J., Paine,M.L., Lei,Y.P., Zhu,D.H.,
          Luskis,J., Xia,Y.-R. and Yang,J.-N.
TITLE     Direct Submission
JOURNAL   Submitted (17-JAN-1996) Malcolm L. Snead, Center for Cranio
          Molecular Biology, University of Southern California, 2250 Alcazar
          St., Los Angeles, CA 90033, USA
REFERENCE 2 (bases 1 to 1654)
AUTHORS  Snead,M.L., Villanueva,J., Paine,M.L., Lei,Y.P., Zhu,D.H.,

```

```

Luskis,J., Xia,Y.-R. and Yang,J.-N.
Direct Submission
Submitted (26-SEP-2002) Center for Cranio Molecular Biology,
University of Southern California, 2250 Alcazar St., Los Angeles, CA
90033, USA
REMARK   Sequence update by submitter
COMMENT   On Sep 26, 2002 this sequence version replaced gi:9789706.
FEATURES
         source
         1..1654
         /organism="Mus musculus"
         /mol_type="mRNA"
         /strain="Swiss-webster"
         /db_xref="taxon:10090"
         /chromosome="2"
         /map="2: D2Mit19 and D2Mit25n"
         221..1507
         /codon_start=1
         /product="von Ebner minor salivary gland protein"
         /protein_id="AA087581.3"
         /db_xref="gi:23327117"
         /translation="MMPDSSRSCHSPCKISLAVPILDSFVHTVRLTIMKRTS
         ANIQLDQPSYDQELVYRIPDMVAGLINTPLKTYEPROMSTFVQALIVERSKG
         PAHLNLSDCSSNESTLRSLKHSFYVNSLAKNVMILVPLQYVKNHLCPTVQA
         FDMYEDFLRLTAPIALSPALERGLISPAIODSNILNLKAKLDSQARQWTFNN
         SATSLMETTPDPAPESLVRODLVNAIVTTLVYKRELVTLRFVLPDVARQLOMDIKE
         INAEANKLGFLOMLKIFTHSPHIVLNEGSAKAAQSVLLEFVPTNPDRPFSIGIE
         ASYEAKQFTEDNRLMLNFNNVSIERIKMISDRLKLFDEVLKDLITLLEYTLNEN
         GRLRPGVMSKSLGIEKAMSVSKGLKLTLPASS"
BASE COUNT  418 a 506 c 394 g 336 t
ORIGIN
Query Match      49.4%; Score 830.4; DB 10; Length 1654;
Best local Similarity 71.0%; Pred. No. 66-188;
Matches 1155; Conservative 0; Mismatches 466; Indels 5; Gaps 4;
QY      57 CGGGCCGAGAGACTCCAGGCTGCCAGCTGGCATCTTG-CAGTGTGCTGCCCTTGACAC 115
Db      14 CAGACCCAGAGACTCTGGACATTCAGTCTCTACTGCTGACCTCACTTCTCAGGACAC 73
QY      116 CTGGGAAGATGGCGGGCCCGGGAGACTCACCTTCTGCTGGTGGTGGGACACCT 175
Db      74 CCAGGAAGATGGCGGGCCCGGGAGACTTATTCACCTCTCTGTGTTGCTGGGAGCACAC 133
QY      176 TGATCAAGCCACCTCAGTCCACTGATCTCATCTCTCGGCCCAAGATCATCAAG 235
Db      134 TGCTCAAGGCTATAGCTATATCCCTCGAGTGTCTCAACCTTGCCAGAAAGTATCCAGA 193
QY      236 AAAAGCTGACAGAGACTGAAAGACACACACCCACACAGATCTTGCAGAGCTGCCG 295
Db      194 AACACCTGACCCAGGACGACGAGGAGACATGATGATCCATCTCCAGGAGTTGCCAC 253
QY      296 TGCTCAGTGGCATGGGGGAAAGCCAGCCGAGGAGATCCCTGTGCTGGGAGCCTGGTGA 355
Db      254 TGCTCAGAGCCATGCAAGATTAAGTGTGGCAG-TATCCCCCATACTGAGACAGCTTGTGCA 312
QY      356 CACCTCTCTGAAGACATCATCTGCTGGAAGGTCAACAGCTTAACATCTCTCACTGCA 415
Db      313 CACCTCTCTGAAGATCATCATCTGATGATGAAGGTCACTCTGCTTAACATCTCTCACTGCA 372
QY      416 GGTGAAGCCCTGGGCAATGACACAGAGCTGTGTAGTCAAGATCCCCCTGGAGCATGTGGC 475
Db      373 TGTGCAAGCTTCAATTATGACACAGAGCTGTGTGAGAAATCCCTCGGAGATGTGGC 432
QY      476 TGGATTCACACAGCCCTGGTGAAGACCATGCTGGAGTTCCATGAGAGAGTGGAGCCCA 535
Db      433 TGGACTTAACACACACACTGATCAACACCATTAAGAGTTCCAAATGAGACCCGAGAGTCCA 492
QY      536 AGCCACATCCGCATGAGACACACAGTGAAGTGGCCCAACCCGCTGCTCAGTCAAGTGG 595
Db      493 AGCCCTCATCCGGGATGAGAGGACGAGAGGCGCCGCCACCTGGAATTCAGGAGTGG 552
QY      596 TGCCACGACCATGGGAGCTTGCGCATCAACTGCTGATTAAGTCTCTCTCTGCTGGTGA 655

```

```

Db      553 CTCACGACATGAGACACCCCTGCGCTCAGCCTGCTTCACAAAGCTCTCTGCTGTGTCAC 612
QY      656 CGCCTTAGCTAAGCAGTGCATGAACCTCTAGTGCATCCCTGCCAAATCTAGTGAAGAAA 715
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      613 CTCCTTGCGAAGAAATGTTATGAAATCTCTGCTGCGACCCCGCCCAATATGCTAAAAA 672
QY      716 CCAGCTGTGCTCCCGTATCGAGGCTTCTTCAATGGCATGTATGACAGACCTCTGACCT 775
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      673 CCACCTGTGCGCTGTGATCCAGCAGGACCTTGTGATGACATGTGACGAAGACTCTGAGACT 732
QY      776 GGTGAAGGTGGCCATGCTCCAGCATGACCGTGTGAGATTTGACCTTCTGTATCCCTGC 835
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      733 GACAAACAGACCCCATTTGCTCTAGTCTGAGACCCCTGAGATTTGGCTTCTGTCTCTGCG 792
QY      836 CATCAAGGCTGACACCATTCAGCTCTACCTGGGGGCCAAGTTGTTGAGACTCAGAGGAAA 895
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      793 TATCCAGGACAGATATATCTCTGTACCTGGAAGGCCAAGCTGCTGAGACTCAGAGCGAG 852
QY      896 GGTGACCAAGTGTTCATTAATCTGACAGCTTCCCTGACAAATGCCACCCCTGGACAACT 955
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      853 GGTAAACCAACTGCTTCAACAACTCTGCACTCTCTGTGATGAGAGACCCACAGAGGCG 912
QY      956 CCGCTTACGCTCATGCGAGTGCAGGACGTGCTGAAGCTGCAGGCTGCTGCTCTC 1015
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      913 CCCCCTTACGCTGACCGTGAAGGACGACCTGGTGAATGCCATTTGTGACACCCCTGGTCC 972
QY      1016 TCCAGAAATTCATGATGCTCTGTGAGCTCTGCTCTGCTGAGAGTGCCTCAGCTGAA 1075
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      973 CAAGAGAGGAGCTTGAATCTCTGCTCAGATTCGTGATTCGTGATGTCGCCCGGCTTACA 1032
QY      1076 GTCAAGCATCGGGCTGATCATGAAGAGCTGCAAGTAAAGCTGGAGTCTACCCAGATCT 1135
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1033 GATGACATCAAGGAATCAATGACAGAGCACCAAGCTGGGGCCACCAAGATGTT 1092
QY      1136 GAAGATCTAATCTCAGGACACCTCCGAGTTTATAGACCAAGGCATGCCAAGGTGCG 1195
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1093 GAAGATCTTACCCACAGACACCCCCACATTTGCTGTAAGAGGAGTGCACAGGCGAC 1152
QY      1196 CCACATGATCTGCTGTAAGTGTTCCTCCACAGTAAGCCCTCCGCTTGTTCACCT 1255
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1153 CCAAGTGTCTGCTGGAAGTGTTCCTTCCCAACATGATGTCGCCGCTTCTTCTCTCT 1212
QY      1256 GGGCATCGAAGCCAGCTCGGAAGTCAAGTTTACACCAAGGTGACCAATTAATCTAA 1315
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1213 CGGCATTTGAGCCAGTTATGAGCTCAAGTCTTACAGAAAGCAACCGGCTTATGCTCAA 1272
QY      1316 CTGGAATTAACATCAGCTCTGATCGATCCAGTGAAGTGAAGTCTGGATGGCTGCTCA 1375
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1273 CTTCATTAACGTCAATTAAGAGCATCAAGCTGATGATCTCAATATCAAACTATTCGA 1332
QY      1376 ACCGTATGTTTGAAGAAACATCATGAGATCATTCACATCTCTGCTCCGAAACA 1435
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1333 TCCTGAAGTCTGAAGAGACACCTGACCAAGATTCCTGGAATACACTCTCTCCCAATA 1392
QY      1436 GAATGGCAAAATTAAGATCTGGGTCCTCAGTGTCAATGTGGAAGCCCTTGGATTGAGGC 1495
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1393 GAATGGCAAACTGAAGAGCTGAGTCCCATGTCAATGTCAAGGCTTGGGATGAGAAA 1452
QY      1496 ACTGAGTCTCAGACCAAGATGAGTCCCTTGTGCTACTCAGAGCTCTCTTGTGAGAAC 1555
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1453 AGCCATGTGCTGTGAGACAGGTCCTCAAGCTCAAGCTCTCTCTCTCAAGAAC 1512
QY      1556 CAGCTCTCC -TGTCTCCAGTGAAGACTTGAATGAGCGCATCAGGAGAGGCTGGTCCC 1614
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1513 TGGCTCCCGCCCTCCTGATGATGAGACCTGAGACAGTGAAGCCCGGCGCAGGTCCC 1572
QY      1615 AGCTGGAGTATGAGGTGTGAGCTCTATAGACATCCCTCTGTGCAATCAATAACACTTG 1674
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1573 AGCCAGGAGTGTGGAAGCTCACTGTGTAGAC--TACCCCTGCAAGTATATAACACTTG 1630
QY      1675 CCGTGTG 1680
        ||||| |||||
Db      1631 CCGGTG 1636

```

```

RESULT 10
AX301908
LOCUS      AX301908
DEFINITION Sequence 15 from Patent WO0174851.
ACCESSION AX301908
VERSION    AX301908.1 GI:17382958
KEYWORDS
SOURCE
ORGANISM  Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  1. Majumder, K., Spaderna, S.K., Taupier, R.J., Padigar, M.,
    Burgess, C.E., Shlmkets, R.A., Spytek, R.A., Liu, X., Patturejan, M. and
    Gusev, V.Y.
    Novel proteins and nucleic acids encoding same
    Patent: WO 0174851-A 15 11-Oct-2001;
    Curegen Corporation (US)
FEATURES
    source
        1..1035
        /organism="Homo sapiens"
        /mol_type="genomic DNA"
        /db_xref="taxon:9606"
        79..1035
        /note="unnamed protein product"
        /codon_start=1
        /protein_id="CAD13090.1"
        /db_xref="GI:1738295"
    CDS
        1..1035
        /translation="MAGPWTFTLGLLAATLIQATLSPTAVLLIGPVYIKRKLTOEL
        RDHNTSILQQLPLLSAMKEPKAGGIPIVGLSVNVLKHIILKTYNTLLOLVKPS
        ANDOLVYKIPLDNFAVETPLKTIIVEHMTLEQATLRMDTSASGPRILSDCAT
        SHGSLRIOLHRLSFLVNALAKOVNVLVPSLPNTVKNOICLVIRASNGWADLIOL
        VKRGSALSPFSPSTTELASRGRKYTKENNNSAALSTMETLDNIFSLVSQDVYKAA
        VAAVLSPEFMTLDSVNVNLSTRQIKGPRPHRNFNLNIGCP"
BASE COUNT      230 a      333 c      261 g      211 t
ORIGIN
Query Match      48.0%; Score 806; DB 6; Length 1035;
Best Local Similarity 91.5%; Pred. No. 4,3e-182;
Matches 906; Conservative 0; Mismatches 35; Indels 49; Gaps 3;
QY      63 GAGGACTCCAGGCTGCCAGTCTGTGATCTGACATCTGCTGCTCCCTGACACTGGGAA 122
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      18 GAGGACTCCAGGCTGCCAGTCTGTGATCTGACATCTGCTGCTCCCTGACACTGGGAA 77
QY      123 GATGGCCGGCCGCTGAGCTTCAACCTTCTGTGTGTTGCTGGACACCTTGATCCA 182
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      78 GATGGCCGGCCGCTGAGCTTCAACCTTCTGTGTGTTGCTGGACACCTTGATCCA 137
QY      183 AGCCACCCCTCAGTCCCTCAGTGTCTGATTCATTCCTCCGCGCCCAAGATCAAGAAAGCT 242
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      138 AGCCACCCCTCAGTCCCTCAGTGTCTGATTCATTCCTCCGCGCCCAAGATCAAGAAAGCT 197
QY      243 GACACAGAGCTGAAGAGACACAGACCCACAGCATCTGACAGACGCTGCCGTGCTCAG 302
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      198 GACACAGAGCTGAAGAGACACAGACCCACAGCATCTGACAGACGCTGCCGTGCTCAG 257
QY      303 TGGCATGCGGGAAAGACCCAGCGGAGG-ATCCCTGTGTGTTGGGACGCTGTGTAACCGCT 361
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      258 TGGCATGCGGGAAAGACCCAGCGGAGGATCCCTGTGTGTTGGGACGCTGTGTAACCGCT 317
QY      362 CCGAAGACATCATCTGCTGTAAGTGCATCAGTATACATCTCCACCTGCAAGTGA 421
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      318 CCGAAGACATCATCTGCTGTAAGTGCATCAGTATACATCTCCACCTGCAAGTGA 377
QY      422 GCCCTGCGCAATGACACAGAGCTGTACTCAAGATCCCTCTGACATGAGTGGCTGAT 481
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      378 GCCCTGCGCAATGACACAGAGCTGTACTCAAGATCCCTCTGACATGAGTGGCTGAT 437
QY      482 CAACACGCCCTGTGTGAAGACATCTGTGATTTCAACATGACGATGAGGCCCAAGCCAC 541
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```



Db	438	CAACAGCGCCCTGGTCCAAGACCAATCGTGGAAATTCACATATGACGATGAGGCCCAAGCAC	497
QY	542	CATCCCGCATGAGACACCAAGTCGAATGGGCCACCCGCCCTGGTCTCAATGACTGTGCCAC	601
Db	498	CATCCCGCATGAGACACCAAGTCGAATGGGCCACCCGCCCTGGTCTCAATGACTGTGCCAC	557
QY	602	CAGCCATGGGAGCCCTGGGCATCCAAACGTGCTCAATAGCTCCCTCCCTGGGAGAACGCCCT	661
Db	558	CAGCCATGGGAGCCCTGGGCATCCAAACGTGCTCAATAGCTCCCTCCCTGGGAGAACGCCCT	617
QY	662	AGCTAAGCAGGTCATGAACCTCTCAAGTGCATTCCTCGGCCCAATGTAGTGAAGAAACAGCT	721
Db	618	AGCTAAGCAGGTCATGAACCTCTCAAGTGCATTCCTCGGCCCAATGTAGTGAAGAAACAGCT	677
QY	722	GTTGTCGCCGTGATGAGGCGCTTCCTCAATGAGCATGTATGACAGCCCTCTGACGTGATGAA	781
Db	678	GTTGTCGCCGTGATGAGGCGCTTCCTCAATGAGCATGTATGACAGCCCTCTGACGTGATGAA	737
QY	782	GGTCCGCCATTTCCCTCAGCAATTGACCGCTGTGGAAATTTGACCTTTCTGATTCCTGGCATCA	841
Db	738	GG-----GTAGGTGCTGCTGCTCTCTCTCCACATTTTTCCT-----	772
QY	842	GGGTGACACCAATTCAGCTCTACCTGAGGGGGCCAGATTTGTGTGACATCACAGGGAAGGTATC	901
Db	773	-----TTACTACGGAAGCTGGCCCTCCAGAACCCGGAAAGGTATC	809
QY	902	CAAGTGGTTCATAATCTCTGCAGCTTCCCTGACATGCCCCAACCCCTGGACCAACATCCGTT	961
Db	810	CAAGTGGTTCATAATCTCTGCAGCTTCCCTGACATGCCCCAACCCCTGGACCAACATCCGTT	869
QY	962	CAGCCTCATGCTGATGACAGACGCTGGTGAAGTTCAGATGGCTGCTGTCTCTCCAGA	1021
Db	870	CAGCCTCATGCTGATGATGACAGACGCTGGTGAAGTTCAGATGGCTGCTGTCTCTCCAGA	929
QY	1022	AGAAATCATGTCCTCGTTTGAGACTGTGTGCT	1051
Db	930	AGAAATCATGTCCTCGTTTGAGACTGTGTGCT	959

	RESULT 11			
LOCUS	AXJ01906	963 bp	DNA	linear PAT 30-NOV-2001
DEFINITION	Sequence 13 from Patent WO0174851;			
ACCESSION	AXJ01906			
VERSION	AXJ01906.1			
KEYWORDS	GI:17382956			
SOURCE	.			
ORGANISM	Homo sapiens (human)			
	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1			
AUTHORS	Matumder, K., Spaderna, S.K., Taupier, R.J., Padigaru, M., Burgess, C.E., Shinkema, R.A., Spytek, K.A., Liu, X., Patturajan, M. and Gusev, V.Y.			
TITLE	Novel proteins and nucleic acids encoding same			
JOURNAL	Patent: WO 0174851-A 13 11-Oct-2001;			
FEATURES	Curagen Corporation (US)			
source	Location/Qualifiers			
	1..963			
	/organism="Homo sapiens"			
	/mol_type="genomic DNA"			
	/db_xref="taxon:9606"			
	1..963			
	/note="unnamed protein product"			
	/codon_start=1			
	/protein_id="CAD13089.1"			
	/db_xref="GI:17382957"			
	/translation="MAGPWTFTLLCGLLAATLIQATLSPYAVILIGPKVIKESITOEI			
	KDHNATSILOOLPLLSAMREKPGAGIVLGSLVNTVKHTPPSLKYTANIILQLOYKA			
	PSADNDQLIAVLPLDMVAGFMTPEIKTVIEFHMTTEQAOTRMPTSGAPRIYLISPC			
	ATSHGSIRIQDLHKLSFLVNALAQVNNILVSLPNLYKNDCPYITASFNGRTADILL			
	QLVAGRSALSPTFSFTTELASRPGKTKMNNSAASLTMPDNLIPSLIVSDVVAK			
	AAVAAYISPEEFWTLDSVYNLSTRHIGPRPHRFNLNIGCP"			

BASE COUNT	217	a	314	c	237	g	195	t
ORIGIN								
Query Match	43.1%	Score 724..2;		DB 6;	Length 963;			
Best Local Similarity	90.1%	Pred. No. 1,'e-162;						
Matches 842; Conservative	0;	Mismatches	38;	Indels	55;	Gaps	4;	
OY	124	ATGCGCGGGCCGTGGACCTTCACCCTTCTCTGTGTGGTTGCTGGCAGGCCACTTGATCCAA	183					
Dd	1	ATTGCCTGGCCCCGTGGACCTTCACCCCTTCTGTGTGGTTGCTGGCAGGCCACTTGATCCAA	60					
OY	184	GCCACCCCTCAAGTCCCATGGAGTTCATATCCCTGGGCCCCAAAAGTCATAAAGAAACCTG	243					
Dd	61	GCCACCCCTCAAGTCCCATGGAGTTCATATCCCTGGGCCCCAAAAGTCATAAAGAAACCTG	120					
OY	244	ACACAGAGAGCTGAAGAAGCACACAACGCCACACAGATCTCTGACAGCAGTGGCCGTGCTCAGT	303					
Dd	121	ACACAGAGAGCTGAAGAAGCACACAACGCCACACAGATCTCTGACAGCAGTGGCCGTGCTCAGT	180					
OY	304	GCCATGGGGGAAAAAGCCAGCCGGAGG-AATCCCTGTGTGGGCACTGTGTGAACCCGTC	362					
Dd	181	GCCATGGGGGAAAAAGCCAGCCGGAGGATCCCTGTGTGGGCACTGTGTGAACCCGTC	240					
OY	363	CTGAAGCAATCA-----TCTGCTGAAGGTATCAAGCTAACATCCTCCACGCTGAC	416					
Dd	241	CTGAAGCAATCAATCCCATCCAGCTTAAGGTATCAAGCTAACATCCTCCACGCTGAC	300					
OY	417	GTGAAGCCCTTCGCCAATGACACAGAGCTGTACTCAAGATCCCCTGGAATGTGCT	476					
Dd	301	GTGAAGCCCTTCGCCAATGACACAGAGCTGTACTCAAGATCCCCTGGAATGTGCT	360					
OY	477	GGATTCAACACGCCCTGTGTACAGACCATGTGTGAGTTCCATAGACGACTGAGGCCAA	536					
Dd	361	GGATTCAACACGCCCTGTGTACAGACCATGTGTGAGTTCCATAGACGACTGAGGCCAA	420					
OY	537	GCCACCAATCCGCATGGAGACACAGTGAAGTGGCCCCACCCGCTGGTCCACAGTGA	596					
Dd	421	GCCACCAATCCGCATGGAGACACAGTGAAGTGGCCCCACCCGCTGGTCCACAGTGA	480					
OY	597	GCCACCAAGCCATGGAGAGCTGGCATCCAATGCTGTGATAAAGCTCTCTTCCTGGTAAC	656					
Dd	481	GCCACCAAGCCATGGAGAGCTGGCATCCAATGCTGTGATAAAGCTCTCTTCCTGGTAAC	540					
OY	657	GCCTTAGCTAAGCAGGTGATGACCTCTCTAGTGGCATCCCTGCCCAATCTAGTAAAAAC	716					
Dd	541	GCCTTAGCTAAGCAGGTGATGACCTCTCTAGTGGCATCCCTGCCCAATCTAGTAAAAAC	600					
OY	717	CAGGTGTGCCCGGATGACAGGCTTCTCTTAATGGCATGTATGAGACCTTCCTGACTG	776					
Dd	601	CAGGTGTGCCCGGATGACAGGCTTCTCTTAATGGCATGTATGAGACCTTCCTGACTG	660					
OY	777	GTGAAGGTGCCATTTCCCTCAGCATTTGACGCTTGGAGTTTGACCTTCTGTATCGGCC	836					
Dd	661	GTGAAG-----GTAGGTGCTTGTCTCTCTCTCCCACTTTTTCT---700						
OY	837	ATCAAGGTGACACCAATTCAGCTCTACCTGGGGGCCAAGTTGTTGACTACAGAGGAAG	896					
Dd	701	-----TTACTACGAGGTGGGCTCCAGCCCGGAAG732						
OY	897	GTGACCAAAGTGTTCATTAATCTGCAAGCTTCCCTGACAAATGCCACCCCTGGACAAATC	956					
Dd	733	GTGACCAAAGTGTTCATTAATCTGCAAGCTTCCCTGACAAATGCCACCCCTGGACAAATC	792					
OY	957	CCGTTCAAGCCCATCGTAGAGTCAGAGAGGTGTGAACCTGCAGAGGGTGGCTGTCTCTCT	1016					
Dd	793	CCGTTCAAGCCCATCGTAGAGTCAGAGAGGTGTGAACCTGCAGAGGGTGGCTGTCTCTCT	852					
OY	1017	CCAGAAAGTAATCATGTGCTCTTTGGACTGTGTGT1051						
Dd	853	CCAGAAAGTAATCATGTGCTCTTTGGACTGTGTGT887						

## RESULT 12



LOCUS	AR243136	1172 bp	DNA	linear	PAT 20-DEC-2002
DEFINITION	AR243136	Sequence 106 from patent US 6475753.			
ACCESSION	AR243136				
VERSION	AR243136.1	GI:27289829			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
BASE COUNT	287 a	358 c	281 g	238 t	8 others
ORIGIN					
Query Match		38.2%;	Score 641;	DB 6;	Length 1172;
Best Local Similarity		99.1%;	Pred. No. 1,4e-142;		
Matches	641;	Conservative	3;	Mismatches	3;
				Indels	0;
				Gaps	0;
QY	56	GC	GGG	CCG	AGAGACTC
Db	2	GC	GGG	CCG	AGAGACTC
QY	116	CT	GGG	AAAG	ATG
Db	62	CT	GGG	AAAG	ATG
QY	176	TG	ATC	CAAG	CC
Db	122	TG	ATC	CAAG	CC
QY	236	AA	AG	CTG	AC
Db	182	AA	AG	CTG	AC
QY	296	TG	CT	AG	TG
Db	242	TG	CT	AG	TG
QY	356	CA	CG	TG	CT
Db	302	CA	CG	TG	CT
QY	416	GG	TAA	AG	CC
Db	362	GG	TAA	AG	CC
QY	476	TG	AT	CA	AG
Db	422	TG	AT	CA	AG
QY	536	AG	CC	AC	CA
Db	482	AG	CC	AC	CA
QY	596	TG	CC	AC	CA
Db	542	TG	CC	AC	CA
QY	656	CG	CT	TA	AG
Db	602	CG	CT	TA	AG

LOCUS	AR243045	1175 bp	DNA	linear	PAT 20-DEC-2002
DEFINITION	Sequence 15 from patent US 6475753.				
ACCESSION	AR243045				
VERSION	AR243045.1	GI:27289738			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1175) Ruben,S.M., Nl,J., Rosen,C.A., Wei,Y.-F., Young,P., Florence,K., Sopper,D.R., Brewer,L.A., Endress,G.A., Carter,K.C., Muenskl,M., Ehner,R., Lafleur,D.W., Olsen,H., Shi,Y., Moore,P.A. and Komatoulis,G. 94 Human Secreted Proteins Patent: US 6475753-A 15 05-NOV-2002; Location/Qualifiers 1..1175 /organism="unknown"				
TITLE	94 Human Secreted Proteins				
JOURNAL	Location/Qualifiers				
FEATURES	1..1175				
BASE COUNT	290 a 359 c 286 g 239 t			1 others	
ORIGIN					
Query Match	37.8%: Score 634.8; DB 6; Length 1175;				
Best Local Similarity	99.5%: Pred. No. 4.4e-141;				
Matches 647; Conservative	0; Mismatches 2; Indels 1; Gaps 1;				
QY	54 GAGCGGGCCGAGGACTCCAGCGTCCGAGGCTGTGGATCTCGACTTGTGCGCCCTTGAC	113			
Db	1 GAGCGGGCCGAGGACTCCAGCGTCCGAGGCTGTGGATCTCGACTTGTGCGCCCTTGAC	60			
QY	114 ACCTGGGAGATGGCCCGCCCGCTGGACCTTACCCCTTCTGTGTGTTGCTGGACGCAC	173			
Db	61 ACCGGGGAGATGGCCCGCCCGCTGGACCTTACCCCTTCTGTGTGTTGCTGGACGCAC	120			
QY	174 CTTGATCCAGGCGCACCGTCAGTCCGACGTTCGACGTCTCATCTCTGGCCCAAAAGTCATCAA	233			
Db	121 CTTGATCCAGGCGCACCGTCAGTCCGACGTTCGACGTCTCATCTCTGGCCCAAAAGTCATCAA	180			
QY	234 AGAAAGCTGACACGAGGAGCTGGAAGGACACAAAGCCACAGACAGATCTGACGAGCTGCC	293			
Db	181 AGAAAGCTGACACGAGGAGCTGGAAGGAGACAAAGCCACAGACAGATCTGACGAGCTGCC	240			
QY	294 GCTGCTCAGTGTCCATGCGGGGAAAGCCAGCCGAGG-ATCCCTGTGCTGGGACGCTGGT	352			
Db	241 GCTGCTCAGTGTCCATGCGGGGAAAGCCAGCCGAGGAGATCCCTGTGCTGGGACGCTGGT	300			
QY	353 GAACACCGTCTGGAAGACATCATCTGGCTTAAGGTATATCAGCTAATCTTCCAGCT	412			
Db	301 GAACACCGTCTGGAAGACATCATCTGGCTTAAGGTATATCAGCTAATCTTCCAGCT	360			
QY	413 GCAGGTGAAGCCTTCGGCCATGTGACAGAGACTGTGTAAAGATCCCGCTGGACATGGT	472			
Db	361 GCAGGTGAAGCCTTCGGCCATGTGACAGAGACTGTGTAAAGATCCCGCTGGACATGGT	420			
QY	473 GGTGGATTCAACAGCCCTGTGTCAAGACCATGTTGAGATTGCACATGAGACTGAGGC	532			
Db	421 GGTGGATTCAACAGCCCTGTGTCAAGACCATGTTGAGATTGCACATGAGACTGAGGC	480			
QY	533 CCAAGGCCACATCCGCATGGACACCAAGTGGACAGTGGCCACCCGCGCTGGTCTCAAGTGA	592			
Db	481 CCAAGGCCACATCCGCATGGACACCAAGTGGACAGTGGCCACCCGCGCTGGTCTCAAGTGA	540			
QY	593 CTGTGGCCACCGCCATGGGAGCCTGGGATTCACATCTGGTGAATPAAAGCTCTCTTCCTGGT	652			
Db	541 CTGTGGCCACCGCCATGGGAGCCTGGGATTCACATCTGGTGAATPAAAGCTCTCTTCCTGGT	600			
QY	653 GAAGCGCTTAGCTAAGCAGGTCAATGAACCTCTAGTGGCATCCCTGCCA 702				
Db	601 GAAGCGCTTAGCTAAGCAGGTCAATGAACCTCTAGTGGCATCCATGCCAA 650				
RESULT 14					
LOCUS	AR273207	382 bp	DNA	linear	PAT 10-APR-2003
LOCUS	AR273207				

```

DEFINITION      Sequence 950 from patent US 6504010.
ACCESSION       AR273207
VERSION         AR273207.1 GI:29705092
KEYWORDS
SOURCE          Unknown.
ORGANISM        Unknown.
REFERENCE       1 (bases 1 to 382)
AUTHORS        Wang,T., Bangur,C.S., Lodes,M.J., Fanger,G.R., Vedvick,T.S.,
                Carter,D., Retter,M.W., Mannion,J., Fan,L.,
                Compositions and methods for the therapy and diagnosis of lung
                cancer
TITLE           Patent: US 6504010-A 950 07-JAN-2003;
                Location/Qualifiers
FEATURES        1..382
SOURCE          /organism="unknown"
BASE COUNT      92 a 103 c 95 g 92 t
ORIGIN
Query Match     22.7%; Score 382; DB 6; Length 382;
Best Local Similarity 100.0%; Pred. No. 1.6e-80;
Matches 382; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY              965 CCTCATCTGAGTGAAGACGTCGTGAAGCTGCATGCGCTGCTCTCTCCAGAGA 1024
                |||||||
DB              1 CCTCATCTGAGTGAAGACGTCGTGAAGCTGCATGCGCTGCTCTCTCCAGAGA 60
QY              1025 ATTCATGCTCTGTTGGAGCTGTGCTTCTGAGAGTCCCATCGGCTGAAGTCAAGCAT 1084
                |||||||
DB              61 ATTCATGCTCTGTTGGAGCTGTGCTTCTGAGAGTCCCATCGGCTGAAGTCAAGCAT 120
QY              1085 CGGGCTGATCAATGAAAAGCTGCAGATTAAGCTGGATCTACCAAGATCGTAGAGATCCT 1144
                |||||||
DB              121 CGGGCTGATCAATGAAAAGCTGCAGATTAAGCTGGATCTACCAAGATCGTAGAGATCCT 180
QY              1145 AACTCAGACACTCCCGAGTTTATATAGACCAAGGCCATGGCAAGTGGCCCAACTGAT 1204
                |||||||
DB              181 AACTCAGACACTCCCGAGTTTATATAGACCAAGGCCATGGCAAGTGGCCCAACTGAT 240
QY              1205 CGTGTGGAAGTGTTCCTCCATGAAAGCCCTCCGCTTGTTCACCTGGGCATCGA 1264
                |||||||
DB              241 CGTGTGGAAGTGTTCCTCCATGAAAGCCCTCCGCTTGTTCACCTGGGCATCGA 300
QY              1265 AGCCAGCTCGGAAGCTCAGTTTACACCAAGGTGACCAACTTATACCTGAATTA 1324
                |||||||
DB              301 AGCCAGCTCGGAAGCTCAGTTTACACCAAGGTGACCAACTTATACCTGAATTA 360
QY              1325 CATCAGCTCTGATCGGATCCAG 1346
                |||||||
DB              361 CATCAGCTCTGATCGGATCCAG 382

RESULT 15
LOCUS          AR276788 382 bp DNA linear PAT 10-APR-2003
DEFINITION    Sequence 950 from patent US 6509448.
ACCESSION     AR276788
VERSION       AR276788.1 GI:29710435
KEYWORDS
SOURCE        Unknown.
ORGANISM      Unknown.
REFERENCE     1 (bases 1 to 382)
AUTHORS      Wang,T., Bangur,C.S., Lodes,M.J., Fanger,G.R., Vedvick,T.S.,
                Carter,D., Retter,M.W., Mannion,J., Fan,L., and Wang,A.
                Compositions and methods for the therapy and diagnosis of lung
                cancer
TITLE         Patent: US 6509448-A 950 21-JAN-2003;
                Location/Qualifiers
FEATURES      1..382
SOURCE        /organism="unknown"
BASE COUNT    92 a 103 c 95 g 92 t
ORIGIN

```

```

Query Match     22.7%; Score 382; DB 6; Length 382;
Best Local Similarity 100.0%; Pred. No. 1.6e-80;
Matches 382; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY              965 CCTCATCTGAGTGAAGACGTCGTGAAGCTGCATGCGCTGCTCTCTCCAGAGA 1024
                |||||||
DB              1 CCTCATCTGAGTGAAGACGTCGTGAAGCTGCATGCGCTGCTCTCTCCAGAGA 60
QY              1025 ATTCATGCTCTGTTGGAGCTGTGCTTCTGAGAGTCCCATCGGCTGAAGTCAAGCAT 1084
                |||||||
DB              61 ATTCATGCTCTGTTGGAGCTGTGCTTCTGAGAGTCCCATCGGCTGAAGTCAAGCAT 120
QY              1085 CGGGCTGATCAATGAAAAGCTGCAGATTAAGCTGGATCTACCAAGATCGTAGAGATCCT 1144
                |||||||
DB              121 CGGGCTGATCAATGAAAAGCTGCAGATTAAGCTGGATCTACCAAGATCGTAGAGATCCT 180
QY              1145 AACTCAGACACTCCCGAGTTTATATAGACCAAGGCCATGGCAAGTGGCCCAACTGAT 1204
                |||||||
DB              181 AACTCAGACACTCCCGAGTTTATATAGACCAAGGCCATGGCAAGTGGCCCAACTGAT 240
QY              1205 CGTGTGGAAGTGTTCCTCCATGAAAGCCCTCCGCTTGTTCACCTGGGCATCGA 1264
                |||||||
DB              241 CGTGTGGAAGTGTTCCTCCATGAAAGCCCTCCGCTTGTTCACCTGGGCATCGA 300
QY              1265 AGCCAGCTCGGAAGCTCAGTTTACACCAAGGTGACCAACTTATACCTGAATTA 1324
                |||||||
DB              301 AGCCAGCTCGGAAGCTCAGTTTACACCAAGGTGACCAACTTATACCTGAATTA 360
QY              1325 CATCAGCTCTGATCGGATCCAG 1346
                |||||||
DB              361 CATCAGCTCTGATCGGATCCAG 382

```

Search completed: October 9, 2003, 19:48:04  
 Job time : 6474.98 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2003, 13:21:47 ; Search time 4071.7 Seconds  
(without alignments)  
10028.129 Million cell updates/sec

Title: US-09-700-770-2

Perfect score: 1680

Sequence: 1 ggtgtcgaagataaaggtc.....tcaataacacttgcctgtg 1680

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 1215238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estnu:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrt1:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	835.2	49.7	945	12	BI772722 603053235
2	829.4	49.4	897	14	CA454720 AGENCOURT
3	791.2	47.1	852	12	BI818205 603032679
4	771	45.9	783	12	BI770190 603053221

C	5	764.4	45.5	818	13	BU684431	UT-CF-ENO
	6	762.4	45.4	807	12	BI823956	BI823956 603039139
	7	746.8	44.5	784	12	BI821790	BI821790 603035865
C	8	743.8	44.3	777	13	BU684288	UT-CF-ENO
	9	738.4	44.0	819	14	CA489712	CA489712 AGENCOURT
C	10	734	43.7	752	12	BM980522	UT-CF-ENO
	11	731.8	43.6	826	10	BG529820	BU529820 602558904
	12	724.8	43.1	887	14	CA488923	CA488923 AGENCOURT
C	13	721.4	42.9	753	13	BU684115	UT-CF-ENO
	14	720	42.9	752	13	BU684110	UT-CF-ENO
C	15	709.4	42.2	757	13	BU684195	UT-CF-ENO
	16	702.8	41.8	752	13	BU684379	UT-CF-ENO
	17	702.6	41.8	785	10	BG530180	BU530180 602558678
C	18	693.4	41.3	738	14	CB306180	CB306180 UT-CF-ENO
	19	684.6	40.8	955	12	BI821769	CA309029 UT-H-PT1-
C	20	677	40.3	707	14	CB305554	CB305554 UT-CF-ENO
	21	671.6	40.0	836	12	BI820886	BI820886 603033924
	22	670	39.9	682	13	BQ109522	BQ109522 Imageqc-7
C	23	652.4	38.8	672	14	CB306411	CB306411 UT-CF-ENO
C	24	652.4	38.8	672	14	CB321690	CB321690 UT-CF-ENO
C	25	640.4	38.1	672	14	CA309029	CA309029 UT-H-PT1-
	26	624.2	37.2	660	10	BG548906	BG548906 602557539
C	27	623.4	37.1	643	13	BU683805	BU683805 UT-CF-ENO
	28	623.2	37.1	796	10	BG540252	BG540252 602569143
C	29	622.4	37.0	644	13	BU683993	BU683993 UT-CF-ENO
	30	619.2	36.9	912	10	BG484717	BG484717 602505896
C	31	619	36.8	656	13	BU683678	BU683678 UT-CF-ENO
	32	618	36.8	658	10	BE061388	BE061388 QVO-BM022
C	33	617.4	36.8	637	14	CB854756	CB854756 UT-CF-ENO
C	34	614.8	36.6	761	13	BU686637	BU686637 UT-CF-ENO
C	35	614.4	36.6	657	12	BM969302	BM969302 UT-CF-ENO
C	36	613	36.5	643	12	BM992632	BM992632 UT-H-DT0-
C	37	608.8	36.2	642	13	BU683945	BU683945 UT-CF-ENO
	38	604	36.0	642	10	BF672220	BF672220 602150403
	39	598.8	35.6	640	10	BG489268	BG489268 602502981
	40	592.4	35.3	634	13	BU683699	BU683699 UT-CF-ENO
C	41	588.8	35.0	754	10	BG547238	BG547238 602574650
	42	587	34.9	602	10	BG530024	BG530024 602558870
	43	581.4	34.6	630	10	BG482764	BG482764 602502549
C	44	581.4	34.6	644	13	BU684008	BU684008 UT-CF-ENO
C	45	572.4	34.1	626	13	BU684353	BU684353 UT-CF-ENO

## ALIGNMENTS

RESULT 1  
LOCUS BI772722 945 bp mRNA linear EST 25-SEP-2001  
DEFINITION 603053235F1 NIH\_MGC\_122 Homo sapiens CDNA clone IMAGE:5202801 5',  
mRNA sequence.  
ACCESSION BI772722  
VERSION BI772722.1 GI:15764300  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 945)  
NIH-MGC http://mgc.ncl.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
Tissue procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLNL1508 row: e column: 10  
High quality sequence stop: 856.





|||||  
Db 541 TGTCCACACGACCCATGGAGGCTCGCATCCACTGCTGCAATGACTCTCTCTCTG 600  
QY 654 AACGCTTAGTAAAGCAGATCATACCTCTAGTGCATCCGCCAATCTGTGAAA 713  
Db 601 AACGCTTAGTAAAGCAGATCATACCTCTAGTGCATCCGCCAATCTGTGAAA 660  
QY 714 AACGCTTAGTAAAGCAGATCATACCTCTAGTGCATCCGCCAATCTGTGAAA 772  
Db 661 AACGCTTAGTAAAGCAGATCATACCTCTAGTGCATCCGCCAATCTGTGAAA 720  
QY 773 GCTGTGAAGGTGCGCCATTCCTCCAGATTCGACCTGCTGG-AGTTGACCTTGTATC 831  
Db 721 GCTGTGAAGGTGCGCCATTCCTCCAGATTCGACCTGCTGG-AGTTGACCTTGTATC 780  
QY 832 CTGCGATCAAGGGGTGACACATTCAGCTTACTCTG-GGGCAAGTGTGAGCTACAG 890  
Db 781 CTGCGATCAAGGGGTGACACATTCAGCTTACTCTG-GGGCAAGTGTGAGCTACAG 840  
QY 891 GGA 894  
Db 841 GGA 844

RESULT 4  
LOCUS B1770190 783 bp mRNA linear EST 25-SEP-2001  
DEFINITION 603053221F1 NIH\_MGC\_122 Homo sapiens cDNA clone IMAGE:520293 5',  
mRNA sequence.  
ACCESSION B1770190  
VERSION B1770190.1 GI:15761768  
KEYWORDS EST.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 783)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
http://image.lnl.gov  
Plate: L1AM1508 row: 1 column: 06  
High quality sequence stop: 782.

FEATURES  
source Location/Qualifiers  
1..783  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:520293"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_122"  
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;  
Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA source  
anonymous pool of 24 week female lung, 16 week female  
spleen, and 20-22 week male spleens. Library is oligo-dT  
primed and directionally cloned (EcoRV site is destroyed  
upon cloning). Average insert size 1.4 kb, insert size  
range 1-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 026. Note:  
this is a NIH-MGC Library."

BASE COUNT 167 a 261 c 199 g 156 t  
ORIGIN

Query Match 45.9%; Score 771; DB 12; Length 783;

Best Local Similarity 99.9%; Pred. No. 1 Be-176;  
Matches 782; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 53 GAGACGGGCGGAGAGCTCCAGCGTGGCCAGTGTGCGATCCTGACCTGCTGTA 112  
Db 1 GAGACGGGCGGAGAGCTCCAGCGTGGCCAGTGTGCGATCCTGACCTGTA 60  
QY 113 CACCTGGGAAGATGCGCGCGCGGAGCTTCAACCTCTCTGTGTGTTGCTGGACCA 172  
Db 61 CACCTGGGAAGATGCGCGCGCGGAGCTTCAACCTCTCTGTGTGTTGCTGGACCA 120  
QY 173 CCTTGATCCAAAGCCACCTTCAGTCCAGTCCAGTTCATCTCCGCGCCAAAGTATCA 232  
Db 121 CTTGATCCAAAGCCACCTTCAGTCCAGTTCATCTCCGCGCCAAAGTATCA 180  
QY 233 AAAAAAAGCTGACACAGAGAGCTGAAGACCAACAGCCACAGATCTGACAGACTGC 292  
Db 181 AAAAAAAGCTGACACAGAGAGCTGAAGACCAACAGCCACAGATCTGACAGACTGC 240  
QY 293 CGCTGCTCAGTGGCATGCGGGGAAAGCCAGCCGAGAG-ATCCCTGTGCTGGGACCTGG 351  
Db 241 CGCTGCTCAGTGGCATGCGGGGAAAGCCAGCCGAGAGATCCCTGTGCTGGGACCTGG 300  
QY 352 TGAACACCGTCTGGAAGACATCATCTGCTGGAAGTCAATCAAGCTTAACATCTCCAGC 411  
Db 301 TGAACACCGTCTGGAAGACATCATCTGCTGGAAGTCAATCAAGCTTAACATCTCCAGC 360  
QY 412 TGCAGTGAAGCCCTGCGCCATGACACAGAGCTGTAGTCAAGATCCCTGGACATGG 471  
Db 361 TGCAGTGAAGCCCTGCGCCATGACACAGAGCTGTAGTCAAGATCCCTGGACATGG 420  
QY 472 TGCCTGATTCAAACAGCGCCCTGGTCAAGACCATCTGAGTTCACATGACAGACTGAGG 531  
Db 421 TGCCTGATTCAAACAGCGCCCTGGTCAAGACCATCTGAGTTCACATGACAGACTGAGG 480  
QY 532 CCCAAGCCACCATCCGATGGAACACAGTGAAGTGGCCCAACCCGCTGTCTCAGTG 591  
Db 481 CCCAAGCCACCATCCGATGGAACACAGTGAAGTGGCCCAACCCGCTGTCTCAGTG 540  
QY 592 ACTGTGCCACAGCCGATGGGAGCGTGGGATCCACTGCTGATTAAGTCTCTCTCTGG 651  
Db 541 ACTGTGCCACAGCCGATGGGAGCGTGGGATCCACTGCTGATTAAGTCTCTCTCTGG 600  
QY 652 TGAACCGCTTAGCTAAGAGTCAAGTGAACCTCTGATGCGATCCCTGCCAATCTAGTA 711  
Db 601 TGAACCGCTTAGCTAAGAGTCAAGTGAACCTCTGATGCGATCCCTGCCAATCTAGTA 660  
QY 712 AAAACAGCTGTGTCTCCGATGAGAGCTTCTCAATGAGCATGTATGACAGCTCTGCG 771  
Db 661 AAAACAGCTGTGTCTCCGATGAGAGCTTCTCAATGAGCATGTATGACAGCTCTGCG 720  
QY 772 AGCTGTGAAGTGGCCATTCCTCCAGATTCGACCTGCTGAGTTGACCTTCTGTATC 831  
Db 721 AGCTGTGAAGTGGCCATTCCTCCAGATTCGACCTGCTGAGTTGACCTTCTGTATC 780  
QY 832 CTG 834  
Db 781 CTG 783.

RESULT 5  
LOCUS B0684431/c 818 bp mRNA linear EST 07-OCT-2002  
DEFINITION UI-CF-ENO-aco-n-04-0-UI-s1 UI-CF-ENO Homo sapiens cDNA clone  
B0684431  
ACCESSION B0684431.1 GI:23537379  
VERSION B0684431.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 818)

**AUTHORS** Bonaldo, M.F., Lennon, G. and Soares, M.B.  
**TITLE** Normalization and subtraction: two approaches to facilitate gene discovery  
**JOURNAL** Genome Res. 6 (9), 791-806 (1996)  
**MEDLINE** 97044477  
**PUBMED** 8889548  
**COMMENT** Contact: McCray, PB  
 McCray Lab  
 University of Iowa  
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
 Tel: 319 356 4866  
 Fax: 319 356 7171  
 Email: paul-mccray@uiowa.edu  
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).  
 Seq primer: M13 FORWARD  
 POLYA-Yes.

# FEATURES

## source

Location/Qualifiers

1. 818 /organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="UI-CF-ENO-aco-n-04-0-UI"

/tissue\_type="Primary Lung Cystic Fibrosis Epithelial Cells"

/dev\_stage="Adult"

/lab\_host="DH10B (Life Technologies) (r1 phage resistant)"

/clone\_1lb="UI-CF-ENO"

/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site.1: Ecor I; Site.2: Not I;

UI-CF-ENO is a cDNA library containing the following

tissue(s): Primary Lung Cystic Fibrosis Epithelial Cells.

The library was constructed according to Bonaldo, Lennon

and Soares, Genome Research, 6:791-806, 1996. First strand

cDNA synthesis was primed with an oligo-dT primer

containing a Not I site. Double stranded cDNA was ligated

to an Ecor I adaptor, digested with Not I, and cloned

directionally into pT73-Pac vector. The oligonucleotide

used to prime the synthesis of first-strand cDNA contains

a library tag sequence that is located between the Not I

site and the (dT)18 tail. The sequence tag for this

library is CAGCTCAGCT.

TAC\_LTB-UI-CF-ENO

TAG\_TISSUE-Human Lung Epithelial Cell Lines untreated LPS

6hr to LPS 24h

TAG\_SEQ-CAGCTCAGCT"

**BASE COUNT** 191 a 197 c 220 g 209 t 1 others

## ORIGIN

**Query Match** 45.58; Score 764.4; DB 13; Length 818;  
**Best Local Similarity** 99.5%; P-adj. 7.4e-175;  
**Matches** 798; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

**QY** 880 TGGACATCAGAGGAAAGGACCAAGGTTCAATACCTGACAGCTTCCCTGCATATGC 939

**Db** 818 TGGACTCAGAGGAA-GTACCAAGTGG-TCAATTAACCTGACAGCTTCCCTGCATATGC 761

**QY** 940 CCACCCGTGACAAATCCCTTACGCTCATCTGATGATGACAGAGTGTGAAAGCTCAG 999

**Db** 760 CCACCCGTGACAAATCCCTTACGCTCATCTGATGATGACAGAGTGTGAAAGCTCAG 701

**QY** 1000 TGGCTGCTGCTCTCTCC-AGAAGATTCATGCTCTGTGACATCTGTCTCTGAG 1058

**Db** 700 TGGCTGCTGCTCTCTCC-AGAAGATTCATGCTCTGTGACATCTGTCTCTGAG 641

**QY** 1059 AGTGGCCATGCGGTGAAGATGAGGCTGATCATATAAAGGCTGCAGATTAAGCTG 1118

**Db** 640 AGTGGCCATGCGGTGAAGATGAGGCTGATCATATAAAGGCTGCAGATTAAGCTG 581

**QY** 1119 GGATCTACCCAGATTCGTGAAGATCCTTAACCTAGGACACTCCAGTTTATAGACAA 1178

**Db** 580 GGATCTACCCAGATTCGTGAAGATCCTTAACCTAGGACACTCCAGTTTATAGACAA 521

**QY** 1179 GGCCATGCCAAGGTGGCCCAACTGATGCTGTGAGATGTTTCCCTCAGTGAAGCCCTC 1238

**Db** 520 GGCCATGCCAAGGTGGCCCAACTGATGCTGTGAGATGTTTCCCTCAGTGAAGCCCTC 461

**QY** 1239 CGCCCTTGTTCACCCCGGCGATCGAAGCCAGCTCGGAAGCTCAGTTTACCAAGGT 1298

**Db** 460 CGCCCTTGTTCACCCCGGCGATCGAAGCCAGCTCGGAAGCTCAGTTTACCAAGGT 401

**QY** 1299 GACCACTTATCTCACTTGAATTAACATCAGCTGATGATGATCAGTGAAGTACTT 1358

**Db** 400 GACCACTTATCTCACTTGAATTAACATCAGCTGATGATGATCAGTGAAGTACTT 341

**QY** 1359 GGGATTTGGCTGTTCCAACTGATGTTTGAAGAAATCATCATCTGATCATCTCC 1418

**Db** 340 GGGATTTGGCTGTTCCAACTGATGTTTGAAGAAATCATCATCTGATCATCTCC 281

**QY** 1419 ATCCTGCTGCGCAACCAAGATGCAATTAAGATCTGGGTCGACATGATGTTAG 1478

**Db** 280 ATCCTGCTGCGCAACCAAGATGCAATTAAGATCTGGGTCGACATGATGTTAG 221

**QY** 1479 GCGTTGGATTCGAGGAGCTGATGCTCTCACTGACCAAGATGCGCTTGTACTTCA 1538

**Db** 220 GCGTTGGATTCGAGGAGCTGATGCTCTCACTGACCAAGATGCGCTTGTACTTCA 161

**QY** 1539 GCGTCTTGTGAAACCCAGCTCTGTCTCTCCAGTGAAGACTTGGATGGACCATCA 1598

**Db** 160 GCGTCTTGTGAAACCCAGCTCTGTCTCTCCAGTGAAGACTTGGATGGACCATCA 101

**QY** 1599 GGGAAAGCTGGGTCGAGCTGGGAGTATGGGTGACCTGATTAAGACATCCCTCTGC 1658

**Db** 100 GGGAAAGCTGGGTCGAGCTGGGAGTATGGGTGACCTGATTAAGACATCCCTCTGC 41

**QY** 1659 AATCAATTAACACTTGGCTGTG 1680

**Db** 40 AATCAATTAACACTTGGCTGTG 19

**RESULT** 6

**BI823956** 807 bp mRNA linear EST 04-Oct-2001

**LOCUS** 603039139F1 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:518036 5',

**DEFINITION** mRNA sequence.

**ACCESSION** BI823956

**VERSION** BI823956.1 GI:15935506

**KEYWORDS** EST.

**SOURCE** Homo sapiens (human)

**ORGANISM** Homo sapiens

**REFERENCE** 1 (bases 1 to 807)

**AUTHORS** Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.

**TITLE** NIH-MGC http://mgc.nci.nih.gov/.

**JOURNAL** National Institutes of Health, Mammalian Gene Collection (MGC)

**COMMENT** Unpublished

Contact: Robert Strausberg, Ph.D.

Email: egadps@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.lnl.gov

Plate: L14M1449 row: m column: 09

High quality sequence stop: 793.

**FEATURES** Location/Qualifiers

1. 807 /organism="Homo sapiens"

/mol\_type="mRNA"



```

/db_xref="taxon:9606"
/clone="IMAGE:5180336"
/lab_host="DH10B"
/clone_1lb="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector:
PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

BASE COUNT      175 a      269 c      202 g      161 t
ORIGIN

Query Match      45.4%; Score 762.4; DB 12; Length 807;
Best Local Similarity 99.5%; Pred. No. 2.3e-174;
Matches 796; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

59 GGCAGAGACTCCAGCTGCCAGTCTGGATCTGCACTTGTGCTCCCTGACACTG 118
|||
4 GGGCGAGAGACTCCAGCTGCCAGTCTGGATCTGCACTTGTGCTCCCTGACACTG 63

119 GGAAGATGGCGCGCGCTGGACCTTCTCTGTGCTTGTGCTGGCAGCCACTTGA 178
64 GGAAGATGGCGCGCGCTGGACCTTCTCTGTGCTTGTGCTGGCAGCCACTTGA 123

179 TCCAGAGCCGCTCAGTCTCCAGTCTGATCTGCTGGCCCAAAAGTCATCAAGAA 238
124 TCCAGAGCCGCTCAGTCTCCAGTCTGATCTGCTGGCCCAAAAGTCATCAAGAA 183

239 AGCTGACACAGAGAGTGAAGGACACACACAGCATCTCTGACAGCTGCCCTGC 298
184 AGCTGACACAGAGAGTGAAGGACACACACAGCATCTCTGACAGCTGCCCTGC 243

299 TGAAGTCCATGGGGGAAAGCCAGCGGAGGATCCCTGTGGGACCTGGTGAMA 357
244 TGAAGTCCATGGGGGAAAGCCAGCGGAGGATCCCTGTGGGACCTGGTGAMA 303

358 CCGTCCGTAAGACATCATCTGCTGAAGTCAATCAGCTTAACATCTCCAGCTCAG 417
304 CCGTCCGTAAGACATCATCTGCTGAAGTCAATCAGCTTAACATCTCCAGCTCAG 363

418 TGAAGCCTCGGCGCAATGACAGAGAGCTGTAAGATCCCTCGACATGGTGCTG 477
364 TGAAGCCTCGGCGCAATGACAGAGAGCTGTAAGATCCCTCGACATGGTGCTG 423

478 GATTCAACACGCCCCCTGGTCAAGACCATGTGAGTTCACATGAGACTGAGGCCAAG 537
424 GATTCAACACGCCCCCTGGTCAAGACCATGTGAGTTCACATGAGACTGAGGCCAAG 483

538 CCACCATCCGATGACAGCAGTGAAGTGGCCGCCCGCGCTGCTCAAGTACTGTG 597
484 CCACCATCCGATGACAGCAGTGAAGTGGCCGCCCGCGCTGCTCAAGTACTGTG 543

598 CCACCATGAGGAGAGCTGCGCATCAACTGCTGATTAAGTCTCTCTCTGCTGTAAG 657
544 CCACCATGAGGAGAGCTGCGCATCAACTGCTGATTAAGTCTCTCTCTGCTGTAAG 603

658 CCTTAGCTAAGCAGTCAATGAACCTCTTAGTGCATCCCTGCCAATTAAGTAAAC 717
604 CCTTAGCTAAGCAGTCAATGAACCTCTTAGTGCATCCCTGCCAATTAAGTAAAC 663

718 AGCTGTCCTCCGATGCGAGGCTTCTTGAATGGCATGTATGAGAGCTCCCTGACCTGG 777
664 AGCTGTCCTCCGATGCGAGGCTTCTTGAATGGCATGTATGAGAGCTCCCTGACCTGG 723

778 TGAAGTGGCCATTTCTCTCAGCATTAACGCTTGGAGTTGACCTTCTGATCTGCA 837
724 TGAAGTGGCCATTTCTCTCAGCATTAACGCTTGGAG-TTGAAGCTTCTGATCTGCA 782

```

```

QY      838 TCAAGGTGACACCATTCAG 857
Db      783 TC-AGGTGACACCATTCAG 801

RESULT 7
B1821790      784 bp      mRNA      linear      EST 04-OCT-2001
LOCUS      60303585F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5176624 5'
DEFINITION      mRNA sequence.
ACCESSION      B1821790
VERSION      B1821790.1 GI:15933340
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
NIH-MGC http://mhc.nci.nih.gov/
1 (bases 1 to 784)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-riemail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM11440 row: b column: 17
High quality sequence stop: 763.
Location/Qualifiers
1..784
/morganism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5176624"
/lab_host="DH10B"
/clone_1lb="NIH_MGC_115"
/note="Organ: pooled brain, lung, testis; Vector:
PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

BASE COUNT      168 a      263 c      200 g      153 t
ORIGIN

Query Match      44.5%; Score 746.8; DB 12; Length 784;
Best Local Similarity 98.7%; Pred. No. 1.4e-170;
Matches 774; Conservative 0; Mismatches 7; Indels 3; Gaps 2;

55 AGCGGCGCAGAGACTCCAGCTGCCAGTCTGGATCTGCACTTGTGCTCCCTGACA 114
1 AGCGGCGCAGAGACTCCAGCTGCCAGTCTGGATCTGCACTTGTGCTCCCTGACA 60

115 CCTGGGAGATGGCGCGCGCTGGAGCTTACCCCTTCTGTGTGCTTGTGCTGACGAC 174
61 CCTGGGAGATGGCGCGCGCTGGAGCTTACCCCTTCTGTGTGCTTGTGCTGACGAC 120

175 TTGATCCAGCAGCAGCCCTGATCCAGTCTGAGTTCATCTCGGCGCAAAAGTCATCAA 234
121 TTGATCCAGCAGCAGCCCTGATCCAGTCTGAGTTCATCTCGGCGCAAAAGTCATCAA 180

235 GAAAGCTGACACAGAGAGTGAAGGACACAGCAGCAGCATCTGAGCAGAGTGGCG 294
181 GAAAGCTGACACAGAGAGTGAAGGACACAGCAGCAGCATCTGAGCAGAGTGGCG 240

```



Db 298 ACTGATCATCCATCCATCTCTGCTGCCGAACAGAAATGCAATTAATGATCTGGGGTC 239

QY 1461 CCAAGTGTATGTTGTAAGGCTTTGGGATTCAGAGCAGCTAGTCTCTCACTGACCAAGAT 1520

Db 238 CCAAGTGTATGTTGTAAGGCTTTGGGATTCAGAGCAGCTAGTCTCTCACTGACCAAGAT 179

QY 1521 GCCCTGTGCTTACTTCACAGCTCTTGTGGAAACCCAGCTCTCTGTCTCCAGTGAAGA 1580

Db 178 GCCCTGTGCTTACTTCACAGCTCTTGTGGAAACCCAGCTCTCTGTCTCCAGTGAAGA 119

QY 1581 CTTGGATGGCAGCAGTATGAGGAGGCTGGTCCAGCTGGAGTATGAGTGGAGTCTCA 1640

Db 118 CTTGGATGGCAGCAGTATGAGGAGGCTGGTCCAGCTGGAGTATGAGTGGAGTCTCA 59

QY 1641 TAGACCATCCCTCTCTGCAATCAATTAACACTTGGCTGTG 1680

Db 58 TAGACCATCCCTCTCTGCAATCAATTAACACTTGGCTGTG 19

RESULT 9 CA489712 819 bp mRNA linear EST 14-NOV-2002

LOCUS CA489712 AGENCOURT.10810488 MAPcl Homo sapiens cDNA clone IMAGE:6722193 5',

DEFINITION mRNA sequence.

ACCESSION CA489712

VERSION CA489712.1 GI:24952503

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM Homo sapiens (human)

REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Euthera; Primates; Carnivora; Homiidae; Homo.

AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cga@briemail.nih.gov

Tissue Procurement: Kristi A. Eglund, Ira Pastan

cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed By: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLNL4284 row: 1 column: 09

High quality sequence stop: 605.

Location/Qualifiers

1. 819

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6722193"

/cell\_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, HERT-HMEL, LNCaP"

/lab\_host="EMD10B"

/clone\_lib="MAPcl"

/note="Vector: pCMV-SPORT6; Site\_1: EcoRV; Site\_2: Not I; Subtracted with brain, liver, lung, kidney and muscle. Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Eglund, James J. Vincent, Robert Strausberg, Bungkok Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins. Manuscript submitted."

BASE COUNT 173 a 276 c 206 g 164 t

ORIGIN

Query Match 44.0%; Score 738.4; DB 14; Length 819;

Best Local Similarity 99.4%; Pred. No. 1.5e-168;

Matches 783; Conservative 0; Mismatches 1; Indels 4; Gaps 4;

QY 63 GAGGACTCCAGCGGCCAGGCTGGCATCTGACCTAGCCCTCGACACCTGGGAA 122

|||||

Db 1 GAGGACTCCAGCGGCCAGGCTGGCATCTGACCTTGCCCTCGACACCTGGGAA 60

QY 123 GATGGCGGGCCGGTGGACCTTACCTTCTCTGTTGGTGGACAGCCACTTATCCA 182

Db 61 GATGGCGGGCCGGTGGACCTTACCTTCTCTGTTGGTGGACAGCCACTTATCCA 120

QY 183 AGCCACCCCTCAGTCCCACTGCAATTCCTCGGCCCCAAAGTCATCAAAAGAGT 242

Db 121 AGCCACCCCTCAGTCCCACTGCAATTCCTCGGCCCCAAAGTCATCAAAAGAGT 180

QY 243 GACACAGAGAGCTGAAGAGACACACAGCCACAGCATCTGACAGAGCTGGCTCAG 302

Db 181 GACACAGAGAGCTGAAGAGAGACACACAGCCACAGCATCTGACAGAGCTGGCTCAG 240

QY 303 TGCATATGGGGGAAAGCCAGCGGAGG-ATCCCTGTGCGGGGACCTGGTAAACCGT 361

Db 241 TGCATATGGGGGAAAGCCAGCGGAGG-ATCCCTGTGCGGGGACCTGGTAAACCGT 300

QY 362 CCTGAAGCAGCATCTGCTGAGGCTGATGATGATGATGATGATGATGATGATGAT 421

Db 301 CCGTAAGCAGCATCTGCTGAGGCTGATGATGATGATGATGATGATGATGATGAT 360

QY 422 GCCCTGGCCAAATGACACAGAGCTCTGATGATGATGATGATGATGATGATGAT 481

Db 361 GCCCTGGCCAAATGACACAGAGCTCTGATGATGATGATGATGATGATGATGAT 420

QY 482 CAACAGGCCCCGTCAGAGACCATGATGATGATGATGATGATGATGATGATGAT 541

Db 421 CAACAGGCCCCGTCAGAGACCATGATGATGATGATGATGATGATGATGATGAT 480

QY 542 CATCGGCAATGACACAGAGCTCTGATGATGATGATGATGATGATGATGATGAT 601

Db 481 CATCGGCAATGACACAGAGCTCTGATGATGATGATGATGATGATGATGATGAT 540

QY 602 CAGGATGGGAGCGCGGATGATGATGATGATGATGATGATGATGATGATGAT 661

Db 541 CAGGATGGGAGCGCGGATGATGATGATGATGATGATGATGATGATGATGAT 600

QY 662 AGCTAAGCAGCATCTGCTGAGGCTGATGATGATGATGATGATGATGATGATGAT 721

Db 601 AGCTAAGCAGCATCTGCTGAGGCTGATGATGATGATGATGATGATGATGATGAT 660

QY 722 GTGTCCCGTATGAGAGCTTCTTCAATGATGATGATGATGATGATGATGATGAT 781

Db 661 GTGTCCCGTATGAGAGCTTCTTCAATGATGATGATGATGATGATGATGATGAT 720

QY 782 GGTGCCAATTCCTGACATGATGATGATGATGATGATGATGATGATGATGAT 838

Db 721 GGTGCCAATTCCTGACATGATGATGATGATGATGATGATGATGATGATGAT 780

QY 839 CAAGGGTG 846

Db 781 CAAGGGTG 788

RESULT 10 BM980522 752 bp mRNA linear EST 21-FEB-2003

LOCUS BM980522/C

DEFINITION UT-CF-EN1-add-c-18-0-UT.s1 UT-CF-EN1 Homo sapiens cDNA clone

UT-CF-EN1-add-c-18-0-UT 3', mRNA sequence.

ACCESSION BM980522

VERSION BM980522.1 GI:19602070

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Carnivora; Homiidae; Homo.

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477



adaptor sequence: 5'-CAAGCGCATTAAGCC-3' and 3' adaptor sequence: 5'-ATTCTAAGCGCGAGGCGGCAGCATG-dt(30)BN-3' (where B = A, C, G, or T). Clones inserted size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by clonech Laboratories (Palo Alto, CA). Note: this is a NIH-MGC Library."

BASE COUNT 179 a 271 c 213 g 163 t  
ORIGIN

Query Match 43.6%; Score 721.8; DB 10; Length 826;  
Best Local Similarity 97.5%; Pred. No. 6.3e-167;  
Matches 806; Conservative 1; Mismatches 13; Indels 7; Gaps 6;

```

QY 42 GGGAGAGGAGGAGCGGGCCGAGAGCTCAAGCGTGCAGAGTCTGSCATCTGCACCTTG 101
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 GGGAGAGGAGGAGAGCGGGCCGAGAGCTCAAGCGTGCAGAGTCTGSCATCTGCACCTTG 61
QY 102 CTGCGCTCTGACACTGCGGAAGATGCGCGCCGCGGACCTTCAACCTCTCTGCGTT 161
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 CTGCGCTCTGACACTGCGGAAGATGCGCGCCGCGGACCTTCAACCTCTCTGCGTT 121
QY 162 GCTGCGACCGCACTGATCCCAAGCCGCTGAGTCCCACTGCGAGTCTCATCTCTGCGCC 221
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 122 GCTGCGACCGCACTGATCCCAAGCCGCTGAGTCCCACTGCGAGTCTCATCTCTGCGCC 181
QY 222 AAAAGTCATCAAAAAGAAAGCTGACACAGAGAGCTGAAGAGCCCAAGCCGACAGATCT 281
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 182 AAAAGTCATCAAAAAGAAAGCTGACACAGAGAGCTGAAGAGCCCAAGCCGACAGATCT 241
QY 282 GCAGAGAGTGGCGGCTGATGAGTGCATGCGGAGAAAGCCAGCGGAGG-ATCCCTGTGCT 340
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 242 GCAGAGAGTGGCGGCTGATGAGTGCATGCGGAGAAAGCCAGCGGAGGATCTCTGTCT 301
QY 341 GGGCAGCGCTGTGTAACACCGCTCTGAGAGCATATCTGTGTAAGGTCTATCACAGCTAA 400
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 302 GGGCAGCGCTGTGTAACACCGCTCTGAGAGCATATCTGTGTAAGGTCTATCACAGCTAA 361
QY 401 CATCTCCAGCTGACAGGTGAAGCCCTCGGCGCAATACAGAGAGAGTCTAGTCAAAATGCC 460
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 362 CATCTCCAGCTGACAGGTGAAGCCCTCGGCGCAATACAGAGAGAGTCTAGTCAAAATGCC 421
QY 461 CCTGACATGATGCTGATGATCAACAGCGCCCTGGTCAAGACCATGAGTTCACAT 520
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 422 CCTGACATGATGCTGATGATCAACAGCGCCCTGGTCAAGACCATGAGTTCACAT 481
QY 521 GACGAGTGAAGGCCCAAGCCATCCGATGAGACACCAAGTGAAGTGCACCGCGCT 580
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 482 GACGAGTGAAGGCCCAAGCCATCCGATGAGACACCAAGTGAAGTGCACCGCGCT 541
QY 581 GGTCTCAAGTACTGTGCGACCAAGCCATGAGAGCGCTCGGCAATCAACTGCTCATTAAGT 640
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 542 GGTCTCAAGTACTGTGCGACCAAGCCATGAGAGCGCTCGGCAATCAACTGCTCATTAAGT 601
QY 641 CTCTCTCCGAGGAAGCGCTT-AGCTAAGCAGATGATGAACCTCTAGTGCATCCCTG 699
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 602 CTCTCTCCGAGGAAGCGCTTAAAGTAAAGCAGATGATGAACCTCTAGTGCATCCCTG 661
QY 700 CCAATCTAGTGA AAAACAGCTGTGTCC--GTATGAGAGGCTTCTCTCAATGAGCATGTA 757
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 662 CCAATCTAGTGA AAAACAGCTGTGTCC--GTATGAGAGGCTTCTCTCAATGAGCATGTA 721
QY 758 TGCAGAGCTT-CCTGCAAGCTGTGTAAGTGCATTTCCCTCAAGCAATGAGCGTGAAT 816
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 722 TGCAGAGCTTCCCTGCAAGCTGTGTAAGTGCATTTCCCTCAAGCAATGAGCG-CTGAGT 780
QY 817 TTGACCTTCTGATCCTGCAATCAAGGTGACACCATTCAGCTCTAC 863
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 781 TGGACCTTCTGATCTGCCATC-AGGTGACCCCATTCAGTTCAC 826

```

RESULT 12

CA488923  
LOCUS CA488923 887 bp mRNA linear EST 14-NOV-2002  
DEFINITION AGENCOURT\_10808455 MAPL Homo sapiens CDNA clone IMAGE:6721128 5',  
RNA sequence.  
ACCESSION CA488923  
VERSION CA488923.1 GI:24951714  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 887)  
AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Kristi A. Eglund, Ira Pastan  
CDNA Library Preparation: Invitrogen Corp  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L14M14281 row: 1 column: 24  
High quality sequence stop: 613.  
location/Qualifiers  
1. 887  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6721128"  
/cell\_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231, hERT-HME1  
/LNCaP"  
/lab\_host="EMD10B"  
/clone\_lib="MAPL"  
/note="Vector: pCMV-SPORT6; Site.1: EcoRV; Site.2: Not I;  
Subtracted with brain, liver, lung, kidney and muscle.  
Directionally cloned. Priming method: oligo-dT. Average  
insert size: 1800 bp. Library amplification: 26,000 fold.  
Kristi A. Eglund, James J. Vincent, Robert Strausberg,  
Bunkook Lee & Ira Pastan. Discovery of new breast  
cancer genes encoding membrane and secreted proteins.  
Manuscript submitted."

BASE COUNT 196 a 285 c 227 g 178 t 1 others  
ORIGIN

Query Match 43.1%; Score 724.8; DB 14; Length 887;  
Best Local Similarity 97.6%; Pred. No. 3.3e-165;  
Matches 778; Conservative 0; Mismatches 13; Indels 6; Gaps 4;

```

QY 54 GAGGGGGCGAGGAGTCCAGCGTGCAGAGTGTGATCTGCACTTGTGCGCTCTGAC 113
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 GAGGGGGCGAGGAGTCCAGCGTGCAGAGTGTGATCTGCACTTGTGCGCTCTGAC 60
QY 114 ACCTGGAAGATGAGCGGCGCGCTGAGACCTTCAACCTCTGTGTGCTGTGAGACGAC 173
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ACCTGGAAGATGAGCGGCGCGCTGAGACCTTCAACCTCTGTGTGCTGTGAGACGAC 120
QY 174 CTGATCCAAAGCACCTTCAGTCCCACTGCAATTTCTATCTCGGCGCCAAAAGTATCAA 233
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 CTGATCCAAAGCACCTTCAGTCCCACTGCAATTTCTATCTCGGCGCCAAAAGTATCAA 180
QY 234 AGAAAAGCTGACACAGAGCTGAAGAGCCACACAGCCACAGACATCTGACAGACTGCC 293
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 AGAAAAGCTGACACAGAGCTGAAGAGCCACACAGCCACAGACATCTGACAGACTGCC 240
QY 294 GCTGCTCAAGTGCATGCGGGAAGAACCGAGAGG-ATCCCTGTGTGCGGAGCGTGGT 352
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 GCTGCTCAAGTGCATGCGGGAAGAACCGAGAGGATCCCTGTGTGCGGAGCGTGGT 300
QY 353 GAACACCGTCTGAAAGCACATCATGTGCTGAAGTCAATCAAGTAAATCTCTCAGGT 412
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

Db 301 GAACACCGCTCTGAGACATCATCTGCTGAAGGTATCATACAGCTACATCTCCAGCT 360  
QY 413 GCAGGTGAGACCCCTCGGCCAATGACGAGAGCTCTAGTGAAGATCCCTCGACATAGT 472  
Db 361 GCAGGTGAGACCCCTCGGCCAATGACGAGAGCTCTAGTGAAGATCCCTCGACATAGT 420  
QY 473 GCGTGAATTAAACAGCCCTGCTGACAGACCATGTGAGTTCACATGACGACTGAGGC 532  
Db 421 GCGTGAATTAAACAGCCCTGCTGACAGACCATGTGAGTTCACATGACGACTGAGGC 480  
QY 533 CCAAGCACCACATCCGATGAGACACAGTGAAGTGGGCCACCCGCTGGTCTCAGTGA 592  
Db 481 CCAAGCACCACATCCGATGAGACACAGTGAAGTGGGCCACCCGCTGGTCTCAGTGA 540  
QY 593 CTGTGCCACCAAGCCATGGAGCCCTGCGCATCCAACTCTGATAGCTCTCTCTCTGCT 652  
Db 541 CTGTGCCACCAAGCCATGGAGCCCTGCGCATCCAACTCTGATAGCTCTCTCTCTGCT 600  
QY 653 GAACGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 712  
Db 601 GAACGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 659  
QY 713 AAACACCTGTGTCCTGATGAGAGGCTTCTCTCAATGAGATGAGAGCTCTGAGCA 772  
Db 660 AAACACCTGTGTCCTGATGAGAGGCTTCTCTCAATGAGATGAGAGCTCTGAGCA 718  
QY 773 GCTGTGAAGTGGCCATTTCCCTCAGCATTTGACCTGCTGCTGCTGCTGCTGCTGCT 829  
Db 719 GCTGTGAAGTGGCCATTTCCCTCAGCATTTGACCTGCTGCTGCTGCTGCTGCTGCT 778  
QY 830 TCCTGCCATCAAGGCTG 846  
Db 779 TCCTGCCATCAAGGCTG 795

RESULT 13  
BU684115/c 753 bp mRNA linear EST 07-OCT-2002  
LOCUS BU684115  
DEFINITION UI-CF-ENO-acn-h-16-0-UI.s1 UI-CF-ENO Homo sapiens cDNA clone  
UI-CF-ENO-acn-h-16-0-UI 3', mRNA sequence.  
ACCESSION BU684115  
VERSION BU684115.1 GI:23536751  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 753)  
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 97044477  
PUBMED 8889548  
COMMENT Contact: McCray, PB  
McCray Lab  
University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171  
Email: paul-mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com) or from Open Biosystems  
(www.openbiosystems.com).  
Seq primer: M13 FORWARD  
POLYA-Yes.

FEATURES  
Source location/Qualifiers  
1..753  
/organism="Homo sapiens"

/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-CF-ENO-acn-h-16-0-UI"  
/tissue\_type="Primary Lung Cystic Fibrosis Epithelial  
Cells"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-CF-ENO"  
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a  
modified polylinker; Site 1: EcoR I; Site 2: Not I;  
UI-CF-ENO is a cDNA library containing the following  
tissue(s): Primary Lung Cystic Fibrosis Epithelial Cells.  
The library was constructed according to Bonaldo, Lennon  
and Soares, Genome Research, 6:791-806, 1996. First strand  
cDNA synthesis was primed with an oligo-dT primer  
containing a Not I site. Double stranded cDNA was ligated  
to an EcoR I adaptor, digested with Not I, and cloned  
directionally into pT73-Pac vector. The oligonucleotide  
used to prime the synthesis of first-strand cDNA contains  
a library tag sequence that is located between the Not I  
site and the (dr)18 tail. The sequence tag for this  
library is CTGCTCAGGT.  
TAG\_Lib=UI-CF-ENO  
TAG\_TISSUE=Human Lung Epithelial Cell Lines untreated LPS  
6hr to LPS 24h  
TAG\_SEQ=CTGCTCAGGT"

BASE COUNT 178 a 183 c 200 g 192 t  
ORIGIN  
Query Match 42.9%; Score 721.4; DB 13; Length 753;  
Best Local Similarity 99.7%; Pred. No. 2e-164;  
Matches 733; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 947 GGACACATCCCGTTCAGCCATCATGATGAGAGAGTGGGAAAGTGCAGTGGCTGC 1006  
Db 753 GGACACATCCCGTTCAGCCATCATGATGAGAGAGTGGGAAAGTGCAGTGGCTGC 694  
QY 1007 TGTGCTCTCTCAGAG-ATTTCATGCTCTCTGAGTCTGCTGCTGCTGCTGCTGCT 1065  
Db 693 TGTGCTCTCTCAGAGAAATTCAATGCTGCTGAGTCTGCTGCTGCTGCTGCTGCT 634  
QY 1066 ATGCGCTGAATCAAGATCGGCGCTGATCATGAAAGCTGCAGATTAAGCTGGATCTA 1125  
Db 633 ATGCGCTGAATCAAGATCGGCGCTGATCATGAAAGCTGCAGATTAAGCTGGATCTA 574  
QY 1126 CCGAGATGTAAGATTCCTAATCAAGACATCCGAGTCTTTTATAGCAAGGCCATG 1185  
Db 573 CCGAGATGTAAGATTCCTAATCAAGACATCCGAGTCTTTTATAGCAAGGCCATG 514  
QY 1186 CCAAGTGGCCCAACTGATCGTGTGAGAGTGTTCCTCCAGTGAAGCCCTCGCCCTT 1245  
Db 513 CCAAGTGGCCCAACTGATCGTGTGAGAGTGTTCCTCCAGTGAAGCCCTCGCCCTT 454  
QY 1246 TGTTCACCTGGGCGATGAGCCAGCTCGAAGCTCACTTTTACCAAGGTGACCAAC 1305  
Db 453 TGTTCACCTGGGCGATGAGCCAGCTCGAAGCTCACTTTTACCAAGGTGACCAAC 394  
QY 1306 TTATATCAATTTGAATTAATCAATCACTGATCGATCGATCACTGATGAATCTGGGATG 1365  
Db 393 TTATATCAATTTGAATTAATCAATCACTGATCGATCGATCACTGATGAATCTGGGATG 334  
QY 1366 GCTGTTCCACATCGATGTTTGAAGAAACATCATCATCATGATCATCATCATCATCAT 1425  
Db 333 GCTGTTCCACATCGATGTTTGAAGAAACATCATCATCATGATCATCATCATCATCAT 274  
QY 1426 TGCCGAACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1485  
Db 273 TGCCGAACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 214  
QY 1486 GATTCGAGGACGCTGAGTCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCTCT 1545  
Db 213 GATTCGAGGACGCTGAGTCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCTCT 154







ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 752)  
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 97044477  
 PUBMED 8889548

COMMENT  
 Contact: McCray, PB  
 McCray Lab  
 University of Iowa  
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
 Tel: 319 356 4866  
 Fax: 319 356 7171  
 Email: paul-mccray@uiowa.edu  
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).  
 Seq primer: M13 FORWARD  
 POLYA-Yes.

FEATURES  
 source location/Qualifiers  
 1..752  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-CF-ENO-aco-1-09-0-UI"  
 /tissue\_type="Primary Lung Cystic Fibrosis Epithelial Cells"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_lib="UI-CF-ENO"  
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I; UI-CF-ENO is a cDNA library containing the following tissue(s): Primary Lung Cystic Fibrosis Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (d)18 tail. The sequence tag for this library is CTGCTCAGCT.  
 TAG-LIB-UI-CF-ENO  
 TAG-TISSUE-Human Lung Epithelial Cell lanes untreated LPS 6hr to LPS 24h  
 TAG-SEQ-CTGCTCAGCT"

BASE COUNT 177 a 184 c 200 g 191 t  
 ORIGIN

Query Match 42.2%; Score 709.4; DB 13; Length 752;  
 Best Local Similarity 99.6%; Pred. No. 1.7e-161;  
 Matches 732; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 947 GGACAAACATCCGCTTCAGCTCATCTGAGTCAGAGAGCTGGAAGCTGCAGTGGCTGC 1006  
 |||||||  
 DB 752 GGACAAACATCCCG-TCAGCCTCATCTGAGTCAGAGAGCTGGAAGCTGCAGTGGCTGC 694  
 |||||||

QY 1007 TGTGCTCTCTCCAGAA-GAATTCATGCTCTCTGTTGACTCTGTGCTCTCTGAGAGTGGCC 1065  
 |||||||  
 DB 693 TGTGCTCTCTCCAGAAAGAAATTCATGCTCTGTTGACTCTGTGCTCTCTGAGAGTGGCC 634  
 |||||||

QY 1066 ATCGGCTGAAGTCAAGCATCGGCTGATCATGAAAAGGCGCAGATTAAGCTGGATCTA 1125  
 |||||||  
 DB 633 ATCGGCTGAAGTCAAGCATCGGCTGATCATGAAAAGGCTGCAATTAAGCTGGATCTA 574  
 |||||||

QY 1126 CCAGATCGTGAAGATCTTAACCTCAGAGACACCTCCGAGTTTATATAGACCAAGCCATG 1185  
 |||||||  
 DB 573 CCAGATCGTGAAGATCTTAACCTCAGAGACACCTCCGAGTTTATATAGACCAAGCCATG 514  
 |||||||

QY 1186 CCAAGTGGGCCCAACTGATGCTGCTGGAAGTGTTCCTCCATGGAAGCCCTCGCCCTT 1245  
 |||||||  
 DB 513 CCAAGTGGGCCCAACTGATGCTGCTGGAAGTGTTCCTCCATGGAAGCCCTCGCCCTT 454  
 |||||||

QY 1246 TGTTCACCTGGGCGATGGAAGCCAGCTCGGAAGCTCAGTTTATACCAAGGTGATCCAAC 1305  
 |||||||  
 DB 453 TGTTCACCTGGGCGATGGAAGCCAGCTCGGAAGCTCAGTTTATACCAAGGTGATCCAAC 394  
 |||||||

QY 1306 TTATACCTCAACTGAATTAACATCAGCTCTGATCCGATCCAGCTGATGAACCTGGATTTG 1365  
 |||||||  
 DB 393 TTATACCTCAACTGAATTAACATCAGCTCTGATCCGATCCAGCTGATGAACCTGGATTTG 334  
 |||||||

QY 1366 GCTGCTTCCAACTGATGTTCTGAAAAAATCATCATCAGATGATCATCATCTGCATCTGC 1425  
 |||||||  
 DB 333 GCTGCTTCCAACTGATGTTCTGAAAAAATCATCATCAGATGATCATCATCTGCATCTGC 274  
 |||||||

QY 1426 TGCCGAACCAAGATGGAATTAGATCTGGGGTCCAGTGTCAATGTTGAAGGCTTTGG 1485  
 |||||||  
 DB 273 TGCCGAACCAAGATGGAATTAGATCTGGGGTCCAGTGTCAATGTTGAAGGCTTTGG 214  
 |||||||

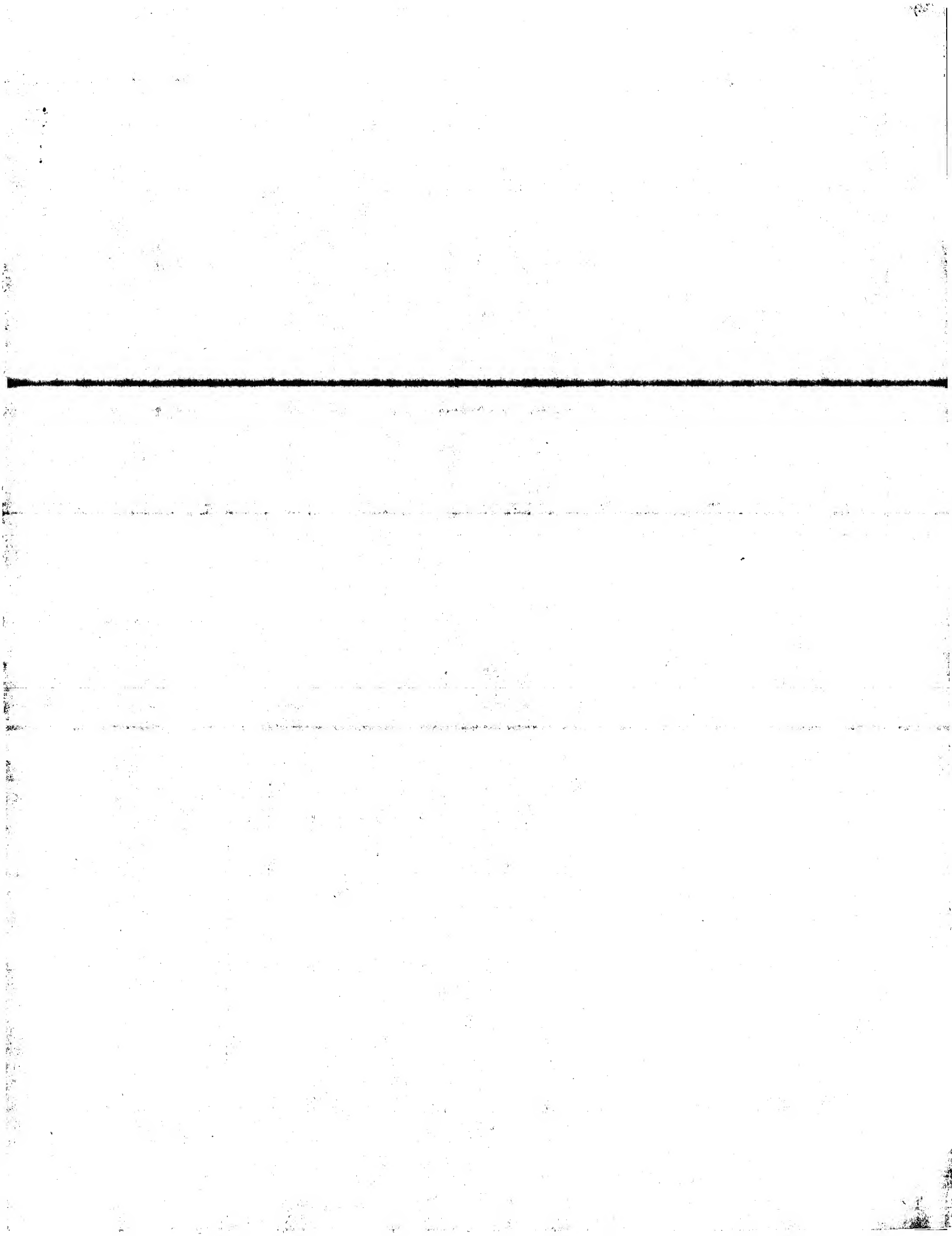
QY 1486 GATTGAGGCGAGTCTGCTCTCACTGACCAAGATGCCCTTGTGCTTAACCTCAGCTCTCT 1545  
 |||||||  
 DB 213 GATTGAGGCGAGTCTGCTCTCACTGACCAAGATGCCCTTGTGCTTAACCTCAGCTCTCT 154  
 |||||||

QY 1546 TGTGGAACCAAGCTCTCTCTCTCTCCAGTGAACATTTGGATGGCAGCATCAGGGAAG 1605  
 |||||||  
 DB 153 TGTGGAACCAAGCTCTCTCTCTCTCCAGTGAACATTTGGATGGCAGCATCAGGGAAG 94  
 |||||||

QY 1606 CTGGGTCACAGCTGGAGTATGGGTGAGCTTATGACCATCCCTCTCGAATCAAT 1665  
 |||||||  
 DB 93 CTGGGTCACAGCTGGAGTATGGGTGAGCTTATGACCATCCCTCTCTCGAATCAAT 34  
 |||||||

QY 1666 AAACACTTGCTGTG 1680  
 |||||||  
 DB 33 AAACACTTGCTGTG 19  
 |||||||

Search completed: October 9, 2003, 23:30:07  
 Job time : 4077.7 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2003, 19:48:32 ; Search time 478.34 Seconds  
(without alignments)  
9113.362 Million cell updates/sec

Title: US-09-700-770-2

Perfect score: 1680

Sequence: 1 ggtgtcagagataaagtgtt.....tcaataacactgtctgtg 1680

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 1731049 seqs, 1297405648 residues

Total number of hits satisfying chosen parameters: 3462098

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_NA:\*

1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/2/pubpna/PTCT\_NEW.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/PCRTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
16: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
17: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1679.2	100.0	1680	US-09-788-990-1	Sequence 1, Appl1
2	1656.2	98.6	2036	US-09-788-990-5	Sequence 5, Appl1
3	1617	96.2	1636	US-09-946-374-127	Sequence 127, App
4	1617	96.2	1636	US-10-015-387A-127	Sequence 127, App
5	1617	96.2	1636	US-10-063-735-77	Sequence 77, Appl
6	1617	96.2	1636	US-10-006-130A-127	Sequence 127, App
7	1617	96.2	1636	US-10-199-672-279	Sequence 279, App
8	1617	96.2	1636	US-10-006-172A-127	Sequence 127, App
9	1617	96.2	1636	US-10-187-749-279	Sequence 279, App
10	1617	96.2	1636	US-10-194-457-279	Sequence 279, App
11	1617	96.2	1636	US-10-184-642-279	Sequence 279, App
12	1617	96.2	1636	US-10-196-747-279	Sequence 279, App
13	1617	96.2	1636	US-10-015-392A-127	Sequence 127, App
14	1617	96.2	1636	US-10-017-253A-127	Sequence 127, App
15	1617	96.2	1636	US-10-173-689-279	Sequence 279, App
16	1617	96.2	1636	US-10-173-690-279	Sequence 279, App

17	1617	96.2	1636	12	US-10-173-691-279	Sequence 279, App
18	1617	96.2	1636	12	US-10-173-692-279	Sequence 279, App
19	1617	96.2	1636	12	US-10-173-694-279	Sequence 279, App
20	1617	96.2	1636	12	US-10-173-698-279	Sequence 279, App
21	1617	96.2	1636	12	US-10-173-699-279	Sequence 279, App
22	1617	96.2	1636	12	US-10-173-707-279	Sequence 279, App
23	1617	96.2	1636	12	US-10-174-569-279	Sequence 279, App
24	1617	96.2	1636	12	US-10-174-583-279	Sequence 279, App
25	1617	96.2	1636	12	US-10-174-587-279	Sequence 279, App
26	1617	96.2	1636	12	US-10-174-589-279	Sequence 279, App
27	1617	96.2	1636	12	US-10-174-591-279	Sequence 279, App
28	1617	96.2	1636	12	US-10-175-736-279	Sequence 279, App
29	1617	96.2	1636	12	US-10-175-742-279	Sequence 279, App
30	1617	96.2	1636	12	US-10-175-744-279	Sequence 279, App
31	1617	96.2	1636	12	US-10-175-745-279	Sequence 279, App
32	1617	96.2	1636	12	US-10-175-748-279	Sequence 279, App
33	1617	96.2	1636	12	US-10-175-751-279	Sequence 279, App
34	1617	96.2	1636	12	US-10-175-754-279	Sequence 279, App
35	1617	96.2	1636	12	US-10-176-480-279	Sequence 279, App
36	1617	96.2	1636	12	US-10-176-489-279	Sequence 279, App
37	1617	96.2	1636	12	US-10-176-754-279	Sequence 279, App
38	1617	96.2	1636	12	US-10-176-755-279	Sequence 279, App
39	1617	96.2	1636	12	US-10-176-759-279	Sequence 279, App
40	1617	96.2	1636	12	US-10-176-920-279	Sequence 279, App
41	1617	96.2	1636	12	US-10-176-922-279	Sequence 279, App
42	1617	96.2	1636	12	US-10-176-924-279	Sequence 279, App
43	1617	96.2	1636	12	US-10-176-984-279	Sequence 279, App
44	1617	96.2	1636	12	US-10-179-508-279	Sequence 279, App
45	1617	96.2	1636	12	US-10-179-512-279	Sequence 279, App

## ALIGNMENTS

RESULT 1  
US-09-788-990-1  
Sequence 1, Application US/09788990  
Publication No. US20030049617A1  
GENERAL INFORMATION:  
APPLICANT: Chen, Sel Yu  
APPLICANT: Ma, Yungling  
TITLE OF INVENTION: Method of Diagnosing, Monitoring, Staging, Imaging and  
FILE REFERENCE: DEX-0140  
CURRENT APPLICATION NUMBER: US/09/788, 990  
CURRENT FILING DATE: 2001-02-20  
PRIOR APPLICATION NUMBER: 60/183,188  
PRIOR FILING DATE: 2000-02-17  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 1  
LENGTH: 1680  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-788-990-1

Query Match 100.0%; Score 1679.2; DB 11; Length 1680;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1678; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY	1	GGTGTGAGATATTAAGTTGACTTCAGACCACTCCCGGAGAGAGAGAGGGG	60
DB	1	GGTGTGAGATATTAAGTTGACTTCAGACCACTCCCGGAGAGAGAGAGGGG	60
QY	61	CCGAGGACTCCAGGCTGCCAGTCTGCATCTGCACTTGCCCTTGACACCTGGG	120
DB	61	CCGAGGACTCCAGGCTGCCAGTCTGCATCTGCACTTGCCCTTGACACCTGGG	120
QY	121	AAGATGGCCGCGCCGTGAGCACTTCACTCTCTGTGTTGCTGAGGACCACTTATC	180
DB	121	AAGATGGCCGCGCCGTGAGCACTTCACTCTCTGTGTTGCTGAGGACCACTTATC	180

181 CAAGCACCCTGATCCACTGAGTTCATCTCTGGGCCCAAAAGTCAATCAAAAG 240  
181 CAAGCACCCTGATCCACTGAGTTCATCTCTGGGCCCAAAAGTCAATCAAAAG 240  
241 CTGACACAGAGAGTGAAGACCAACAGCCAGCATCTCTGAGAGAGTGGCGGCTC 300  
241 CTGACACAGAGAGTGAAGACCAACAGCCAGCATCTCTGAGAGAGTGGCGGCTC 300  
301 AGTGCATGGGGGAAAAAGCCGAGAGATCCCTGTGTGGGAGAGCTGGTGAACACG 360  
301 AGTGCATGGGGGAAAAAGCCGAGAGATCCCTGTGTGGGAGAGCTGGTGAACACG 360  
361 TCTGAAAGACATCATCTGCTGAGAGTCAATCAAGTAAATCTCTCACTGAGTGA 420  
361 TCTGAAAGACATCATCTGCTGAGAGTCAATCAAGTAAATCTCTCACTGAGTGA 420  
421 AGCCCTGGCCATGACACAGAGAGTGTCTAGTCAAGATCCCTGGAGATGGTGGAT 480  
421 AGCCCTGGCCATGACACAGAGAGTGTCTAGTCAAGATCCCTGGAGATGGTGGAT 480  
481 TCAACAGCCCTGTGTCAAGACATCTGTGAGTTCACATGAGAGAGTGGCCAAAGCA 540  
481 TCAACAGCCCTGTGTCAAGACATCTGTGAGTTCACATGAGAGAGTGGCCAAAGCA 540  
541 CCATCCGATGAGACACAGTGAAGTGGCCCAAGTGGCCCAAGTGGCCCAAGTGGCA 600  
541 CCATCCGATGAGACACAGTGAAGTGGCCCAAGTGGCCCAAGTGGCCCAAGTGGCA 600  
601 CCAGCCATGGGAGCTGCGATCCAACTGCTGCAATAGCTCTGCTGAGAGGCT 660  
601 CCAGCCATGGGAGCTGCGATCCAACTGCTGCAATAGCTCTGCTGAGAGGCT 660  
661 TAGCTAAGCAGGTCATGAACCTCTAGTGCATCCCTGCCCAATCTAGTAAAAACAGC 720  
661 TAGCTAAGCAGGTCATGAACCTCTAGTGCATCCCTGCCCAATCTAGTAAAAACAGC 720  
721 TGTGTCCCTGATGAGAGTCTCTCAATGATGATGAGAGTCTCTGAGTGGTGA 780  
721 TGTGTCCCTGATGAGAGTCTCTCAATGATGATGAGAGTCTCTGAGTGGTGA 780  
781 AGGTGCCATTTCCCTCAGATGACGCTGCTGAGAGTGGTGAAGTGGTGAAGTGA 840  
781 AGGTGCCATTTCCCTCAGATGACGCTGCTGAGAGTGGTGAAGTGGTGAAGTGA 840  
841 AGGTGCCATTTCCCTCAGATGACGCTGCTGAGAGTGGTGAAGTGGTGAAGTGA 900  
841 AGGTGCCATTTCCCTCAGATGACGCTGCTGAGAGTGGTGAAGTGGTGAAGTGA 900  
901 CCAGAGTGTCAATTAATCTGACAGCTTCCCTGACATGACCCAGCTGGACATCCCGT 960  
901 CCAGAGTGTCAATTAATCTGACAGCTTCCCTGACATGACCCAGCTGGACATCCCGT 960  
961 TCAGCCTCATGATGAGTCAAGAGTGGTGAAGTGGTGAAGTGGTGAAGTGGTGA 1020  
961 TCAGCCTCATGATGAGTCAAGAGTGGTGAAGTGGTGAAGTGGTGAAGTGGTGA 1020  
1021 AAGAAATTCATGCTGTGTGAGTCTGTGTCTCTGAGAGTGGCCATGGCTGAAGTCAA 1080  
1021 AAGAAATTCATGCTGTGTGAGTCTGTGTCTCTGAGAGTGGCCATGGCTGAAGTCAA 1080  
1081 GCATCGGGCTGATCAATGAAGAGTGGTGAAGTGGTGAAGTGGTGAAGTGGTGA 1140  
1081 GCATCGGGCTGATCAATGAAGAGTGGTGAAGTGGTGAAGTGGTGAAGTGGTGA 1140  
1141 TCTTAATCTAGGACACTCCGAGATTTTATAGACCAAGGCAATGCCAAGTGGCCAA 1200  
1141 TCTTAATCTAGGACACTCCGAGATTTTATAGACCAAGGCAATGCCAAGTGGCCAA 1200  
1201 TGAATGCTGAGAGTGTTCCTCCAGTGAAGCCCTCCGCTTTGTTTACCTGGGCA 1260  
1201 TGAATGCTGAGAGTGTTCCTCCAGTGAAGCCCTCCGCTTTGTTTACCTGGGCA 1260  
1261 TCAGAGCCAGCTCGAAGCTCAGTTTACACCAAGGTGACCAATTATACCTGA 1320

1261 TCAGAGCCAGCTCGAAGCTCAGTTTACACCAAGGTGACCAATTATACCTGA 1320  
1321 ATAAATCAGCTGTGATGGATCCAGTGTGATGAACCTGGAGTGGCTGGTCAACCTG 1380  
1321 ATAAATCAGCTGTGATGGATCCAGTGTGATGAACCTGGAGTGGCTGGTCAACCTG 1380  
1381 ATGTTCTGAAAAATCATCATCTGATGATCAATCCATCTCTGTCGCGAACAAGT 1440  
1381 ATGTTCTGAAAAATCATCATCTGATGATCAATCCATCTCTGTCGCGAACAAGT 1440  
1441 GCAAAATTAAGATCTGGGGTCCAGTGTCAATGCTGAAGGCTTGGATTCAGACAGCTG 1500  
1441 GCAAAATTAAGATCTGGGGTCCAGTGTCAATGCTGAAGGCTTGGATTCAGACAGCTG 1500  
1501 AGTCTCAGTACGACCAAGAGATGCCCTGTGTCTGCTCAAGCTCTGTGGAACCAAGCT 1560  
1501 AGTCTCAGTACGACCAAGAGATGCCCTGTGTCTGCTCAAGCTCTGTGGAACCAAGCT 1560  
1561 CTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAGGAGAGCTGGTCCAGCTGG 1620  
1561 CTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAGGAGAGCTGGTCCAGCTGG 1620  
1621 GAGTATGGGTGATGCTCTATGACCATCTCTCTGCAATCAATTAACCTTGGCTG 1680  
1621 GAGTATGGGTGATGCTCTATGACCATCTCTCTGCAATCAATTAACCTTGGCTG 1680

RESULT 2  
US-09-788-990-5  
; Sequence 5, Application US/09788990  
; Publication No. US2003049617A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Sei Yu  
; APPLICANT: Sun, Yongming  
; TITLE OF INVENTION: Method of Diagnosing, Monitoring, Staging, Imaging and  
; FILE REFERENCE: DEX-0140  
; CURRENT APPLICATION NUMBER: US/09/788,990  
; PRIOR FILING DATE: 2001-02-20  
; PRIOR APPLICATION NUMBER: 60/183,188  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 2036  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-788-990-5

Query Match 98.6%; Score 1656.2; DB 11; Length 2036;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1678; Conservative 2; Mismatches 0; Indels 3; Gaps 2;

1 GGTGTGAGATATTAAGTGTGACTTCCAGACCCACTGCCGGGAGAG--GAGRGAGCG 58  
38 GGTGTGAGATATTAAGTGTGACTTCCAGACCCACTGCCGGGAGAGAGGAGCG 97  
59 GGCAGAGACTCCAGAGTGGCCAGGCTGGCAATCTGCAATCTGCTGCTGACACTG 157  
98 GGCAGAGACTCCAGAGTGGCCAGGCTGGCAATCTGCAATCTGCTGCTGACACTG 157  
119 GGAAGATGGCCGCGCTGAGACTTCAACCTTCTGTGGTTGTGGAGGACCACTTGA 178  
158 GGAAGATGGCCGCGCTGAGACTTCAACCTTCTGTGGTTGTGGAGGACCACTTGA 217  
179 TCAGAGCCAGCTCAGTCCACTGACAGTCTCAATCTCGGCGCCAAAGTCAATCAAGAA 238  
218 TCAGAGCCAGCTCAGTCCACTGACAGTCTCAATCTCGGCGCCAAAGTCAATCAAGAA 277  
239 AGCTGACACAGAGCTGAAGAGACCAAGCCACAGCATCTCTGACAGAGCTCGCTGG 298

Db 278 AGTGTACACAGGAGCTGTAAGGACCAACAGCCACACGATCTGTGACAGCACTGCCCTGCC 337  
QY 299 TCAGTGCATGCGGGGAAAAGCCAGCCGAGG-ATCCCTGTGTGGGAGCGCTGGTGAACA 357  
Db 338 TCAGTGCATGCGGGGAAAAGCCAGCCGAGGAGCATCCCTGTGTGGGAGCGCTGGTGAACA 397  
QY 358 CCGTCTGGAAGCAATCATCTGGCTGAAGGTCAATCAGAGTAAATCTCTCAGCTGACAG 417  
Db 398 CCGTCTGGAAGCAATCATCTGGCTGAAGGTCAATCAGAGTAAATCTCTCAGCTGACAG 457  
QY 418 TGAAGCCCTGGGCAATGACAGAGAGTGTATCAAGATCCCGCTGGAGCATGTGGCTG 477  
Db 458 TGAAGCCCTGGGCAATGACAGAGAGTGTATCAAGATCCCGCTGGAGCATGTGGCTG 517  
QY 478 GATTCAACAGCCCTGTGTCAAGACATCGTGAAGTTCACATAGACACTGAGGCCAG 537  
Db 518 GATTCAACAGCCCTGTGTCAAGACATCGTGAAGTTCACATAGACACTGAGGCCAG 577  
QY 538 CCACCATCCGATGAGACACAGTGAAGTGGCCCAACCGCTGTGCTCAAGTACTGTG 597  
Db 578 CCACCATCCGATGAGACACAGTGAAGTGGCCCAACCGCTGTGCTCAAGTACTGTG 637  
QY 598 CCACCATCCGATGAGAGCGCATCCAACTGCTGAATAAGTCTCTCTGCTGGTGAAG 657  
Db 638 CCACCATCCGATGAGAGCGCATCCAACTGCTGAATAAGTCTCTCTGCTGGTGAAG 697  
QY 658 CCTTAGCTAAGCAGATCATGACCTCTAGTGCATCCCTGCCAATCTAGTGAATAAC 717  
Db 698 CCTTAGCTAAGCAGATCATGACCTCTAGTGCATCCCTGCCAATCTAGTGAATAAC 757  
QY 718 AGCTGTGCTCCGTGTGATGAGGCTCTCTCAATGGCATGTATGACAGACTCTGACGTG 777  
Db 758 AGCTGTGCTCCGTGTGATGAGGCTCTCTCAATGGCATGTATGACAGACTCTGACGTG 817  
QY 778 TGAAGGTGCCATTTCCCTGAGATGACGTGCGGAGTTGACCTCTGATCCCTGCA 837  
Db 818 TGAAGGTGCCATTTCCCTGAGATGACGTGCGGAGTTGACCTCTGATCCCTGCA 877  
QY 838 TCAAGGTGACACCATTCACCTCTACTGCGGGGCAAGTGTGACTCAAGGGAAG 897  
Db 878 TCAAGGTGACACCATTCACCTCTACTGCGGGGCAAGTGTGACTCAAGGGAAG 937  
QY 898 TGACCAAGTGTTCATTAATCTGACACTTCCCTGCAAGGCCACCTGACAACTCC 957  
Db 938 TGACCAAGTGTTCATTAATCTGACACTTCCCTGCAAGGCCACCTGACAACTCC 997  
QY 958 CGTTACGCTCATGCTGAGTCAAGAGTGTGAAGTGTGAAGTGTGCTGCTCTC 1017  
Db 998 CGTTACGCTCATGCTGAGTCAAGAGTGTGAAGTGTGAAGTGTGCTGCTCTC 1057  
QY 1018 CAGAGAATTCATGCTGCTGTGAGACTGTGCTTCTGAGAGTGGCCATCGCTGAAGT 1077  
Db 1058 CAGAGAATTCATGCTGCTGTGAGACTGTGCTTCTGAGAGTGGCCATCGCTGAAGT 1117  
QY 1078 CAAGCATCGGGCTGATCAATGAAAAGGCTCAGATAAGCTGAGATCAACAGATCTGA 1137  
Db 1118 CAAGCATCGGGCTGATCAATGAAAAGGCTCAGATAAGCTGAGATCAACAGATCTGA 1177  
QY 1138 AGATCCATACGAGGAGACATCCGAGTTTATATAGCAAGGCAAGGCAAGGTGGCCC 1197  
Db 1178 AGATCCATACGAGGAGACATCCGAGTTTATATAGCAAGGCAAGGCAAGGTGGCCC 1237  
QY 1198 AACTGATGCTGTGAAGTGTTCCTCTCAGTGAAGCCCTCGCCCTTGTTCACCTGG 1257  
Db 1238 AACTGATGCTGTGAAGTGTTCCTCTCAGTGAAGCCCTCGCCCTTGTTCACCTGG 1297  
QY 1258 GCATCGAAGCCAGCTCGGAAGCTCAGTTTACACCAAGGTGACCAATATATCAACT 1317  
Db 1298 GCATCGAAGCCAGCTCGGAAGCTCAGTTTACACCAAGGTGACCAATATATCAACT 1357  
QY 1318 TGAATTAACATCAGTGTGATCGGATCAAGTGAATCACTCGGGATGGGCTGCTCAAC 1377  
Db 1358 TGAATTAACATCAGTGTGATCGGATCAAGTGAATCACTCGGGATGGGCTGCTCAAC 1417

QY 1378 CTGATGTTCTGAAAAACATCATCACTGAGATCAATCCATCTGCTGCGGAACCGA 1437  
Db 1418 CTGATGTTCTGAAAAACATCATCACTGAGATCAATCCATCTGCTGCGGAACCGA 1477  
QY 1438 ATGGCAAAATTAACATCTGGGGGTCCCAAGTCTCATTTGGTGAAGGCTTGGATTTGAGGACAG 1497  
Db 1478 ATGGCAAAATTAACATCTGGGGGTCCCAAGTCTCATTTGGTGAAGGCTTGGATTTGAGGACAG 1537  
QY 1498 CTGATGTTCTGAAAAACATCACTGAGATCAATCCATCTGCTGCGGAACCGA 1557  
Db 1538 CTGATGTTCTGAAAAACATCACTGAGATCAATCCATCTGCTGCGGAACCGA 1597  
QY 1558 GCTCTCTGTTCTCCCAATGAAAGTGTGATGAGCAGCCATCAGGGAAGGCTGGGTCCAGC 1617  
Db 1598 GCTCTCTGTTCTCCCAATGAAAGTGTGATGAGCAGCCATCAGGGAAGGCTGGGTCCAGC 1657  
QY 1618 TGGAGATATGGGTGTGAGCTCTATAGACATCCCTCTCTGCAATCAATAACACTTGGCT 1677  
Db 1658 TGGAGATATGGGTGTGAGCTCTATAGACATCCCTCTCTGCAATCAATAACACTTGGCT 1717  
QY 1678 GTG 1680  
Db 1718 GTG 1720

RESULT 3  
US-09-946-374-127  
; Sequence 127, Application US/09946374  
; Publication No. US20030073129A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Bolstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paonli, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830PICI  
; CURRENT APPLICATION NUMBER: US/09/946,374  
; CURRENT FILING DATE: 2001-09-04  
; PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098749  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098750  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098803  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098821  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098843  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/099536  
; PRIOR FILING DATE: 1998-09-09







;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; TITLE OF INVENTION: Acids Encoding the Same  
;; FILE REFERENCE: P28301C54  
;; CURRENT APPLICATION NUMBER: US/10/015,387A  
;; PRIORITY FILING DATE: 2001-12-12  
;; Prior Application removed - See File Wrapper or Palm  
;; NUMBER OF SEQ ID NOS: 477  
;; SEQ ID NO 127  
;; LENGTH: 1636  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-015-387A-127

Query Match 96.2%; Score 1617; DB 12; Length 1636;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1628; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 51 GRGAGCGCGCGGAGGATCCAGCGTGGCCAGGTGTGGCATCTGCACCTGTGCTGCTCT 110  
DB 1 GAGGAGCGGCGCGGAGGATCCAGCGTGGCCAGGTGTGGCATCTGCACCTGTGCTGCTCT 60  
QY 111 GACACCTGGGAGGATGGCGCGCGCGGAGGATCCAGCGTGGCCAGGTGTGGCATCTGCACG 170  
DB 61 GACACCTGGGAGGATGGCGCGCGCGGAGGATCCAGCGTGGCCAGGTGTGGCATCTGCACG 120  
QY 171 CACCTTGAATCCAGGACCGCTCAGTCCAGTGCAGCTTGTCTCATCTCGGCCCCAAAGTCA 230  
DB 121 CACCTTGAATCCAGGACCGCTCAGTCCAGTGCAGCTTGTCTCATCTCGGCCCCAAAGTCA 180  
QY 231 CAAAGAAAAAGCTGACACAGGAGCTAAGGACACCAAGCGCACAGATCTCTGACAGCT 290  
DB 181 CAAAGAAAAAGCTGACACAGGAGCTAAGGACACCAAGCGCACAGATCTCTGACAGCT 240  
QY 291 GCCCGTGTCAAGTGCATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 349  
DB 241 GCCCGTGTCAAGTGCATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300  
QY 350 GGTGAACACCGTCTGAAAGCATATCTGCTGAAGGTCTATCAGAGTCAATCACTCTCTCA 409  
DB 301 GGTGAACACCGTCTGAAAGCATATCTGCTGAAGGTCTATCAGAGTCAATCACTCTCTCA 360  
QY 410 GCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 469  
DB 361 GCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420  
QY 470 GGTGCGTGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 529  
DB 421 GGTGCGTGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480  
QY 530 GGGCCAGGACCATCCGATGAGACAGAGTGAAGTGGCCCGCCGCTGTGCTCTAG 589  
DB 481 GGGCCAGGACCATCCGATGAGACAGAGTGAAGTGGCCCGCCGCTGTGCTCTAG 540  
QY 590 TGACTGTGACACGACGATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 649  
DB 541 TGACTGTGACACGACGATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600  
QY 650 GGTGAACGCTTACGATGAAGAGGATGATCACTCTAGTGCATCTGCTGCTGCTGCTGCT 709  
DB 601 GGTGAACGCTTACGATGAAGAGGATGATCACTCTAGTGCATCTGCTGCTGCTGCTGCTGCT 660  
QY 710 GAAAAACAGGCTGTCCCGTGTGATGAGGCTTCTTCAATGGAGATGATGACAGCTCTCT 769  
DB 661 GAAAAACAGGCTGTCCCGTGTGATGAGGCTTCTTCAATGGAGATGATGACAGCTCTCT 720  
QY 770 GAGGTGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 829  
DB 721 GAGGTGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780  
QY 830 TCTTCGATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 889  
DB 781 TCTTCGATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840

QY 890 GGGAAAGGTGACCAAGTGTTCATTAATCACTGACGCTTCCCTGACATGATGCCACCTGGA 949  
DB 841 GGGAAAGGTGACCAAGTGTTCATTAATCACTGACGCTTCCCTGACATGATGCCACCTGGA 900  
QY 950 CAACATCCCGTTCACGCTCATGCTGAGTGCAGAGAGCTGTGAAAGTGCATGCTGCTGT 1009  
DB 901 CAACATCCCGTTCACGCTCATGCTGAGTGCAGAGAGCTGTGAAAGTGCATGCTGCTGT 960  
QY 1010 GCTCTCTCAGAGAAATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1069  
DB 961 GCTCTCTCAGAGAAATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
QY 1070 GCTGAAGTCAAGCATCGGCGCTGATCAATGAAAGGCTCAGATAGTGGATCAACCA 1129  
DB 1021 GCTGAAGTCAAGCATCGGCGCTGATCAATGAAAGGCTCAGATAGTGGATCAACCA 1080  
QY 1130 GATGCTGAAGATCCCTAATCAAGACACTCCGAGTCTTTATAGCAAGGCGCATGCGCA 1189  
DB 1081 GATGCTGAAGATCCCTAATCAAGACACTCCGAGTCTTTATAGCAAGGCGCATGCGCA 1140  
QY 1190 GGTGCGCCAGCATGATGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1249  
DB 1141 GGTGCGCCAGCATGATGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200  
QY 1250 CACCTGTGGCATCGAAGCGAGCTGGAAGCTCAGTTTACACCAAGGTGACCACTTAT 1309  
DB 1201 CACCTGTGGCATCGAAGCGAGCTGGAAGCTCAGTTTACACCAAGGTGACCACTTAT 1260  
QY 1310 ACTGACCTTGAATTAATCAATCAGCTGTGATGAGTCCAGTGAATGAACTGTGGATGGCTG 1369  
DB 1261 ACTGACCTTGAATTAATCAATCAGCTGTGATGAGTCCAGTGAATGAACTGTGGATGGCTG 1320  
QY 1370 GTTCCAACTGATGTTCTGAAAAAATCATCATCACTGATCATCTGCTGCC 1429  
DB 1321 GTTCCAACTGATGTTCTGAAAAAATCATCATCACTGATCATCTGCTGCC 1380  
QY 1430 GAACCAAGATGGCAATTAATGATCTGGGCTGCCAGTGTGATGTTGTAAGGCTTGGATT 1489  
DB 1381 GAACCAAGATGGCAATTAATGATCTGGGCTGCCAGTGTGATGTTGTAAGGCTTGGATT 1440  
QY 1490 CGAGGACACTGATGCTCTCACTGACCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1549  
DB 1441 CGAGGACACTGATGCTCTCACTGACCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500  
QY 1550 GAAACCAAGCTCTCTCTGCTCTCCAGTGAAGATTTGATGAGGAGGAGGAGGAGGAGGAG 1609  
DB 1501 GAAACCAAGCTCTCTCTGCTCTCCAGTGAAGATTTGATGAGGAGGAGGAGGAGGAGGAG 1560  
QY 1610 GTTCCAGCTGGAGATGAGGAGTGTGAGCTCTATAGCAATCCCTCTCTGCAATCAATAAC 1669  
DB 1561 GTTCCAGCTGGAGATGAGGAGTGTGAGCTCTATAGCAATCCCTCTCTGCAATCAATAAC 1620  
QY 1670 ACTTGCCTGTG 1680  
DB 1621 ACTTGCCTGTG 1631

RESULT 5  
US-10-063-735-77  
; Sequence 77, Application US/10063735  
; Publication No. US20030138882A1  
; GENERAL INFORMATION:  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey J.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William T.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; ACIDS ENCODING THE SAME

```

? FILE REFERENCE: P3230R1C
? CURRENT APPLICATION NUMBER: US/10/063,735
? CURRENT FILING DATE: 2002-05-08
? PILOT Application removed - See Palm or File wrapper
? NUMBER OF SEQ ID NOS: 170
? SEQ ID NO 77
? LENGTH: 1636
? TYPE: DNA
? ORGANISM: Homo Sapien
? US-10-063-735-77

```

Query Match	96.2%	Score 1617	DB 12	Length 1636
Best Local Similarity	99.8%	Pred. No. 0		
Matches 1628	Conservative	1	Mismatches	1
			Indels	1
			Gaps	1

QY	51	GRGAGAGGGGCGCGAGACTCCAGGGTCCCGCAGGCTGGCATCTCGACCTTCCTGGCCCT	110
Db	1	GAGAGGCGGGCCGAGGAGACTCCAGCGTGCCCGAGGCTGGCATCTTCGTGTGCCCTCT	60
QY	111	GACACCGGGGAAAGTGGCCGGCCGCGTGGAGCTTCAACCTTCTCTGTGGTTTGTGTGGACG	170
Db	61	GACACCGGGGAAAGTGGCCGGCCGCGTGGAGCTTCAACCTTCTCTGTGGTTTGTGTGGACG	120
QY	171	CACCTTATCCAAAGCCACACCTCACTCCACTGCAGTTTCTCATCTCGGCGCCAAAAGTCAT	230
Db	121	CACCTTATCCAAAGCCACACCTCACTCCACTGCAGTTTCTCATCTCGGCGCCAAAAGTCAT	180
QY	231	CAAGAAAAGCTGACACAGGAGCTGAAAGGACACACGCCACACAGCATCTCGACAGCT	290
Db	181	CAAGAAAAGCTGACACAGGAGCTGAAAGGACACACGCCACACAGCATCTCGACAGCT	240
QY	291	GCCGCTGCTGATGCTCCATMGCGGGGAAAAAGCCAGCCGGAAG - ATCCCTGTGTGGGGAGCT	349
Db	241	GCCGCTGCTGATGCTCCATMGCGGGGAAAAAGCCAGCCGGAAGCATCTCTGTGTGGGAGCTT	300
QY	350	GGTGAACACGCTGCTGAAGACATATCTGTGGCTGAAGGTCATACAGCTAACATCTTCCA	409
Db	301	GGTGAACACGCTGCTGAAGACATATCTGTGGCTGAAGGTCATACAGCTAACATCTTCCA	360
QY	410	GCTCAGGTGAAGCGCTCGGGCATTMGACACAGAGGTGTATGCAAGATCCCGCTGGACAT	469
Db	361	GCTCAGGTGAAGCGCTCGGGCATTMGACACAGAGGTGTATGCAAGATCCCGCTGGACAT	420
QY	470	GGTGTGTGATTCACAACGCGCCCTGGTCAAGACATCGTGAAGTTCCACATGACAGCTGA	529
Db	421	GGTGTGTGATTCACAACGCGCCCTGGTCAAGACATCGTGAAGTTCCACATGACAGCTGA	480
QY	530	GGGCCAAGCCACATCCGGATGGACACAGTGGCAAGTGGGCCCAACCGCGCTGGTCTGAG	589
Db	481	GGGCCAAGCCACATCCGGATGGACACAGTGGCAAGTGGGCCCAACCGCGCTGGTCTGAG	540
QY	590	TGACTGTGCCACACGACATGGGAGCTTCGGCATCCAACTGCTGCATAAGCTCTCTCTCT	649
Db	541	TGACTGTGCCACACGACATGGGAGCTTCGGCATCCAACTGCTGCATAAGCTCTCTCTCT	600
QY	650	GGTGAAGCGCTTACTTAAGCAAGTGCATGAAACCTCTTATGGCATTCCTGGCCAACTGAGT	709
Db	601	GGTGAAGCGCTTACTTAAGCAAGTGCATGAAACCTCTTATGGCATTCCTGGCCAACTGAGT	660
QY	710	GAAAAACAGCTGTGTCCCGTATCGAGGCTTCTCTCAATGGCATGTATGAGACCTCT	769
Db	661	GAAAAACAGCTGTGTCCCGTATCGAGGCTTCTCTCAATGGCATGTATGAGACCTCTCT	720
QY	770	GCAGCTGTGAAGGTGCCATTTTCCCTCAGCATTGACCGTCTGGAGTTTGACTTCTGTGA	829
Db	721	GCAGCTGTGTGAAGGTGCCATTTTCCCTCAGCATTGACCGTCTGGAGTTTGACTTCTGTGA	780
QY	830	TCTCGCATCAAGGGTGACACATTCAGCTTACTCTGGGGCCAAAGTTGTGGACTTACA	889
Db	781	TCTCGCATCAAGGGTGACACATTCAGCTTACTCTGGGGCCAAAGTTGTGGACTTACA	840
QY	890	GGGAAGGTGACCAAGTGTTCATTAATCTGACGCTTCCGTGACAAATGCCACCTTGA	949

Db	84	GGGAAAGTACCAAGTGGTTCAATTAATCTGACGCTTCCTTGACATGGCCACCTCGA	900
QY	950	CAACATCCCGTTACGCTCATCTGTAGTCAGAGACGTGGTGAAGCTGCAGTGGCTGT	1009
Db	901	CAACATGCCCTTCAGCTTCATCGAGTACAGAGAGCTGGTGAAGAGCTCAGAGCTGCTGT	960
QY	1010	GCCTCTCCGAAAGAAATTCATAGTCCCTGGTGGAGATCTGTGTTCTCTGAGATGCCCCATCG	1069
Db	961	GCCTCTCCGAAAGAAATTCATAGTCCCTGGTGGAGATCTGTGTTCTCTGAGATGCCCCATCG	1020
QY	1070	GCTGAAGTCAAGCATCGGGCGATCATGTGAAAAGGCTGCAGATTAAGCGGGATCTACCA	1129
Db	1021	GCTGAAGTCAAGCATCGGGCGATCATGTGAAAAGGCTGCAGATTAAGCTGGATCTACCA	1080
QY	1130	GATCGTGAAGATCCCTAACTCAGAGACACTCCGAGTTTATATAGACCAAGGCCATGCCAA	1189
Db	1081	GATCGTGAAGATCCCTAACTCAGAGACACTCCGAGTTTATATAGACCAAGGCCATGCCAA	1140
QY	1190	GGTGGGCCCACTGATCTGCTGGAAAGTTCCTCCAGTGAAGCCTCCGCTTTGT	1249
Db	1141	GGTGGGCCCACTGATCTGCTGGAAAGTTCCTCCAGTGAAGCCTCCGCTTTGT	1200
QY	1250	CACCCGSGGATCGAAGACGACGTGGAGAGCTCACTTTTACACCAAGSTGACCAACTAT	1309
Db	1201	CACCCGSGGATCGAAGACGACGTGGAGAGCTCACTTTTACACCAAGSTGACCAACTAT	1260
QY	1310	ACTCAACTTGAAATTAACATCAGAGCTGTGATCCGATCCAGCTGATGAATCTGGATTGGCTG	1369
Db	1261	ACTCAACTTGAAATTAACATCAGAGCTGTGATCCGATCCAGCTGATGAATCTGGATTGGCTG	1320
QY	1370	GTTTCAACCTGATGTTGTGAAAACATCATCTAGATCATTCAGACTTCATCTGCTGCC	1429
Db	1321	GTTTCAACCTGATGTTGTGAAAACATCATCTAGATCATTCAGACTTCATCTGCTGCC	1380
QY	1430	GAACCAAGATGGCAAAATTAAGATCTGGGGTCCCACTGATGGTGAAGGCTTGGGAT	1489
Db	1381	GAACCAAGATGGCAAAATTAAGATCTGGGGTCCCACTGATGGTGAAGGCTTGGGAT	1440
QY	1490	CGAGGAGAGTGAAGCTCTACCTGACCAAGAGATGACCTTGTGCTTACTCCAGGCTCCTTGTG	1549
Db	1441	CGAGGAGAGTGAAGCTCTACCTGACCAAGAGATGACCTTGTGCTTACTCCAGGCTCCTTGTG	1500
QY	1550	GAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGGCCATGAGGAAAGCTGG	1609
Db	1501	GAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGGCCATGAGGAAAGCTGG	1560
QY	1610	GTCCCACTGGGATATGGGTGATGAGCTTATACCATTCCTCTCTGCAATCAATAAC	1669
Db	1561	GTCCCACTGGGATATGGGTGATGAGCTTATACCATTCCTCTCTGCAATCAATAAC	1620
QY	1670	ACTTGCCTGTG 1680	
Db	1621	ACTTGCCTGTG 1631	
RESULT 6			
US-10-006-130A-127			
; Sequence 127, Application US/10006130A			
; Publication No. US20030148375A1			
GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Bolstein, David			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Eaton, Dan I.			
; APPLICANT: Ferrara, Napoleone			
; APPLICANT: Fong, Sherman			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Grimaldi, Christopher J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Hillan, Kenneth J.			
; APPLICANT: Pan, James			

```

; APPLICANT: Paoli, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: F2830PIC7
; CURRENT APPLICATION NUMBER: US/10/006,130A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 127
; LENGTH: 1636
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-006-130A-127

Query Match      96.2%; Score 1617; DB 12; Length 1636;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1628; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 51 GGGAGCGGGCCGAGGACTCCAGCTGCGCCAGGCTGGCATCCCTGACCTTGCCCTCT 110
    |||
Db 1 GAGGAGCGGGCCGAGGACTCCAGCTGCGCCAGGCTGGCATCCCTGACCTTGCCCTCT 60

QY 111 GACACCTGGGAAGATGGCGCGCCGCTGGACCTTCACCTTCTCTGTGTGCTGGCAGC 170
    |||
Db 61 GACACCTGGGAAGATGGCGCGCCGCTGGACCTTCACCTTCTCTGTGTGCTGGCAGC 120

QY 171 CACCTTGATCCAGCAACCCCTCAGTCCAGCTGAGTTCATCTCTGCGCCCAAAAGCAT 230
    |||
Db 121 CACCTTGATCCAGCAACCCCTCAGTCCAGCTGAGTTCATCTCTGCGCCCAAAAGCAT 180

QY 231 CAAAGAAAAGCTGACACAGAGAGCTGAGAGACCAACAGCCACAGCATCTCGACAGCT 290
    |||
Db 181 CAAAGAAAAGCTGACACAGAGAGCTGAGAGACCAACAGCCACAGCATCTCGACAGCT 240

QY 291 GCGGCTGCTAGTGCATGGGGGAAAAAGCCAGCGGAGG-ATGCCGTGCTGGGCAAGCT 349
    |||
Db 241 GCGGCTGCTAGTGCATGGGGGAAAAAGCCAGCGGAGGCACTCTGTGCTGGGCAAGCT 300

QY 350 GGTGAACACCCGCTCCTGAAGCACAATCATCTGCTGAAGGTCATCACAGCTAACTCTCTCA 409
    |||
Db 301 GGTGAACACCCGCTCCTGAAGCACAATCATCTGCTGAAGGTCATCACAGCTAACTCTCTCA 360

QY 410 GCTGCAAGGTAAAGCCCTCGGCCAATGACAGAGAGCTCTAGTAAAGTCCCCCTGGACAT 469
    |||
Db 361 GCTGCAAGGTAAAGCCCTCGGCCAATGACAGAGAGCTCTAGTAAAGTCCCCCTGGACAT 420

QY 470 GGTGGTGAAGTGAACAGCCGCTGTCGAAGACCATGCTGGAAGTTCACATGAGCACTGA 529
    |||
Db 421 GGTGGTGAAGTGAACAGCCGCTGTCGAAGACCATGCTGGAAGTTCACATGAGCACTGA 480

QY 530 GGGCCAGAGCCACATCCGATGAGACACAGTGAAGTGGCCCAACCCGCTGTCTCAG 589
    |||
Db 481 GGGCCAGAGCCACATCCGATGAGACACAGTGAAGTGGCCCAACCCGCTGTCTCAG 540

QY 590 TGACTGTGCCACCAAGCCATGGAGCCCTGGCATTCAACTGCTGATAGCTCTCTCTCT 649
    |||
Db 541 TGACTGTGCCACCAAGCCATGGAGCCCTGGCATTCAACTGCTGATAGCTCTCTCTCTCT 600

QY 650 GGTGAAGCCCTTAGCTAAGCAGGTGATGAACCTCTAGTGCACATCCCTGCCCAATCTAGT 709
    |||
Db 601 GGTGAAGCCCTTAGCTAAGCAGGTGATGAACCTCTAGTGCACATCCCTGCCCAATCTAGT 660

QY 710 GAAAAACACAGCTGTGTCCGTGATGAGAGCTTCTCTTAATGGCAATGATGACAGCTCT 769
    |||
Db 661 GAAAAACACAGCTGTGTCCGTGATGAGAGCTTCTCTTAATGGCAATGATGACAGCTCT 720

QY 770 GCACTGTGTAAGGTGCCATTTCTCTCAGCATTTGACATTCCTGGAAGTTGACCTTCTGTA 829
    |||
Db 721 GCACTGTGTAAGGTGCCATTTCTCTCAGCATTTGACATTCCTGGAAGTTGACCTTCTGTA 780

QY 830 TCCGCGCATCAAGGGGTGACACACATTCAGCTCTACCTGCGGGGCCAAGTTGTTGACCTACA 889
    |||
Db 781 TCCGCGCATCAAGGGGTGACACACATTCAGCTCTACCTGCGGGGCCAAGTTGTTGACCTACA 840

```

```

QY 890 GGGAAAGGTGACCAAGTGTTCATTAATTAATCTGACAGCTTCCCTGACAAATGCCACCTGGA 949
    |||
Db 841 GGGAAAGGTGACCAAGTGTTCATTAATTAATCTGACAGCTTCCCTGACAAATGCCACCTGGA 900

QY 950 CAACATCCCGTTGAGCTCATGCTGATGATGAGAGAGCTGGTGAAGAGCTGCAGTGGCTGT 1009
    |||
Db 901 CAACATCCCGTTGAGCTCATGCTGATGATGAGAGAGCTGGTGAAGAGCTGCAGTGGCTGT 960

QY 1010 GCTCTCTCAGAAAGATTCATGCTGCTGTTGAGCTGCTGCTTCCGAGAGTGGCCATGCG 1069
    |||
Db 961 GCTCTCTCAGAAAGATTCATGCTGCTGTTGAGCTGCTGCTTCCGAGAGTGGCCATGCG 1020

QY 1070 GCTGAAGTCAAGCATCGGCTGATCAATGAAAAAGCTGACAGATTAAGCTGGATCTACCCA 1129
    |||
Db 1021 GCTGAAGTCAAGCATCGGCTGATCAATGAAAAAGCTGACAGATTAAGCTGGATCTACCCA 1080

QY 1130 GATCGTGAAGATCTTAATCAGAGACACTCCCGAGTTTATTAAGACCAAGGCCATGCCAA 1189
    |||
Db 1081 GATCGTGAAGATCTTAATCAGAGACACTCCCGAGTTTATTAAGACCAAGGCCATGCCAA 1140

QY 1190 GGTGGCCCAACATGATGCTGCTGGAAGTGTTCCTCCTCAGTGAAGCCCTCGGCTTGTGT 1249
    |||
Db 1141 GGTGGCCCAACATGATGCTGCTGGAAGTGTTCCTCCTCAGTGAAGCCCTCGGCTTGTGT 1200

QY 1250 CACCTTGGGCAATCGAAGCCAGCTCGGAAGCTCAGTTTACACCAAGGTGACCAACTTAT 1309
    |||
Db 1201 CACCTTGGGCAATCGAAGCCAGCTCGGAAGCTCAGTTTACACCAAGGTGACCAACTTAT 1260

QY 1310 ACTCAACTGGAATTAATCATCATGCTGATGATGATGATGATGATGATGATGATGATGATG 1369
    |||
Db 1261 ACTCAACTGGAATTAATCATCATGCTGATGATGATGATGATGATGATGATGATGATGATG 1320

QY 1370 GTTCAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1429
    |||
Db 1321 GTTCAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380

QY 1430 GAACCAAGATGCAAAATTAAGATCTGGGCTCCAGAGTCAATGCTGTAAGGCTTGGGAT 1489
    |||
Db 1381 GAACCAAGATGCAAAATTAAGATCTGGGCTCCAGAGTCAATGCTGTAAGGCTTGGGAT 1440

QY 1490 CGAGGAGCTGAGTCTCTCACTGACACAGAGATGACCTTGTGCTTACTGACGCTCTGTG 1549
    |||
Db 1441 CGAGGAGCTGAGTCTCTCACTGACACAGAGATGACCTTGTGCTTACTGACGCTCTGTG 1500

QY 1550 GAAACCCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1609
    |||
Db 1501 GAAACCCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1560

QY 1610 GTCCCAAGCTGGAGATGAGGTGTGAGCTCTATAGACCATCCCTCTGCAATCAATTAAC 1669
    |||
Db 1561 GTCCCAAGCTGGAGATGAGGTGTGAGCTCTATAGACCATCCCTCTGCAATCAATTAAC 1620

QY 1670 ACTTGCTGTG 1680
    |||
Db 1621 ACTTGCTGTG 1631

```

# RESULT 7

```

; Sequence 279, Application US/10199672
; Publication No. US2003018442A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.

```

APPLICANT: Zhang, Zhenli  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3430R1C1  
CURRENT APPLICATION NUMBER: US/10/199,672  
CURRENT FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: US/10/052,586  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059266  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063120  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063121  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063486  
PRIOR FILING DATE: 1997-10-21  
PRIOR APPLICATION NUMBER: 60/063540  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063541  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063544  
PRIOR FILING DATE: 1997-10-28  
Remainding Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 279  
LENGTH: 1636  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-199-672-279

Query Match 96.2% Score 1617; DB 12; Length 1636;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1620; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 51 GGGAGGCGGCGGAGAGCTCCAGGCTCCAGGCTGCTGGCATTCCTGCTGCTCCCTCT 110  
DB 1 GAGGAGCGGCGGCGGAGCTCCAGGCTCCAGGCTGCTGGCATTCCTGCTGCTCCCTCT 60  
QY 111 GACACCTGGGAAGATGGCCCGGCGGCTGGACCTTCACCTTCCTGCTGCTGCTGCGAGC 170  
DB 61 GACACCTGGGAAGATGGCCCGGCGGCTGGACCTTCACCTTCCTGCTGCTGCTGCGAGC 120  
QY 171 CACCTTATCCAAAGCCACCTCAGTCCAGTCCAGTTCATCTCTGCGCCAAAGTCAT 230  
DB 121 CACCTTATCCAAAGCCACCTCAGTCCAGTTCATCTCTGCGCCAAAGTCAT 180  
QY 231 CAAAGAAAGCTGACACAGAGAGTGAAGGACACACAGCCACAGATCTCTGACAGACT 290  
DB 181 CAAAGAAAGCTGACACAGAGAGTGAAGGACACACAGCCACAGATCTCTGACAGACT 240  
QY 291 GCGGCTGCTAGTGGCTATGGGGGAAAGCCAGCGGAGG-ATCCCTGCTGCGGAGCT 349  
DB 241 GCGGCTGCTAGTGGCTATGGGGGAAAGCCAGCGGAGGATCCCTGCTGCGGAGCT 300  
QY 350 GGTGACACCGCTCTGAAGGACATCATCTGCTGAAGGTCAATCAGATTAATCTTCA 409  
DB 301 GGTGACACCGCTCTGAAGGACATCATCTGCTGAAGGTCAATCAGATTAATCTTCA 360  
QY 410 GCTGACAGTGAAGCCCTCGGCGCATGACACAGAGAGCTCTAGTCAAGATCCCTCGGACAT 469  
DB 361 GCTGACAGTGAAGCCCTCGGCGCATGACACAGAGAGCTCTAGTCAAGATCCCTCGGACAT 420  
QY 470 GGTGCTGATTCACACGCGCCCTGGTCAAGACATGTTGAGATTCACATGACAGCTGA 529  
DB 421 GGTGCTGATTCACACGCGCCCTGGTCAAGACATGTTGAGATTCACATGACAGCTGA 480  
QY 530 GGGCCAAAGCCACATCGGAGTGAACACAGTGAAGTGAAGTGGCCCAAGCCGCTGCTCAG 589  
DB 481 GGGCCAAAGCCACATCGGAGTGAACACAGTGAAGTGAAGTGGCCCAAGCCGCTGCTCAG 540

QY 590 TGACTGTGCGACGACGACCATGGAGGAGCTGGCGATCCAACTGCTGATTAAGCTTCCTCTCT 649  
DB 541 TGACTGTGCGACGACGACCATGGAGGAGCTGGCGATCCAACTGCTGATTAAGCTTCCTCTCT 600  
QY 650 GGTGAAGCGCTTACTTAAGCAGGATGATGAACCTCTTGTGCTGATCCCTGCCCAATTAAT 709  
DB 601 GGTGAAGCGCTTACTTAAGCAGGATGATGAACCTCTTGTGCTGATCCCTGCCCAATTAAT 660  
QY 710 GAAAGACAGTGTGCTGCTGCTGATGAGGCTTCTTAAGGACATGATGACAGCTCT 769  
DB 661 GAAAGACAGTGTGCTGCTGCTGATGAGGCTTCTTAAGGACATGATGACAGCTCT 720  
QY 770 GCACTGTGAGAGTGGCCATTTCCCTCAGCATGACCGTCTGGAGTTGACCTTCTGTA 829  
DB 721 GCACTGTGAGAGTGGCCATTTCCCTCAGCATGACCGTCTGGAGTTGACCTTCTGTA 780  
QY 830 TCTGCGCATCAAGGCTGACACATTCATGCTTACCTGGGGCCAAAGTTTGGACTACA 889  
DB 781 TCTGCGCATCAAGGCTGACACATTCATGCTTACCTGGGGCCAAAGTTTGGACTACA 840  
QY 890 GGGAAAGGTGACCAAGTGTTCATTACTGACGCTTCCCTGACATGCCCCACCTGGA 949  
DB 841 GGGAAAGGTGACCAAGTGTTCATTACTGACGCTTCCCTGACATGCCCCACCTGGA 900  
QY 950 CAACATCCCGTTACGCTCATCTGAGTCAAGAGAGTGTGAAGCTCAGTGGCTGCT 1009  
DB 901 CAACATCCCGTTACGCTCATCTGAGTCAAGAGAGTGTGAAGCTCAGTGGCTGCT 960  
QY 1010 GCTCTCTCAGAGAAATTCATGCTGCTGTTGGACTGTGCTGCTGCTGAGAGTCCCATCG 1069  
DB 961 GCTCTCTCAGAGAAATTCATGCTGCTGTTGGACTGTGCTGCTGCTGAGAGTCCCATCG 1020  
QY 1070 GCTGAGTCAAGATCGGCGGCTGATCAATGAAGGCTGACATTAAGCTGGGATCTACCCA 1129  
DB 1021 GCTGAGTCAAGATCGGCGGCTGATCAATGAAGGCTGACATTAAGCTGGGATCTACCCA 1080  
QY 1130 GATCGTGAAGATCTTAATCTCAGGACACTCCGAGTTTATTAAGACCAAGGCCATGCA 1189  
DB 1081 GATCGTGAAGATCTTAATCTCAGGACACTCCGAGTTTATTAAGACCAAGGCCATGCA 1140  
QY 1190 GGTGCGCCAACTGATGCTGCTGGAAGTGTTCCTCCAGTGAAGCCCTCGCCCTTGT 1249  
DB 1141 GGTGCGCCAACTGATGCTGCTGGAAGTGTTCCTCCAGTGAAGCCCTCGCCCTTGT 1200  
QY 1250 CACCTGCGGATCAAGAGCAGCTGGAAGCTCAGTTTATTAAGACCAAGGCCATTA 1309  
DB 1201 CACCTGCGGATCAAGAGCAGCTGGAAGCTCAGTTTATTAAGACCAAGGCCATTA 1260  
QY 1310 ACTCACTTGAATTAATCACTGATCGGATCGAGCTGATGAATGAATCTGGATTTGGCTG 1369  
DB 1261 ACTCACTTGAATTAATCACTGATCGGATCGAGCTGATGAATGAATCTGGATTTGGCTG 1320  
QY 1370 GTTCAACCTGATGTTGCTGAAAAATCATCATGATGATGATTCATCATCTGCTGCT 1429  
DB 1321 GTTCAACCTGATGTTGCTGAAAAATCATCATGATGATGATTCATCATCTGCTGCT 1380  
QY 1430 GAACCAAGATGGAATTAATGATCTGGGGGTCCAGTGCATTTGGTGAAGGCTTGGGAT 1489  
DB 1381 GAACCAAGATGGAATTAATGATCTGGGGGTCCAGTGCATTTGGTGAAGGCTTGGGAT 1440  
QY 1490 CGAGGAGCTGAGTCTCCTCAGTGAACAGATGCTGCTGCTTACTCAGGCTCCTTGTG 1549  
DB 1441 CGAGGAGCTGAGTCTCCTCAGTGAACAGATGCTGCTGCTTACTCAGGCTCCTTGTG 1500  
QY 1550 GAAACCCAGCTCTCTCTCTCCAGTGAAGCTTGGATGGACCATGAGGAAAGCTGG 1609  
DB 1501 GAAACCCAGCTCTCTCTCTCCAGTGAAGCTTGGATGGACCATGAGGAAAGCTGG 1560  
QY 1610 GTCCAGCTGGAGATGAGTGTGAGTCTATAGACATCTCCTCTGCTCAATCAATAAC 1669  
DB 1561 GTCCAGCTGGAGATGAGTGTGAGTCTATAGACATCTCCTCTGCTCAATCAATAAC 1620

OY 1670 ACTGCTGTG 1680  
DB 1621 ACTGCTGTG 1631

RESULT 8  
US-10-006-172A-127

Sequence 127, Application US/10006172A  
Publication No. US20030153000A1

## GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830PIC11  
CURRENT APPLICATION NUMBER: US/10/006,172A  
PRIOR FILING DATE: 2002-03-19  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098803  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098821  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098843  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/099536  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099596  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099598  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099602  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099642  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099741  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099754  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099763  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099792  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099808  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099812  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099815  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099816  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100385  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100388  
PRIOR FILING DATE: 1998-09-15

PRIOR APPLICATION NUMBER: 60/100390  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100584  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100661  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100662  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100664  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100683  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100684  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100710  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100711  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100848  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100849  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100919  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/100930  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/101014  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101068  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101071  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/101279  
PRIOR FILING DATE: 1998-09-22  
PRIOR APPLICATION NUMBER: 60/101471  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101472  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101474  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101475  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101476  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101477  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101479  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101741  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101743  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101915  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/102207  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102240  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102307  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102330  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102331  
PRIOR FILING DATE: 1998-09-29  
PRIOR APPLICATION NUMBER: 60/102484  
PRIOR FILING DATE: 1998-09-30  
PRIOR APPLICATION NUMBER: 60/102487

Query Match 96.2%; Score 1617; DB 12; Length 1636;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1628; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Db 61 GACACCTGGGAAGATGGCCGCCCGTGAGACCTTACCCCTTCTCTGTGTGCTGGAGC 120

QY 111 GACACCTGGGAAGATGGCCGCCCGTGAGACCTTACCCCTTCTGTGTGCTGGAGC 170

Db 61 GACACCTGGGAAGATGGCCGCCCGTGAGACCTTACCCCTTCTGTGTGCTGGAGC 120

QY 171 CACCTTGATCCAAAGCCACCTCAGTCCACACTGAGTTTCATCTCGGGCCAAAGTCAT 230

Db 121 CACCTTGATCCAAAGCCACCTCAGTCCACACTGAGTTTCATCTCGGGCCAAAGTCAT 180

QY 231 CAAAGAAAAGCTGACACAGAGAGTGAAGACCAACAGCCACAGCATCTCGAGCAGCT 290

Db 181 CAAAGAAAAGCTGACACAGAGAGTGAAGACCAACAGCCACAGCATCTCGAGCAGCT 240

QY 291 GCGGCTGCTCAGTGCATGGGGGAAAAAGCCAGCCGAGG - ATCCCTGTGTGGGAGCCCT 349

Db 241 GCGGCTGCTCAGTGCATGGGGGAAAAAGCCAGCCGAGGATCCCTGTGTGGGAGCCCT 300

QY 350 GGTGAACACCGCTCCTGAAGCAGATCATCTGGTGAAGGTCATCAGACGTAACTCTCCA 409

Db 301 GGTGAACACCGCTCCTGAAGCAGATCATCTGGTGAAGGTCATCAGACGTAACTCTCCA 360

QY 410 GCTGCAAGTGAAGCCCTCGGCCAATGACAGAGCTGCTAAGTCAAGATCCCTGGACAT 469

Db 361 GCTGCAAGTGAAGCCCTCGGCCAATGACAGAGCTGCTAAGTCAAGATCCCTGGACAT 420

QY 470 GGTGGCTGATGTAACAGCCGCCCTGGTCAAGACATCGTGGATGCCATGACAGACTGA 529

Db 421 GGTGGCTGATGTAACAGCCGCCCTGGTCAAGACATCGTGGATGCCATGACAGACTGA 480

QY 530 GGCCCAAGCCACCATCCGATGAGACACAGTGAAGTGGCCACCCGCTGGTCTCAG 589

Db 481 GGCCCAAGCCACCATCCGATGAGACACAGTGAAGTGGCCACCCGCTGGTCTCAG 540

QY 590 TGACTGTGCCACCAAGCCATGGAGCCCTGCGATCCAACTGCTGCATAAAGCTCTCTCT 649

Db 541 TGACTGTGCCACCAAGCCATGGAGCCCTGCGATCCAACTGCTGCATAAAGCTCTCTCT 600

QY 650 GGTGAACGCTTGAAGTGAAGGTCATGAACCTCTAAGTCCCTGCGCAATCAGT 709

Db 601 GGTGAACGCTTGAAGTGAAGGTCATGAACCTCTAAGTCCCTGCGCAATCAGT 660

QY 710 GAAAAACACGCTGTGCCGTGATGAGGCTTCCTTCAATGGCATGTATGACAGACTCT 769

Db 661 GAAAAACACGCTGTGCCGTGATGAGGCTTCCTTCAATGGCATGTATGACAGACTCT 720

QY 770 GCAGCTGCTGAAGTGGCCATTTCCCTCAGCATTTGACAGCTGTGACATCTCTCTGA 829

Db 721 GCAGCTGCTGAAGTGGCCATTTCCCTCAGCATTTGACAGCTGTGACATCTCTCTGA 780

QY 830 TCCCTGCATCAAGGGTGAACACATTCAGTCTAAGCTGGGGCCAAAGTTGTGGACTACA 889

Db 781 TCCCTGCATCAAGGGTGAACACATTCAGTCTAAGCTGGGGCCAAAGTTGTGGACTACA 840

QY 890 GGGAAAGGTGACCAAGTGTTCATTAATCTGTGACGTTCCCTGACAAATGCCACCCCTGA 949

Db 841 GGGAAAGGTGACCAAGTGTTCATTAATCTGTGACGTTCCCTGACAAATGCCACCCCTGA 900

QY 950 CAACATCCCGTTACAGCTCATCTGAGTCAAGAGCTGTAAAGCTCAGTGGCTGT 1009

Db 901 CAACATCCCGTTACAGCTCATCTGAGTCAAGAGCTGTAAAGCTCAGTGGCTGT 960

QY 1010 GCTCTCTCCAGAAATTCATGCTGCTGGAGCTGTGCTCTCTCTAGAGTGGCCATCG 1069

Db 961 GCTCTCTCCAGAAATTCATGCTGCTGGAGCTGTGCTCTCTCTAGAGTGGCCATCG 1020

QY 1070 GCTGAAGTCAAGATCGGGCTGATCAATGAAAAGCTGACAGATTAAGCTGGATCTACCA 1129

Db 1021 GCTGAAGTCAAGATCGGGCTGATCAATGAAAAGCTGACAGATTAAGCTGGATCTACCA 1080

QY 1130 GATCGTGAAGATCTTAATCTAGAGACACTCCCGAGTTTATATAGACCAAGGCCATGCGAA 1189

Db 1081 GATCGTGAAGATCTTAATCTAGAGACACTCCCGAGTTTATATAGACCAAGGCCATGCGAA 1140

QY 1190 GGTGGCCCAACTGATCGTGTGAAGTGTTCCTCCAGTGAAGCCCTCGGCCCTTGT 1249

Db 1141 GGTGGCCCAACTGATCGTGTGAAGTGTTCCTCCAGTGAAGCCCTCGGCCCTTGT 1200

QY 1250 CACCCTGGGATCGAAGCCAGCTCGAAGCTCAGTTTATACCAAAAGGTGACCACTTAT 1309  
DB 1201 CACCTGGGATCGAAGCCAGCTCGAAGCTCAGTTTATACCAAAAGGTGACCACTTAT 1260  
QY 1310 ACTCACTTGAATAACATCAGCTCTGATCGATCCAGCTGATGAATCTGGGATTGGCTG 1369  
DB 1261 ACTCACTTGAATAACATCAGCTCTGATCGATCCAGCTGATGAATCTGGGATTGGCTG 1320  
QY 1370 GTCCAACTGATGTTCTGAAAAACATCATCATGATCATCCATCCATCCCTGCTGCC 1429  
DB 1321 GTCCAACTGATGTTCTGAAAAACATCATCATGATCATCCATCCATCCCTGCTGCC 1380  
QY 1430 GAACAGATGAGCAATTAAGATCTGGGTCACATGTCATCTGTAAGAGCCCTGGGAT 1489  
DB 1381 GAACAGATGAGCAATTAAGATCTGGGTCACATGTCATCTGTAAGAGCCCTGGGAT 1440  
QY 1490 CGAGCAGCTGATGCTCTGATGACCAAGATGCTTGTGCTTACTCCAGCTCTTGTG 1549  
DB 1441 CGAGCAGCTGATGCTCTGATGACCAAGATGCTTGTGCTTACTCCAGCTCTTGTG 1500  
QY 1550 GAAACCCAGCTCTCTGCTCCAGTGAAGATGATGAGCCATGAGCCATGAGGAGCTG 1609  
DB 1501 GAAACCCAGCTCTCTGCTCCAGTGAAGATGATGAGCCATGAGCCATGAGGAGCTG 1560  
QY 1610 GTCCAGCTGAGATGAGTGGTGTGAGCTTATAGCAATCCCTCTCTCAATCAATAAC 1669  
DB 1561 GTCCAGCTGAGATGAGTGGTGTGAGCTTATAGCAATCCCTCTCTCAATCAATAAC 1620  
QY 1670 ACTGCTGCTG 1680  
DB 1621 ACTGCTGCTG 1631

RESULT 9  
US-10-187-749-279  
Sequence 279, Application US/10187749  
Publication No. US20030153036A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3430R1C1  
CURRENT APPLICATION NUMBER: US/10/187,749  
CURRENT FILING DATE: 2002-07-01  
PRIOR APPLICATION NUMBER: US/10/052,586  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059266  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063120  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063121  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063486  
PRIOR FILING DATE: 1997-10-21  
PRIOR APPLICATION NUMBER: 60/063540  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063541  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063544

QY 1250 CACCCTGGGATCGAAGCCAGCTCGAAGCTCAGTTTATACCAAAAGGTGACCACTTAT 1309  
DB 1201 CACCTGGGATCGAAGCCAGCTCGAAGCTCAGTTTATACCAAAAGGTGACCACTTAT 1260  
QY 1310 ACTCACTTGAATAACATCAGCTCTGATCGATCCAGCTGATGAATCTGGGATTGGCTG 1369  
DB 1261 ACTCACTTGAATAACATCAGCTCTGATCGATCCAGCTGATGAATCTGGGATTGGCTG 1320  
QY 1370 GTCCAACTGATGTTCTGAAAAACATCATCATGATCATCCATCCATCCCTGCTGCC 1429  
DB 1321 GTCCAACTGATGTTCTGAAAAACATCATCATGATCATCCATCCATCCCTGCTGCC 1380  
QY 1430 GAACAGATGAGCAATTAAGATCTGGGTCACATGTCATCTGTAAGAGCCCTGGGAT 1489  
DB 1381 GAACAGATGAGCAATTAAGATCTGGGTCACATGTCATCTGTAAGAGCCCTGGGAT 1440  
QY 1490 CGAGCAGCTGATGCTCTGATGACCAAGATGCTTGTGCTTACTCCAGCTCTTGTG 1549  
DB 1441 CGAGCAGCTGATGCTCTGATGACCAAGATGCTTGTGCTTACTCCAGCTCTTGTG 1500  
QY 1550 GAAACCCAGCTCTCTGCTCCAGTGAAGATGATGAGCCATGAGCCATGAGGAGCTG 1609  
DB 1501 GAAACCCAGCTCTCTGCTCCAGTGAAGATGATGAGCCATGAGCCATGAGGAGCTG 1560  
QY 1610 GTCCAGCTGAGATGAGTGGTGTGAGCTTATAGCAATCCCTCTCTCAATCAATAAC 1669  
DB 1561 GTCCAGCTGAGATGAGTGGTGTGAGCTTATAGCAATCCCTCTCTCAATCAATAAC 1620  
QY 1670 ACTGCTGCTG 1680  
DB 1621 ACTGCTGCTG 1631

Query Match 96.2%; Score 1617; DB 12; Length 1636;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1628; Conservative 1; Mismatches 1; Indels 1; Gaps 1;  
US-10-187-749-279

QY 51 GRGAGAGGCGCGGAGGATGCTCCAGGCTGCGGAGCTGCTGATCTGCACTTCTGCTCT 110  
DB 1 GAGGAGGCGCGCGGAGGATGCTCCAGGCTGCGGAGCTGCTGATCTGCACTTCTGCTCT 60  
QY 111 GACACCTGGAAGATGCGCGCGCGCGGAGCTTCACTTCTGCTGCTGCTGCTGCTGCT 170  
DB 61 GACACCTGGAAGATGCGCGCGCGCGGAGCTTCACTTCTGCTGCTGCTGCTGCTGCT 120  
QY 171 CACCTGATCCAGGACCTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 230  
DB 121 CACCTGATCCAGGACCTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
QY 231 CAAGAAAGCTGACACAGAGCTGGAAGACCAACGCGCACAGATCTGCAAGAGCT 290  
DB 181 CAAGAAAGCTGACACAGAGCTGGAAGACCAACGCGCACAGATCTGCAAGAGCT 240  
QY 291 GCGGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 349  
DB 241 GCGGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
QY 350 GGTGAAACACCTGCTGGAAGACATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 409  
DB 301 GGTGAAACACCTGCTGGAAGACATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
QY 410 GCTGAGGTGAAAGCTTGGGCTGATGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 469  
DB 361 GCTGAGGTGAAAGCTTGGGCTGATGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
QY 470 GGTGAGGTGAAAGCTTGGGCTGATGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 529  
DB 421 GGTGAGGTGAAAGCTTGGGCTGATGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
QY 530 GGTGAGGTGAAAGCTTGGGCTGATGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 589  
DB 481 GGTGAGGTGAAAGCTTGGGCTGATGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
QY 590 TGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 649  
DB 541 TGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
QY 650 GGTGAGGTGAAAGCTTGGGCTGATGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 709  
DB 601 GGTGAGGTGAAAGCTTGGGCTGATGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
QY 710 GGTGAGGTGAAAGCTTGGGCTGATGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 769  
DB 661 GGTGAGGTGAAAGCTTGGGCTGATGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
QY 770 GGTGAGGTGAAAGCTTGGGCTGATGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 829  
DB 721 GGTGAGGTGAAAGCTTGGGCTGATGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
QY 830 GGTGAGGTGAAAGCTTGGGCTGATGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 889  
DB 781 GGTGAGGTGAAAGCTTGGGCTGATGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
QY 890 GGTGAGGTGAAAGCTTGGGCTGATGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 949  
DB 841 GGTGAGGTGAAAGCTTGGGCTGATGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 900



```
OY 950 CACATCCGTCAGCCTCATCTGAGTCAGAGCCTGCTGAAAGCTCAGTGGCTGCT 1009
    |||||
Db 901 CACATCCCGTCAGCCTCATCTGAGTCAGAGCCTGCTGAAAGCTCAGTGGCTGCT 960
OY 1010 GCTCTCCGAAAGAAATTCATGAGTCTGTTGAGTCTGTTGCTGTAAGTGGCCATG 1069
    |||||
Db 961 GCTCTCCGAAAGAAATTCATGAGTCTGTTGAGTCTGTTGCTGTAAGTGGCCATG 1020
OY 1070 GCTGAAGTCAAGCATCGGGCTGATCAATGAAAGGCTGACATGAAGTGGATACCA 1129
    |||||
Db 1021 GCTGAAGTCAAGCATCGGGCTGATCAATGAAAGGCTGACATGAAGTGGATACCA 1080
OY 1130 GATGCTAAGATCTTAATCAAGACACTCCCGAGTTTATATAGACCAAGGCTACCA 1189
    |||||
Db 1081 GATGCTAAGATCTTAATCAAGACACTCCCGAGTTTATATAGACCAAGGCTACCA 1140
OY 1190 GGTGGCCCACTGATGCTGCTGGAAGTTCCTCCAGTGAAGCCCTCCGCTTGT 1249
    |||||
Db 1141 GGTGGCCCACTGATGCTGCTGGAAGTTCCTCCAGTGAAGCCCTCCGCTTGT 1200
OY 1250 CACCTGGGATCGAAGCCAGCTGGAAGCTCAAGTTTACACAAAGTGACAACTTAT 1309
    |||||
Db 1201 CACCTGGGATCGAAGCCAGCTGGAAGCTCAAGTTTACACAAAGTGACAACTTAT 1260
OY 1310 ACTCACTTGAATTAATCAATCACTCTGATCGGATCCAGCTGATGAAGTGGATGCTG 1369
    |||||
Db 1261 ACTCACTTGAATTAATCAATCACTCTGATCGGATCCAGCTGATGAAGTGGATGCTG 1320
OY 1370 GTTCCACCTGATGCTGTAAGAAACATCAATCAATCAATCAATCAATCAATCAAT 1429
    |||||
Db 1321 GTTCCACCTGATGCTGTAAGAAACATCAATCAATCAATCAATCAATCAATCAAT 1380
OY 1430 GAACCAAGATGCAAAATTAAGATCTGGGGTCCAGTGTCAATGCTGGAAGGCTT 1489
    |||||
Db 1381 GAACCAAGATGCAAAATTAAGATCTGGGGTCCAGTGTCAATGCTGGAAGGCTT 1440
OY 1490 CGAGGAGCTGAGTCTCACTGACACCAAGAGATGCCCTTGTCTACTCCAGCTCTTGTG 1549
    |||||
Db 1441 CGAGGAGCTGAGTCTCACTGACACCAAGAGATGCCCTTGTCTACTCCAGCTCTTGTG 1500
OY 1550 GAACCCAGCTCTCTCTGCTCCAGTGAAGCTTGAATGAGCAGCATCAGGAAGGCTG 1609
    |||||
Db 1501 GAACCCAGCTCTCTCTGCTCCAGTGAAGCTTGAATGAGCAGCATCAGGAAGGCTG 1560
OY 1610 GTCCAGCTGGAGTATGGGTGAGCTCTATAGACCATCCCTCTGCAATCAATTAAC 1669
    |||||
Db 1561 GTCCAGCTGGAGTATGGGTGAGCTCTATAGACCATCCCTCTGCAATCAATTAAC 1620
OY 1670 ACTTGCTGTG 1680
    |||||
Db 1621 ACTTGCTGTG 1631
```

```
RESULT 10
US-10-194-457-279
; Sequence 279, Application US/10194457
; Publication No. US20030153037A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jilan
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C296
; CURRENT APPLICATION NUMBER: US/10/194,457
```

```
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 279
; LENGTH: 1636
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-194-457-279

Query Match 96.2%; Score 1617; DB 12; Length 1636;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1628; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

OY 51 GRGAGGGGGGGGAGACTCCAGGCTGCGGACCTGCGCATCTGCTGCTGCT 110
    |||||
Db 1 GAGAGCGGGGGGAGACTCCAGGCTGCGGACCTGCGCATCTGCTGCTGCT 60
OY 111 GACACCTGGGAAATGCGCGGCGCGGACCTTCTGTTGCTGCGAGC 170
    |||||
Db 61 GACACCTGGGAAATGCGCGGCGCGGACCTTCTGTTGCTGCGAGC 120
OY 171 CACCTGTATCCAGCACCCCTCAGTCCGACCTGCTCATCTGCGCCAAAAGTAT 230
    |||||
Db 121 CACCTGTATCCAGCACCCCTCAGTCCGACCTGCTCATCTGCGCCAAAAGTAT 180
OY 231 CAAAGAAAGCTGACACAGAGCTGAAGAGCACAAAGCCAGCATCTGAGCAGCT 290
    |||||
Db 181 CAAAGAAAGCTGACACAGAGCTGAAGAGCACAAAGCCAGCATCTGAGCAGCT 240
OY 291 GCCGCTGCTAGTGCATGCGGGAAGAGCCAGCGAGG-ATCCCTGCTGCGAGCT 349
    |||||
Db 241 GCCGCTGCTAGTGCATGCGGGAAGAGCCAGCGAGGATCCCTGCTGCGAGCT 300
OY 350 GGTGAACACGCTCTGTAAGACATCTGCTGAAGGTATCAACAGTAATCTTCA 409
    |||||
Db 301 GGTGAACACGCTCTGTAAGACATCTGCTGAAGGTATCAACAGTAATCTTCA 360
OY 410 GCTGAGGTGAAGCCCTGCGCATGACAGAGAGCTGTATCAAGATCCCTGAGCAT 469
    |||||
Db 361 GCTGAGGTGAAGCCCTGCGCATGACAGAGAGCTGTATCAAGATCCCTGAGCAT 420
OY 470 GGTGCTGATTAACACAGCCCTGCTGTAAGACATCTGAGTTCACATGACAGATGA 529
    |||||
Db 421 GGTGCTGATTAACACAGCCCTGCTGTAAGACATCTGAGTTCACATGACAGATGA 480
OY 530 GGGCCAAAGCCATCGCATGACACAGTGAAGTGGCCCAAGCCGCTGCTCAG 589
    |||||
Db 481 GGGCCAAAGCCATCGCATGACACAGTGAAGTGGCCCAAGCCGCTGCTCAG 540
OY 590 TGAATGCGCCAGCCATGAGGAGCTGCGCATCACTGCTGATGAAGTCTCTCTCT 649
    |||||
Db 541 TGAATGCGCCAGCCATGAGGAGCTGCGCATCACTGCTGATGAAGTCTCTCTCT 600
```

QY 650 GGTGAAGCGCTTAGTACAGAGGTATGAACTCTCTAGTGCATCCCTGCCAATCTAGT 709  
 |||||||  
 Db 601 GGTGAAGCGCTTAGTACAGAGGTATGAACTCTCTAGTGCATCCCTGCCAATCTAGT 660  
 QY 710 GAAAAACAGCTGTGTCCGTGATGACAGGCTTCTTCAATGGCATATAGCAGACTCT 769  
 |||||||  
 Db 661 GAAAAACAGCTGTGTCCGTGATGACAGGCTTCTTCAATGGCATATAGCAGACTCT 720  
 QY 770 GCAGCTGGGAAGGTGCCATTTCCCTCAGCATTTGACCGCTGGATTTGACCTTCTGTA 829  
 |||||||  
 Db 721 GCAGCTGGGAAGGTGCCATTTCCCTCAGCATTTGACCGCTGGATTTGACCTTCTGTA 780  
 QY 830 TCCTGCATCAAGGTGACACATTCAGCTTACCTGGGGGCCAAGTTGTTGGACTACAA 889  
 |||||||  
 Db 781 TCCTGCATCAAGGTGACACATTCAGCTTACCTGGGGGCCAAGTTGTTGGACTACAA 840  
 QY 890 GGGAAAGGTGACCAAGTGTGTAATTAATCTGACGTTCCCTTACAAATGCCACCTGGA 949  
 |||||||  
 Db 841 GGGAAAGGTGACCAAGTGTGTAATTAATCTGACGTTCCCTTACAAATGCCACCTGGA 900  
 QY 950 CAACATCCGCTGACGCTCATCTGATGATGACGAGCTGGTGAAGCTGACAGTGGCTGCT 1009  
 |||||||  
 Db 901 CAACATCCGCTTACGCTCATCTGATGATGACGAGCTGGTGAAGCTGACAGTGGCTGCT 960  
 QY 1010 GCTCTCTCAGAAAGATTCATGCTGCTGTTGACCTGTGCTCTGAGAGTGCCTCATCG 1069  
 |||||||  
 Db 961 GCTCTCTCAGAAAGATTCATGCTGCTGTTGACCTGTGCTCTGAGAGTGCCTCATCG 1020  
 QY 1070 GCTGAAGTCAAGATCGGGCTGATTCATGAAAGGCGCATAGCTGGGATCTACCCA 1129  
 |||||||  
 Db 1021 GCTGAAGTCAAGATCGGGCTGATTCATGAAAGGCGCATAGCTGGGATCTACCCA 1080  
 QY 1130 GATCGTGAATCTTAATCTAGCAGACACTCCGAGTTTATATAGCAAGCCATGCA 1189  
 |||||||  
 Db 1081 GATCGTGAATCTTAATCTAGCAGACACTCCGAGTTTATATAGCAAGCCATGCA 1140  
 QY 1190 GGTGGCCCAACTGATGCTGTGGAAGTGTTCCTCCAGTGAAGCCCTCCGCCCTTGT 1249  
 |||||||  
 Db 1141 GGTGGCCCAACTGATGCTGTGGAAGTGTTCCTCCAGTGAAGCCCTCCGCCCTTGT 1200  
 QY 1250 CACCTGGGATGAGACGCGAGCTCGGAAGCTCAGTTTACACAAAGGTGACCAACTAT 1309  
 |||||||  
 Db 1201 CACCTGGGATGAGACGCGAGCTCGGAAGCTCAGTTTACACAAAGGTGACCAACTAT 1260  
 QY 1310 ACTCACTTGAATTAATCACTGATCGATCGATCGATGATGAACTCTGGATTTGCTG 1369  
 |||||||  
 Db 1261 ACTCACTTGAATTAATCACTGATCGATCGATCGATGATGAACTCTGGATTTGCTG 1320  
 QY 1370 GTTCAACCTGATGTCTGAAAAAATCATCATCATGATCATCATCATCATCATCATCAT 1429  
 |||||||  
 Db 1321 GTTCAACCTGATGTCTGAAAAAATCATCATCATGATCATCATCATCATCATCATCAT 1380  
 QY 1430 GAACCAATGAGCAATTAAGATCTGGGGTCCAGTGTCAATTTGTAAGGCTTGGGAT 1489  
 |||||||  
 Db 1381 GAACCAATGAGCAATTAAGATCTGGGGTCCAGTGTCAATTTGTAAGGCTTGGGAT 1440  
 QY 1490 CGAGGAGCTGATGCTCACTGACCAAGATGCCCTTGTGCTTACTCCAGCTCTTGTG 1549  
 |||||||  
 Db 1441 CGAGGAGCTGATGCTCACTGACCAAGATGCCCTTGTGCTTACTCCAGCTCTTGTG 1500  
 QY 1550 GAAACCCAGCTCTCTCTCTCCAGTGAAGACTTGGATGGAGCAATCAGGAGAGCTGG 1609  
 |||||||  
 Db 1501 GAAACCCAGCTCTCTCTCTCCAGTGAAGACTTGGATGGAGCAATCAGGAGAGCTGG 1560  
 QY 1610 GTCCACAGTGGAGTATGAGTGTAGGCTTATAGCATCCCTCTGCAATCAATTAAC 1669  
 |||||||  
 Db 1561 GTCCACAGTGGAGTATGAGTGTAGGCTTATAGCATCCCTCTGCAATCAATTAAC 1620  
 QY 1670 ACTTGCCTGTG 1680  
 |||||||  
 Db 1621 ACTTGCCTGTG 1631

RESULT 11  
 US-10-184-642-279  
 ; Sequence 279, Application US/10184642  
 ; Publication No. US20030157635A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3430R1C194  
 ; CURRENT APPLICATION NUMBER: US/10/184,642  
 ; PRIOR APPLICATION REMOVED - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 612  
 ; SEQ ID NO 279  
 ; LENGTH: 1636  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-184-642-279  
 Query Match 96.2%; Score 1617; DB 12; Length 1636;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1636; Conservative 1; Mismatches 1; Indels 1; Gaps 1;  
 QY 51 GRGAGCGGGCGAGAGCTCAAGCTGCGCAGGTGCGCATCTGCTGCTGCTCT 110  
 |||||||  
 Db 1 GAGAGCGGGCGAGAGCTCAAGCTGCGCAGGTGCGCATCTGCTGCTGCTCT 60  
 QY 111 GACACCTGGGAGAGATGGCGCGCGGTGAGACTTCAACCTTCTCTGTGTTGCTGGCAGC 170  
 |||||||  
 Db 61 GACACCTGGGAGAGATGGCGCGCGGTGAGACTTCAACCTTCTCTGTGTTGCTGGCAGC 120  
 QY 171 CACCTTGATCAAGCCACCCCTCAGTCCCACTGAGTTTCAATCCTGGGCCAAGATCAT 230  
 |||||||  
 Db 121 CACCTTGATCAAGCCACCCCTCAGTCCCACTGAGTTTCAATCCTGGGCCAAGATCAT 180  
 QY 231 CAAAGAAAAGCTGACACAGAGCTGAAGACCAACAGCCACAGCATCCTGACAGCT 290  
 |||||||  
 Db 181 CAAAGAAAAGCTGACACAGAGCTGAAGACCAACAGCCACAGCATCCTGACAGCT 240  
 QY 291 GCGGCTGCTAGTGCATGCGGGGAAAAAGCCAGCCGAGG-ATGCCCTGTGCTGGCAGCCT 349  
 |||||||  
 Db 241 GCGGCTGCTAGTGCATGCGGGGAAAAAGCCAGCCGAGGATCCTGTGCTGGCAGCCT 300  
 QY 350 GGTGACACCGCTCCTGAGACATCATCTGCGTGAAGGTCATGACAGTAACTCCTCCA 409  
 |||||||  
 Db 301 GGTGACACCGCTCCTGAGACATCATCTGCGTGAAGGTCATGACAGTAACTCCTCCA 360  
 QY 410 GCTGACAGTGAAGCCCTCGGCAATGACAGAGCTGACTAGTCAAGATCCCTGACAT 469  
 |||||||  
 Db 361 GCTGACAGTGAAGCCCTCGGCAATGACAGAGCTGACTAGTCAAGATCCCTGACAT 420  
 QY 470 GGTGCTGGATTAACAGCGCCCTGGTCAAGACATCTGGGATTCACATGACGACTGA 529  
 |||||||  
 Db 421 GGTGCTGGATTAACAGCGCCCTGGTCAAGACATCTGGGATTCACATGACGACTGA 480  
 QY 530 GGCCCAAGCCACCATCCGATGACACCAAGTGAAGTGGCCCAAGCCGCTGCTCTGAC 589  
 |||||||  
 Db 481 GGCCCAAGCCACCATCCGATGACACCAAGTGAAGTGGCCCAAGCCGCTGCTCTGAC 540  
 QY 590 TGACTGTGCCACAGCCATGGAGGCTGGCATCAACTGCTCATTAAGCTCTCTCTCT 649  
 |||||||  
 Db 541 TGACTGTGCCACAGCCATGGAGGCTGGCATCAACTGCTCATTAAGCTCTCTCTCTCT 600

QY 650 GGTGAACGGCTTACGTAAGAGGTGATGAACCTCTAGTCCCTGCGCAATCTAGT 709  
 DB 601 GGTGAACGGCTTACGTAAGAGGTGATGAACCTCTAGTCCCTGCGCAATCTAGT 709  
 QY 710 GAAAAACGAGCTGTCCGATGAGGCTTCCATGGATGATGACACCTCT 769  
 DB 661 GAAAAACGAGCTGTCCGATGAGGCTTCCATGGATGATGACACCTCT 769  
 QY 770 GCAGCTGTGAAGGTCCCATTTCCCTCAGCATTTGACCGCTGGATTTGACCTTCTGA 829  
 DB 721 GCAGCTGTGAAGGTCCCATTTCCCTCAGCATTTGACCGCTGGATTTGACCTTCTGA 829  
 QY 830 TCTGCTCATCAGAGGTGACACCATTCAGCTCTACCTGGGGGCCAAGTTGTTGACCTACA 889  
 DB 781 TCTGCTCATCAGAGGTGACACCATTCAGCTCTACCTGGGGGCCAAGTTGTTGACCTACA 889  
 QY 890 GGGAAAGGTGACCAAGTGTCTCAATACCTGCAAGTGTCCCTGACCAAGTCCCTGGA 949  
 DB 841 GGGAAAGGTGACCAAGTGTCTCAATACCTGCAAGTGTCCCTGACCAAGTCCCTGGA 949  
 QY 950 CAACATCCGTTGAGCTCATCTGAGTCAAGAGCTGGTGAAGCTGACAGTGGCTGCT 1009  
 DB 901 CAACATCCGTTGAGCTCATCTGAGTCAAGAGCTGGTGAAGCTGACAGTGGCTGCT 1009  
 QY 1010 GCTCTCTCAGAAATTCATGAGTCTCTGTTGACCTGTGCTCTGAGAGTCCCATCG 1069  
 DB 961 GCTCTCTCAGAAATTCATGAGTCTCTGTTGACCTGTGCTCTGAGAGTCCCATCG 1069  
 QY 1070 GGTGAAGTCAAGATGGGCTGTGATGATGAAGAGTGGCAGATAGCTGGATCTACCA 1129  
 DB 1021 GGTGAAGTCAAGATGGGCTGTGATGATGAAGAGTGGCAGATAGCTGGATCTACCA 1129  
 QY 1130 GATCTGAAGATCTCACTAGAGACACTCCGAGTTTATATAGACCAAGGCTACCA 1189  
 DB 1081 GATCTGAAGATCTCACTAGAGACACTCCGAGTTTATATAGACCAAGGCTACCA 1189  
 QY 1190 GGTGGCCCACTATGCTGTGGAAGTGTTCCTCCAGTGAAGCCCTCCGCTTGT 1249  
 DB 1141 GGTGGCCCACTATGCTGTGGAAGTGTTCCTCCAGTGAAGCCCTCCGCTTGT 1249  
 QY 1250 CACCTGGGATGAGAGCCAGTGGAGGCTGATTTACCAAGGCTGACCAACTAT 1309  
 DB 1201 CACCTGGGATGAGAGCCAGTGGAGGCTGATTTACCAAGGCTGACCAACTAT 1309  
 QY 1310 ACTCAACTGATATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1369  
 DB 1261 ACTCAACTGATATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1369  
 QY 1370 GTTCCAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1429  
 DB 1321 GTTCCAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1429  
 QY 1430 GAACCAAGATGGAATTAAGATCTGGGAGCCAGTCAATGGTGAAGGCTTGGAT 1489  
 DB 1381 GAACCAAGATGGAATTAAGATCTGGGAGCCAGTCAATGGTGAAGGCTTGGAT 1489  
 QY 1490 CGAGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1549  
 DB 1441 CGAGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1549  
 QY 1550 GAAACCACTGCTCTGCTCTCCAGTGAAGACTTGGATGGCAGCCTACAGGAGGCTG 1609  
 DB 1501 GAAACCACTGCTCTGCTCTCCAGTGAAGACTTGGATGGCAGCCTACAGGAGGCTG 1609  
 QY 1610 GTCCAGCTGGAGTATGGTGTGAGTCTATAGACATCCCTCTGCAATGAATTAAC 1669  
 DB 1561 GTCCAGCTGGAGTATGGTGTGAGTCTATAGACATCCCTCTGCAATGAATTAAC 1669  
 QY 1670 ACTTGCTGTG 1680  
 DB 1621 ACTTGCTGTG 1631

RESULT 12  
 US-10-196-747-279  
 ; Sequence 279, Application US/10196747  
 ; Publication No. US20030162250A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zhenlin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3430R1C346  
 ; CURRENT APPLICATION NUMBER: US/10/196,747  
 ; PRIOR APPLICATION REMOVED - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 612  
 ; SEQ ID NO 279  
 ; LENGTH: 1636  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-196-747-279  
 Query Match 96.28; Score 1617; DB 12; Length 1636;  
 Best Local Similarity 99.88; Pred. No. 0;  
 Matches 1628; Conservative 1; Mismatches 1; Indels 1; Gaps 1;  
 QY 51 GGGAGGCGGCGGAGGAGCTCAGGTCGCGGAGTGGATCTGCACTTGGCTGCT 110  
 DB 1 GAGGAGCGGCGGAGGAGCTCAGGTCGCGGAGTGGATCTGCACTTGGCTGCT 60  
 QY 111 GACACCTGGGAGAGTGGCGCGGCGGAGTGGATCTGCACTTGGCTGCTGCGAGC 170  
 DB 61 GACACCTGGGAGAGTGGCGCGGCGGAGTGGATCTGCACTTGGCTGCTGCGAGC 120  
 QY 171 CACCTGATCAAGACCACTCAGTCCACTGATGATGATGATGATGATGATGATGATGAT 230  
 DB 121 CACCTGATCAAGACCACTCAGTCCACTGATGATGATGATGATGATGATGATGATGAT 180  
 QY 231 CAAAGAAAGCTGACAGAGGAGTGAAGGACCAAGGACCAAGGACCAAGGACCAAGGAC 290  
 DB 181 CAAAGAAAGCTGACAGAGGAGTGAAGGACCAAGGACCAAGGACCAAGGACCAAGGAC 240  
 QY 291 GCCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 349  
 DB 241 GCCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
 QY 350 GGTGAACACCTGCTGTAAGCAATCATCTGCTGAAGGATCATCAAGCTAATCTTCCA 409  
 DB 301 GGTGAACACCTGCTGTAAGCAATCATCTGCTGAAGGATCATCAAGCTAATCTTCCA 360  
 QY 410 GGTGAAGTGAAGGCTGCGCAATGACAGAGGCTCTGTAAGATTCCTGCGAT 469  
 DB 361 GGTGAAGTGAAGGCTGCGCAATGACAGAGGCTCTGTAAGATTCCTGCGAT 420  
 QY 470 GGTGGTGAATTAACAGCGCCCTGCTGTAAGGATGATGATGATGATGATGATGATGAT 529  
 DB 421 GGTGGTGAATTAACAGCGCCCTGCTGTAAGGATGATGATGATGATGATGATGATGAT 480  
 QY 530 GGGCCAAAGCCATCCGATGGAACACAGCAAGTGAAGTGGCCCAAGGCTGCTGAG 589  
 DB 481 GGGCCAAAGCCATCCGATGGAACACAGCAAGTGAAGTGGCCCAAGGCTGCTGAG 540  
 QY 590 TGAAGTGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 649  
 DB 541 TGAAGTGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600

OY	650	GGTAAAGCCTTACCTAAGAGGATGAAGCACTCTAGTGCATACCTGGCCAAATCAAGT	709
Db	601	GGTAAAGCCTTACCTAAGAGGATGAAGCACTCTAGTGCATACCTGGCCAAATCAAGT	660
OY	710	GAATAACCACTGTGTCCCGTATGATGAGGCTTCCTTCAATGGCATGTATGACACTCCT	769
Db	661	GAATAACCACTGTGTCCCGTATGATGAGGCTTCCTTCAATGGCATGTATGACACTCCT	720
OY	770	GCACCTGTGAAGGTGGCCAAATTCGCCACATTTGACCGTCGTGGAGTTTACCTTCGTGA	829
Db	721	GCACCTGTGAAGGTGGCCAAATTCGCCACATTTGACCGTCGTGGAGTTTACCTTCGTGA	780
OY	830	TCCTGCCATCAAGGGGTGACACCAATTCAGCTCTACCTGGGGGCCAAAGTTGTTGACTACA	889
Db	781	TCCTGCCATCAAGGGGTGACACCAATTCAGCTCTACCTGGGGGCCAAAGTTGTTGACTACA	840
OY	890	GGGAAAGGTACCAAGTGTCTCAATTAATCTCGACGCTTCCTCTGCATATGCCCAACCCGTGA	949
Db	841	GGGAAAGGTACCAAGTGTCTCAATTAATCTCGACGCTTCCTCTGCATATGCCCAACCCGTGA	900
OY	950	CAACATCCCGTTACAGCCTCATCTGAGTCTGAGATCGAGAGTGTTGAAACCTCAGTGGCTGTGT	1009
Db	901	CAACATCCCGTTACAGCCTCATCTGAGTCTGAGAGTGTTGAAACCTCAGTGGCTGTGT	960
OY	1010	GCTCTCTCCAGAGAAATTCATGTCTGTGTTGGACTCTGTGCTTCTGAGAGTGGCCATCG	1069
Db	961	GCTCTCTCCAGAAATTCATGTCTGTGTTGGACTCTGTGCTTCTGAGAGTGGCCATCG	1020
OY	1070	GCTGAAGTCAGACATCGGGGCTGATCAATGAAAGAGGTCGACATTAAGCGGGATCTACCCA	1129
Db	1021	GCTGAAGTCAGACATCGGGGCTGATCAATGAAAGAGGTCGACATTAAGCGGGATCTACCCA	1080
OY	1130	GATCGTGAAGATCCTTAACCTACGAGCACTCCGAGTTTATTAAGACCAAGGCCATGACCAA	1189
Db	1081	GATCGTGAAGATCCTTAACCTACGAGCACTCCGAGTTTATTAAGACCAAGGCCATGACCAA	1140
OY	1190	GGTGGCCCACTGATGCTGCTGAGAGTGTTCCTCCAGTGAACCCCTGGCCCTTGTGT	1249
Db	1141	GGTGGCCCACTGATGCTGCTGAGAGTGTTCCTCCAGTGAACCCCTGGCCCTTGTGT	1200
OY	1250	CACCCCTGGGCACTGAAAGCCAGCTGGGAAGCTCAGTTTATACCAACAAAGGTGACCAACTTAT	1309
Db	1201	CACCCCTGGGCACTGAAAGCCAGCTGGGAAGCTCAGTTTATACCAACAAAGGTGACCAACTTAT	1260
OY	1310	ACTCAACTGTGAATTAACATCAGCTCTGATCGGATCCAGTGAATGAACCTTGGGATTTGGCTG	1369
Db	1261	ACTCAACTGTGAATTAACATCAGCTCTGATCGGATCCAGTGAATGAACCTTGGGATTTGGCTG	1320
OY	1370	GTTCCAAACCTATGTTGTGAAGAAACATATCATAGTAGATGCATATCCACTCATCTGCTGCTCC	1429
Db	1321	GTTCCAAACCTATGTTGTGAAGAAACATATCATAGTAGATGCATATCCACTCATCTGCTGCTCC	1380
OY	1430	GAACCAAGATGGCAAAATTAAGATCGGGGCTCCCAAGTGTCAATTTGTGAAGGCTTTGGGATT	1489
Db	1381	GAACCAAGATGGCAAAATTAAGATCGGGGCTCCCAAGTGTCAATTTGTGAAGGCTTTGGGATT	1440
OY	1480	CGAGGCACTAGTCTCATCTGACCAAGCAAGATGCCCTTGTGCTTACTCCAGGCTCCTTGTG	1549
Db	1441	CGAGGCACTAGTCTCATCTGACCAAGCAAGATGCCCTTGTGCTTACTCCAGGCTCCTTGTG	1500
OY	1550	GAAGCAACAGCTCTCTGTCTGCCAGTGAAGACTTGGATGGAGAGCATCAGGAAAGGCTGG	1609
Db	1501	GAAGCAACAGCTCTCTGTCTGCCAGTGAAGACTTGGATGGAGAGCATCAGGAAAGGCTGG	1560
OY	1610	GTCCAGCTGGAGATGAGGTGTGAGCTCTATAGACATCCCTCTCTGCAATCAATAAAC	1669
Db	1561	GTCCAGCTGGAGATGAGGTGTGAGCTCTATAGACATCCCTCTCTGCAATCAATAAAC	1620
OY	1670	ACTTGCCTGTG 1680	
Db	1621	ACTTGCCTGTG 1631	

Db 241 GCGCTCTAGTCCATGCGGGAAGCCAGCGGAGCATCCCTGTGGCACCT 300  
QY 350 GGTGAACACCGCTCTGAAGACATCATCTGCTGAAGGTCAATCAGCTACATCTTCA 409  
Db 301 GGTGAACACCGCTCTGAAGACATCATCTGCTGAAGGTCAATCAGCTACATCTTCA 360  
QY 410 GCTGACAGTGAAGCCCTGGCCAAATGACAGAGAGCTCTAGTAAAGTCCCTGACAT 469  
Db 361 GCTGACAGTGAAGCCCTGGCCAAATGACAGAGAGCTCTAGTAAAGTCCCTGACAT 420  
QY 470 GGTGGCTGAATTAACACGCCCCCTGGTCAAGACCATGTGAGAGTCCACATGACACTGA 529  
Db 421 GGTGGCTGAATTAACACGCCCCCTGGTCAAGACCATGTGAGAGTCCACATGACACTGA 480  
QY 530 GGGCCCAAGCCACCATCCGATGACACACAGTGAAGTGGCCCCACCCGCTGGTCTCAG 589  
Db 481 GGGCCCAAGCCACCATCCGATGACACACAGTGAAGTGGCCCCACCCGCTGGTCTCAG 540  
QY 590 TGACTGTGCACACAGCCATGGAGCCCTGGCATCAACTGCTGCATTAAGCTCTCTCTCT 649  
Db 541 TGACTGTGCACACAGCCATGGAGCCCTGGCATCAACTGCTGCATTAAGCTCTCTCTCT 600  
QY 650 GGTGAACGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 709  
Db 601 GGTGAACGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 660  
QY 710 GAAAAACACAGCTGTGCTCCGTGATGAGGCTCCCTCAATGGCATGTATGACAGCTCT 769  
Db 661 GAAAAACACAGCTGTGCTCCGTGATGAGGCTCCCTCAATGGCATGTATGACAGCTCT 720  
QY 770 GCAAGCTGTGAAGTGGCCATTTCCCTGACAGATTAAGCTGTGAGTTGACCTTCTGTA 829  
Db 721 GCAAGCTGTGAAGTGGCCATTTCCCTGACAGATTAAGCTGTGAGTTGACCTTCTGTA 780  
QY 830 TCCGTCATGAAGGTGACACATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 889  
Db 781 TCCGTCATGAAGGTGACACATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 840  
QY 890 GGGAAAGGTGACCAAGTGTTCATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 949  
Db 841 GGGAAAGGTGACCAAGTGTTCATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 900  
QY 950 CAACATCCGCTTGAAGCTCATCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1009  
Db 901 CAACATCCGCTTGAAGCTCATCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 960  
QY 1010 GCTCTCTCCAGAGAAATTCATGCTGCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 1069  
Db 961 GCTCTCTCCAGAGAAATTCATGCTGCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
QY 1070 GCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1129  
Db 1021 GCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1080  
QY 1130 GATGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1189  
Db 1081 GATGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1140  
QY 1190 GGTGGCCCAACTGATGTGCTGAAGTGTTCCTCCAGTGAAGCCCTCGCCCTTGTGT 1249  
Db 1141 GGTGGCCCAACTGATGTGCTGAAGTGTTCCTCCAGTGAAGCCCTCGCCCTTGTGT 1200  
QY 1250 CACCTTGGGATGGAAGCCAGCTGGAAGTCAAGTTTAAACCAAGGTGAAGCAACTAT 1309  
Db 1201 CACCTTGGGATGGAAGCCAGCTGGAAGTCAAGTTTAAACCAAGGTGAAGCAACTAT 1260  
QY 1310 ACTCAACTGAATTAACATCACTGCTGATGATGATGATGATGATGATGATGATGATGATG 1369  
Db 1261 ACTCAACTGAATTAACATCACTGCTGATGATGATGATGATGATGATGATGATGATGATG 1320  
QY 1370 GTTCCAACTGATGTTTGAAGAAATCATCATCTGAGATCATCTCCATCTCTGCTGCC 1429

Db 1321 GTTCCAACTGATGTTTGAAGAAATCATCATCTGAGATCATCTCCATCTCTGCTGCC 1380  
QY 1430 GAACCCAGATGGCAAAATTAAGATCTGGGTCCAGTCAATGCTGAAGCCCTGGAT 1489  
Db 1381 GAACCCAGATGGCAAAATTAAGATCTGGGTCCAGTCAATGCTGAAGCCCTGGAT 1440  
QY 1490 CGAGGAGCTGAGTCTCTACTGACCAAGATGACCTTGTCTTACTCAGCTCTCTGTG 1549  
Db 1441 CGAGGAGCTGAGTCTCTACTGACCAAGATGACCTTGTCTTACTCAGCTCTCTGTG 1500  
QY 1550 GAAACCCAGCTCTCTCTCTCTCCAGTGAAGCTTGAAGTGAAGTGAAGTGAAGTGAAG 1609  
Db 1501 GAAACCCAGCTCTCTCTCTCTCCAGTGAAGCTTGAAGTGAAGTGAAGTGAAGTGAAG 1560  
QY 1610 GTCCAGCTGGAGTATGGGTGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1669  
Db 1561 GTCCAGCTGGAGTATGGGTGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1620  
QY 1670 ACTTGCCTGTG 1680  
Db 1621 ACTTGCCTGTG 1631

## RESULT 14

US-10-017-253A-127  
Sequence 127, Application US/10017253A  
Publication No. US20030166055A1

GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830P162  
CURRENT APPLICATION NUMBER: US/10/017, 253A  
CURRENT FILING DATE: 2001-12-13

PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098803  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098821  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098843  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/099536  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099596  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099598  
PRIOR FILING DATE: 1998-09-09  
Remainder Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 477  
SEQ ID NO 127  
LENGTH: 1636  
TYPE: DNA  
ORGANISM: Homo sapiens

US-10-017-253A-127

Query Match 96.2%; Score 1617; DB 12; Length 1636;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1628; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

```
QY 51 GGGAGCGGGCGAGGATCCAGCGCTGGCCAGCTGGCATCTGCACTTGTGCTCT 110
DB 1 GGGAGCGGGCGAGGATCCAGCGCTGGCCAGCTGGCATCTGCACTTGTGCTCT 60
QY 111 GACACCTGGGAAAGATGGCGCGCGGCGGACCTTACCCCTCTGCTGGTGGTGGCAGC 170
DB 61 GACACCTGGGAAAGATGGCGCGCGGCGGACCTTACCCCTCTGCTGGTGGTGGCAGC 120
QY 171 CACCTTGATCAAGCCACCTCAGTCCACCTGCACTGATCTCATCTTGGCCAAAGTCTAT 230
DB 121 CACCTTGATCAAGCCACCTCAGTCCACCTGCACTGATCTCATCTTGGCCAAAGTCTAT 180
QY 231 CAAAGAAAAGCTGACACAGGAGCTGAAGGACCAACAGCCACAGCATCTGCGACGAGCT 290
DB 181 CAAAGAAAAGCTGACACAGGAGCTGAAGGACCAACAGCCACAGCATCTGCGACGAGCT 240
QY 291 GCGCGCTGCAAGGCGATGGGAAAAGCGCGGAGG-ATCCCTGCTGGGCGAGCT 349
DB 241 GCGCGCTGCAAGGCGATGGGAAAAGCGCGGAGGCGATCCCTGCTGGGCGAGCT 300
QY 350 GGTGAACACCGCTCTGAGACACATCATCTGCTGAAGGTCAATCAGTAACTCCCTCA 409
DB 301 GGTGAACACCGCTCTGAGACACATCATCTGCTGAAGGTCAATCAGTAACTCCCTCA 360
QY 410 GCTGCAAGTGAAGCCCTCGGCCATATACAGAGCTGCTAAGTCAAGATCCCTGAGCAT 469
DB 361 GCTGCAAGTGAAGCCCTCGGCCATATACAGAGCTGCTAAGTCAAGATCCCTGAGCAT 420
QY 470 GGTGCTGATTCACACAGCCCTGCTGCAAGACCATCTGAGATGCAATGACGAGCTG 529
DB 421 GGTGCTGATTCACACAGCCCTGCTGCAAGACCATCTGAGATGCAATGACGAGCTG 480
QY 530 GGGCCACAGCCACCATCCGATGACACAGTGCAGTGGCCGCCCGCTGCTCTCAG 589
DB 481 GGGCCACAGCCACCATCCGATGACACAGTGCAGTGGCCGCCCGCTGCTCTCAG 540
QY 590 TGACTGTGCGACACAGCATGGAGCTGGGACATCCCACTGCTCAATAGCTCTCTCTCT 649
DB 541 TGACTGTGCGACACAGCATGGAGCTGGGACATCCCACTGCTCAATAGCTCTCTCTCT 600
QY 650 GGTGAACGCTTGTAGTACAGGATCATGAACCTCTAGTGGCATCTGCTGCGCAATCTAGT 709
DB 601 GGTGAACGCTTGTAGTACAGGATCATGAACCTCTAGTGGCATCTGCTGCGCAATCTAGT 660
QY 710 GAAAAACAGCTGTGTCCGTGATGAGAGCTTCTTCAATGGCATGTATGACAGCTCTCT 769
DB 661 GAAAAACAGCTGTGTCCGTGATGAGAGCTTCTTCAATGGCATGTATGACAGCTCTCT 720
QY 770 GAGAGCTGGAAGTGGTCCCTTCCAGCATTTGACCGCTGGAGATTTGACCTTCTCTA 829
DB 721 GAGAGCTGGAAGTGGTCCCTTCCAGCATTTGACCGCTGGAGATTTGACCTTCTCTA 780
QY 830 TCTGTCATCAAGGAGTACACATTCAGTCTTACCTGAGGAGCCAAATTTGTTGAGCTACA 889
DB 781 TCTGTCATCAAGGAGTACACATTCAGTCTTACCTGAGGAGCCAAATTTGTTGAGCTACA 840
QY 890 GGGAAAAGTGAACCAAGTGTTCATTAATCTGTGACAGCTTCCCTGACAAAGCCACCTGGA 949
DB 841 GGGAAAAGTGAACCAAGTGTTCATTAATCTGTGACAGCTTCCCTGACAAAGCCACCTGGA 900
QY 950 CAAACATCCCGTTACAGCTCATGTGAGTACGACGCTGGAGGAAAGCTGCAAGTGGCTCTCT 1009
DB 901 CAAACATCCCGTTACAGCTCATGTGAGTACGACGCTGGAGGAAAGCTGCAAGTGGCTCTCT 960
QY 1010 GCTCTCTCAGAAAGATTCATGCTGTTGAGCTGTGAGCTGTGAGAGTGGCCATCG 1069
DB 961 GCTCTCTCAGAAAGATTCATGCTGTTGAGCTGTGAGCTGTGAGAGTGGCCATCG 1020
```

```
QY 1070 GCTGAAGTCAGACATCGGGCTGATCAATGAAAAAGCTGCAGATTAAGCTGGATCTACCA 1129
DB 1021 GCTGAAGTCAGACATCGGGCTGATCAATGAAAAAGCTGCAGATTAAGCTGGATCTACCA 1080
QY 1130 GATCTGGAAGATCTTACTACAGACACCTCCGAGATTTTATPAGACCAAGCCATGCCAA 1189
DB 1081 GATCTGGAAGATCTTACTACAGACACCTCCGAGATTTTATPAGACCAAGCCATGCCAA 1140
QY 1190 GGTGGCCCAACTGATGTGCTGGAAATGTTTCCCTCCAGTGAAGCCCTCGCCCTTGT 1249
DB 1141 GGTGGCCCAACTGATGTGCTGGAAATGTTTCCCTCCAGTGAAGCCCTCGCCCTTGT 1200
QY 1250 CACCCCTGGCATGGAAGCCAGCTCGGAACCTGATTTTACACCAAGTGAACACTTAT 1309
DB 1201 CACCCCTGGCATGGAAGCCAGCTCGGAACCTGATTTTACACCAAGTGAACACTTAT 1260
QY 1310 ACTCAACTTGAATACATACAGCTCTGATCGATGACAGCTGATGAACTCTGGAGTTGGCTG 1369
DB 1261 ACTCAACTTGAATACATACAGCTCTGATCGATGACAGCTGATGAACTCTGGAGTTGGCTG 1320
QY 1370 GTTCCAACTGATGTGTTCTGAAAAACATCACTGATGATCATCCATCCTGCTGCTG 1429
DB 1321 GTTCCAACTGATGTGTTCTGAAAAACATCACTGATGATCATCCATCCTGCTGCTG 1380
QY 1430 GAACCAAGATGGCAATTAAGATCTGGGGTCCAGTGTGATGTTGGTGAAGGCTTGGGAT 1489
DB 1381 GAACCAAGATGGCAATTAAGATCTGGGGTCCAGTGTGATGTTGGTGAAGGCTTGGGAT 1440
QY 1490 CGAGGAGCTGAGTCTCTACTGACCAAGAGTCCCTTGTGCTTACTTCCAGCTCTTGTG 1549
DB 1441 CGAGGAGCTGAGTCTCTACTGACCAAGAGTCCCTTGTGCTTACTTCCAGCTCTTGTG 1500
QY 1550 GAAACCCAGCTCTCTGCTCTCCAGTGAAGACTTGGATGGAGCCATCCAGGGAAGGCTG 1609
DB 1501 GAAACCCAGCTCTCTGCTCTCCAGTGAAGACTTGGATGGAGCCATCCAGGGAAGGCTG 1560
QY 1610 GTCCAGCTGGGAGTATGGGTGATGAGCTCTATAGACATCCCTCTGCAATCAATTAAC 1669
DB 1561 GTCCAGCTGGGAGTATGGGTGATGAGCTCTATAGACATCCCTCTGCAATCAATTAAC 1620
QY 1670 ACTTGGCTGTG 1680
DB 1621 ACTTGGCTGTG 1631
```

RESULT 15  
US-10-173-689-279  
Sequence 279, Application US/10173689  
Publication No. US2003016104A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3430R1C10  
CURRENT APPLICATION NUMBER: US/10/173,689  
Prior Application removed - See file wrapper or Palm  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 279  
LENGTH: 1636  
TYPE: DNA  
ORGANISM: Homo Sapient



US-10-173-689-279

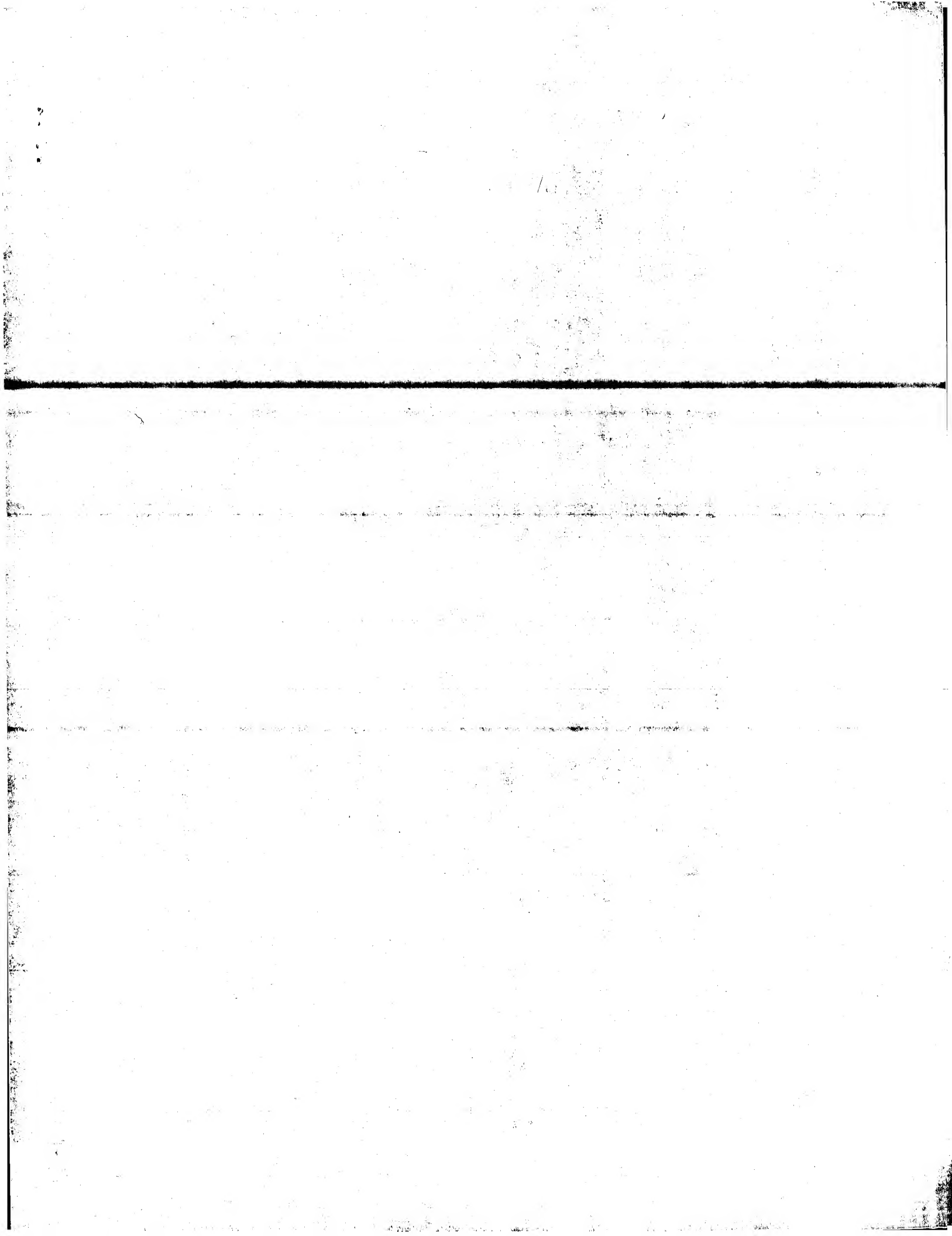
Query Match 96.28; Score 1617; DB 12; Length 1636;  
Best Local Similarity 99.88; Pred. No. 0;  
Matches 1628; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 51 GGGAGCGGGCCGAGAGCTCCAGGCTGCGCCAGGCTCTGGCATCCGCACTTGTGCTGCGAGC 170  
DB 1 GAGGAGCGGGCCGAGAGCTCCAGGCTGCGCCAGGCTCTGGCATCCGCACTTGTGCTGCGAGC 170  
QY 111 GACACCTGGGAGAGTGGCGGGCCGCTGGACCTTCCACCTTCTGTGTGTTGGTGGAGC 170  
DB 61 GACACCTGGGAGAGTGGCGGGCCGCTGGACCTTCCACCTTCTGTGTGTTGGTGGAGC 170  
QY 171 CACCTTGATCCAAAGCCACCTCAGTCCAGTTCATCTCTCTGCGCCAAAGTAT 230  
DB 121 CACCTTGATCCAAAGCCACCTCAGTTCATCTCTCTGCGCCAAAGTAT 230  
QY 231 CAAAGAAAGCTGACACAGAGCTGAAAGACACACACGCAACGCAATCTCTGACAGCT 290  
DB 181 CAAAGAAAGCTGACACAGAGCTGAAAGACACACACGCAACGCAATCTCTGACAGCT 290  
QY 291 GCGGCTGCTAGTGCCTAGTGGGAAAGCCAGCGAGG - ATCCCTGTGGTGGGAGCT 349  
DB 241 GCGGCTGCTAGTGCCTAGTGGGAAAGCCAGCGAGGCTCTGCTGGGAGAGCT 300  
QY 350 GGTGAACACCGCTCGAAGCATCATCTGCTGAAGGTATCATACAGCTAATCATCTCA 409  
DB 301 GGTGAACACCGCTCGAAGCATCATCTGCTGAAGGTATCATACAGCTAATCATCTCA 360  
QY 410 GGTGACAGTGAAGCCCTCGGCAATGACAGAGCTGCTAGTCAAGTATCCCTGAGCAT 469  
DB 361 GGTGACAGTGAAGCCCTCGGCAATGACAGAGCTGCTAGTCAAGTATCCCTGAGCAT 420  
QY 470 GGTGCTGATGATTAACAGCCCTGCTCAAGACCATGCTGAGTTCACATGACAGCTGA 529  
DB 421 GGTGCTGATGATTAACAGCCCTGCTCAAGACCATGCTGAGTTCACATGACAGCTGA 480  
QY 530 GGGCCAAAGCCACATCCGATGACACACAGTGAAGTGGCCCAACCCGCTGTCTCAG 589  
DB 481 GGGCCAAAGCCACATCCGATGACACACAGTGAAGTGGCCCAACCCGCTGTCTCAG 540  
QY 590 TGAAGTGGCCACAGCCATGGGAGCTGGCCATCAACTGCTGATTAAGCTCTCTCTCT 649  
DB 541 TGAAGTGGCCACAGCCATGGGAGCTGGCCATCAACTGCTGATTAAGCTCTCTCTCT 600  
QY 650 GGTGAAGCCTTAGCTAAGAGCTCATGAACCTCTAGTGGCAATCCCTGGCCAAATTAAT 709  
DB 601 GGTGAAGCCTTAGCTAAGAGCTCATGAACCTCTAGTGGCAATCCCTGGCCAAATTAAT 660  
QY 710 GAAAAACAGCTGTGCTCCGTGATGAGGCTTCTCTCAATGCAATGATGACAGCTCT 769  
DB 661 GAAAAACAGCTGTGCTCCGTGATGAGGCTTCTCTCAATGCAATGATGACAGCTCT 720  
QY 770 GCAAGCTGTAAGGTGGCCATTTCCCTGACATGACCTGCTGGAAGTTGACCTTCTGTA 829  
DB 721 GCAAGCTGTAAGGTGGCCATTTCCCTGACATGACCTGCTGGAAGTTGACCTTCTGTA 780  
QY 830 TCCGTCATGAAGGCTGACACATTAAGCTCTAAGCTGGGGCCAAAGTTGTTGACTGACA 889  
DB 781 TCCGTCATGAAGGCTGACACATTAAGCTCTAAGCTGGGGCCAAAGTTGTTGACTGACA 840  
QY 890 GGGAAAGGTGACCAAGTGTTCATTAATCTGACAGCTTCCCTGACAAATGGCCACCTGGA 949  
DB 841 GGGAAAGGTGACCAAGTGTTCATTAATCTGACAGCTTCCCTGACAAATGGCCACCTGGA 900  
QY 950 CAACATCCCTGTCAGCTCATCGTGAATCAAGAGCTGTGAAGCTGACAGTGGCTGCTGT 1009  
DB 901 CAACATCCCTGTCAGCTCATCGTGAATCAAGAGCTGTGAAGCTGACAGTGGCTGCTGT 960  
QY 1010 GCTCTCTCAGAAAGATTAATGATGCTGCTGGAAGCTGCTGCTGCTGAGAGTGGCCATCG 1069  
DB 961 GCTCTCTCAGAAAGATTAATGATGCTGCTGGAAGCTGCTGCTGCTGAGAGTGGCCATCG 1020

QY 1070 GCTGAAGTCAAGCATCGGGCTGATCAATGAAGGCTGACAGATTAAGCTGGGATCTACCA 1129  
DB 1021 GCTGAAGTCAAGCATCGGGCTGATCAATGAAGGCTGACAGATTAAGCTGGGATCTACCA 1080  
QY 1130 GATCGTAAGATCTTAAGTCAAGGACACTCCGAGATTTTTATTAAGCAAGGCCATGCAAA 1189  
DB 1081 GATCGTAAGATCTTAAGTCAAGGACACTCCGAGATTTTTATTAAGCAAGGCCATGCAAA 1140  
QY 1190 GGTGGCCCAAGTATGCTGCTGGAAGTGTTCCTCCAGTGAAGCCCTCGGCTTGTGT 1249  
DB 1141 GGTGGCCCAAGTATGCTGCTGGAAGTGTTCCTCCAGTGAAGCCCTCGGCTTGTGT 1200  
QY 1250 CACCTGGGATCGAAGCCAGCTGGAAGCTCAAGTATTAACCAAGGTGACCAACTTAT 1309  
DB 1201 CACCTGGGATCGAAGCCAGCTGGAAGCTCAAGTATTAACCAAGGTGACCAACTTAT 1260  
QY 1310 ACTCAACTTGAATTAACATCAAGCTGATCGGATCCAGCTGATGAAGTGGGATGCTG 1369  
DB 1261 ACTCAACTTGAATTAACATCAAGCTGATCGGATCCAGCTGATGAAGTGGGATGCTG 1320  
QY 1370 GTTCAACCTGATGTCTGAAAAACATCATCACTGAGTCAATCCATCCGCTGCC 1429  
DB 1321 GTTCAACCTGATGTCTGAAAAACATCATCACTGAGATCAATCCATCCATCTGCTGCC 1380  
QY 1430 GAACCAAGATGCAAAATTAAGATCTGGGGTCCCAAGTGTATTTGTAAGGCTTGGGAT 1489  
DB 1381 GAACCAAGATGCAAAATTAAGATCTGGGGTCCCAAGTGTATTTGTAAGGCTTGGGAT 1440  
QY 1490 CGAGGCAAGTGAATCTCACTGACCAAGAGATGCCCTTGTGTTACTCCAGCTCTTGTG 1549  
DB 1441 CGAGGCAAGTGAATCTCACTGACCAAGAGATGCCCTTGTGTTACTCCAGCTCTTGTG 1500  
QY 1550 GAAACCAAGCTCTCTGCTCCAGTGAAGACTTGATGGAGCATCAGGGAAGGCTGG 1609  
DB 1501 GAAACCAAGCTCTCTGCTCCAGTGAAGACTTGATGGAGCATCAGGGAAGGCTGG 1560  
QY 1610 GTCCAGCTGGGATGAGTGGTGAAGCTCTAATAGACATCCCTCTGCAATCAATTAAC 1669  
DB 1561 GTCCAGCTGGGATGAGTGGTGAAGCTCTAATAGACATCCCTCTGCAATCAATTAAC 1620  
QY 1670 ACTTGCCTGTG 1680  
DB 1621 ACTTGCCTGTG 1631

Search completed: October 10, 2003, 05:45:28  
Job time : 483.34 secs







Db 122 TGATTCAGGACCGCTTCAGTCCACATGCACTTCATCTCGGCCCCAAAAGTCATCAAG 181  
QY 236 AAAAGCTGACACAGAGCTGAAGAGACCAACGCGCACAGCATCTCAGAGCTGCGC 295  
Db 182 AAAAGCTGACACAGAGCTGAAGAGACCAACGCGCACAGCATCTCAGAGCTGCGC 241  
QY 296 TGCTCAGTGCATGCGGGAAAAGCCAGCGGAGAGTCCGTGTGGGACGCTGTGAA 355  
Db 242 TGCTCAGTGCATGCGGGAAAAGCCAGCGGAGAGTCCGTGTGGGACGCTGTGAA 301  
QY 356 CACCGTCCTGAGCAGCATCTGGCTGAAGGTTCATACAGTAACTCCCTCCAGCTGCA 415  
Db 302 CACCGTCCTGAGCAGCATCTGGCTGAAGGTTCATACAGTAACTCCCTCCAGCTGCA 361  
QY 416 GTGAAGCCCTCGGCAATGACAGAGAGCTGCTAGTCAAGATCCCTCGGACATGTGCG 475  
Db 362 GTGAAGCCCTCGGCAATGACAGAGAGCTGCTAGTCAAGATCCCTCGGACATGTGCG 421  
QY 476 TGATTCACAGCGCTCGTGTCAAGACATCTGAGGTTCACATGACGACTGAGGCCA 535  
Db 422 TGATTCACAGCGCTCGTGTCAAGACATCTGAGGTTCACATGACGACTGAGGCCA 481  
QY 536 AGCCACCATCCGATGACACAGTGCATGAGTGGCCCGCGCTGGTCTCAGTGAAGT 595  
Db 482 AGCCACCATCCGATGACACAGTGCATGAGTGGCCCGCGCTGGTCTCAGTGAAGT 541  
QY 596 TGCCACCAAGCATGAGGAGCTCGCATTCACATCTGTCATAGCTCTCTCTGTGTGA 655  
Db 542 TGCCACCAAGCATGAGGAGCTCGCATTCACATCTGTCATAGCTCTCTCTGTGTGA 601  
QY 656 CGCCTAGCTAAGCAGGTATGAACTCCAGTGCATCCCTGCCA 702  
Db 602 CGCCTAGCTAAGCAGGTATGAACTCCAGTGCATCCCTGCCA 648

RESULT 2  
US-09-461-325-15  
; Sequence 15, Application US/09461325A  
; Patent No. 6475753  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 94 Human Secreted Proteins  
; FILE REFERENCE: P2029P1  
; CURRENT APPLICATION NUMBER: US/09/461,325A  
; EARLIER APPLICATION NUMBER: PCT/US99/13418  
; EARLIER FILING DATE: 1999-06-15  
; EARLIER APPLICATION NUMBER: 60/089,507  
; EARLIER FILING DATE: 1998-06-16  
; EARLIER APPLICATION NUMBER: 60/089,508  
; EARLIER FILING DATE: 1998-06-16  
; EARLIER APPLICATION NUMBER: 60/089,509  
; EARLIER FILING DATE: 1998-06-16  
; EARLIER APPLICATION NUMBER: 60/089,510  
; EARLIER FILING DATE: 1998-06-16  
; EARLIER APPLICATION NUMBER: 60/090,112  
; EARLIER FILING DATE: 1998-06-22  
; EARLIER APPLICATION NUMBER: 60/090,113  
; EARLIER FILING DATE: 1998-06-22  
; NUMBER OF SEQ ID NOS: 532  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 1175  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-461-325-15

Query Match 37.8%; Score 634.8; DB 4; Length 1175;  
Best Local Similarity 99.5%; Pred. No. 4,2e-162;  
Matches 647; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 54 GAGCGGCGGAGAGTCCAGCTGCGCAGGTCTGCGATCTCAGTGTGCTGCTGTGAC 113  
|||||

Db 1 GAGCGGCGGAGAGTCCAGCTGCGCAGGTCTGCGATCTCAGTGTGCTGCTGTGAC 60  
QY 114 ACCTGGGAATATGGCCGCGCCGTGGACCTTCACCTCTCTGTGTGTGCTGGACGAC 173  
Db 61 ACCTGGGAATATGGCCGCGCCGTGGACCTTCACCTCTCTGTGTGTGCTGGACGAC 120  
QY 174 CTGTATCCAGGACACCTCAGTCCAGTGTGATCTGATCTGCGGCCAAAGTCATCA 233  
Db 121 CTGTATCCAGGACACCTCAGTCCAGTGTGATCTGATCTGCGGCCAAAGTCATCA 180  
QY 234 AGAAAGCTGACACAGAGAGCTGAAGGACCAACAGCCACAGCATCTCGACAGCTGCC 293  
Db 181 AGAAAGCTGACACAGAGAGCTGAAGGACCAACAGCCACAGCATCTCGACAGCTGCC 240  
QY 294 GCTGCTCAGTGCATGCGGGAAGAAAGCCAGCCGAGG-ATCCCTGTGTGTGGCAGCTG 352  
Db 241 GCTGCTCAGTGCATGCGGGAAGAAAGCCAGCCGAGGATCCCTGTGTGTGGCAGCTG 300  
QY 353 GAACACCGTCTGAGACATCATCTGGCTGAAGGTTCATGACAGTAACTCCCTCCAGT 412  
Db 301 GAACACCGTCTGAGACATCATCTGGCTGAAGGTTCATGACAGTAACTCCCTCCAGT 360  
QY 413 GCAAGTGAAGCCCTCGGACCATGACAGAGAGCTGTGATCAAGATCCCTGGACATGT 472  
Db 361 GCAAGTGAAGCCCTCGGACCATGACAGAGAGCTGTGATCAAGATCCCTGGACATGT 420  
QY 473 GGTGATTCACAGCGCCCTGTGTCAAGACATCTGAGGTTCACATGACGACTGAGGC 532  
Db 421 GGTGATTCACAGCGCCCTGTGTCAAGACATCTGAGGTTCACATGACGACTGAGGC 480  
QY 533 CCAAGCCACCATCCGATGACACAGTGCATGAGTGGCCCGCGCTGGTCTCAGTGA 592  
Db 481 CCAAGCCACCATCCGATGACACAGTGCATGAGTGGCCCGCGCTGGTCTCAGTGA 540  
QY 593 CTGTGCGCACGACCATGAGGAGCTCGCATTCACATCTGTCATAGCTCTCTCTGTGT 652  
Db 541 CTGTGCGCACGACCATGAGGAGCTCGCATTCACATCTGTCATAGCTCTCTCTGTGT 600  
QY 653 GAACGCTTAGCTAAGCAGGTATGAACTCCAGTGCATCCCTGCCA 702  
Db 601 GAACGCTTAGCTAAGCAGGTATGAACTCCAGTGCATCCCTGCCA 650

RESULT 3  
US-09-702-705-950  
; Sequence 950, Application US/09702705  
; Patent No. 6504010  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Lodes, Michael A.  
; APPLICANT: Fanger, Gary  
; APPLICANT: Vedvick, Tom  
; APPLICANT: Carter, Darrick  
; APPLICANT: Retter, Marc  
; APPLICANT: Mannion, Jane  
; APPLICANT: Fan, Liqun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.478C14  
; CURRENT APPLICATION NUMBER: US/09/702,705  
; NUMBER OF SEQ ID NOS: 1833  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 950  
; LENGTH: 382  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-702-705-950

Query Match 22.7%; Score 382; DB 4; Length 382;  
Best Local Similarity 100.0%; Pred. No. 6.4e-94;  
Matches 382; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Db 531 AAGCTCCAAAGTGAATAGCGCCCTGTCGAGCAAGTCTGTTGAGGCGCTGTGAAGCTG 590  
528 GAGGCCCAAGCCACATCCGCATGAGACACAGTGAAGTGGCCCGCCGCTGGTCTC 587  
Db 591 GACATCACTGACAGAAATCTTACGTGAGAGATTAAGCAGAGAGATCCACCTGGTCTT 650  
588 AGTACTGTGCGCACAGCCATGGAGCGCTGCGATCCACTGCTGATCAACTCT--CTCC 644  
Db 651 GGTACTGACGACCATTCCTCCCTGGAAAGCTCAAAATTTCTGCTGTGATGACTGGCC 710  
645 TTCTGTGTAAGCCCTTACGTAGCAGGTATCAACTCTGATGCTGCTGCTGCTGCTGCT 704  
Db 711 CTCCCAATTCAGAGCTCTTCTGACAGGCTTCACAGGATCTTGAATTAAGTCTGCTGAG 770  
705 CTAGTGAAGAAACAGGCTGTCGCGGTGATGAGAGCTCTTCAATGGCATGTATGAGAC 764  
Db 771 TTGTTTCAAGGCGCAACGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 830  
645 CTCTGCTGCA 772  
Db 831 CTGCTGCA 838

RESULT 6  
US-09-252-991A-5267  
; Sequence 5267, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; NUMBER OF SEQ ID NOS: 33142  
; LENGTH: 1302  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-5267

Query Match 2.6%; Score 43.8; DB 4; Length 1302;  
Best Local Similarity 45.9%; Pred. No. 0.039;  
Matches 150; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

QY 304 GCCATGCGGAAAAAGCCAGCGGAGGANTCCCTGTGCTGGGACGCTGTGATACCGCTCC 363  
Db 534 GCTACAGAGTAAAGATCATGATGAGCGAGCCCGCTGGCGCTCGGCACTCTCGGATACCC 593  
QY 364 TGAAGACATCATCTGTGCTGAGGTATCATCACTTAACATCTCCAGCTGACGTGAGC 423  
Db 594 TGAACAGCAACATCTGTGCTGAGGTATCATCACTTAACATCTCCAGCTGAGGAAA 653  
QY 424 CTTGCGGCAATGACGAGAGCTCTAGTCAAGATCCCTGGACATGAGTGGCTGATCA 483  
Db 654 ACATGCGGAGAGCGAGCGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 713  
QY 484 ACAGCGCCCTGTGCTGACAGACCATGTGAGTTCACATGACAGTGAAGGCCCAAGCA 543  
Db 714 CTTGCTGTGCTGCGCAAGCGGCTGCGCGGAGCAAGGTATGATCCCTGATCAACACCTG 773  
QY 544 TCCGATGAGACACCATGTGAGTGGCCCAAGCGCTGCTGCTGCTGCTGCTGCTGCTG 603  
Db 774 CTTATGTCACCTGTGTCAAGGCGGAGATGATCATCCGATCAAGCCGCAACTGGCGA 833  
QY 604 GGCATGGAGCGCTGGCATCCAACTGC 630  
Db 834 CCATGCGGACCTGTGCGCCACGTTTC 860

RESULT 7  
US-09-252-991A-5207  
; Sequence 5207, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; NUMBER OF SEQ ID NOS: 33142  
; LENGTH: 1401  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-5207

Query Match 2.6%; Score 43.8; DB 4; Length 1401;  
Best Local Similarity 45.9%; Pred. No. 0.041;  
Matches 150; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

QY 304 GCCATGCGGAAAAAGCCAGCGGAGGANTCCCTGTGCTGGGACGCTGTGATACCGCTCC 363  
Db 785 GCTACAGAGTAAAGATCATGATGAGCGAGCCCGCTGGCGCTCGGCACTCTCGGATACCC 844  
QY 364 TGAAGACATCATCTGTGCTGAGGTATCATCACTTAACATCTCCAGCTGACGTGAGC 423  
Db 845 TGAACAGCAACATCTGTGCTGAGGTATCATCACTTAACATCTCCAGCTGAGGAAA 904  
QY 424 CTTGCGGCAATGACGAGAGCTCTAGTCAAGATCCCTGGACATGAGTGGCTGATCA 483  
Db 905 ACATGCGGAGAGCGAGCGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 964  
QY 484 ACAGCGCCCTGTGCTGACAGACCATGTGAGTTCACATGACAGTGAAGGCCCAAGCA 543  
Db 965 CTTGCTGTGCTGCGCAAGCGGCTGCGCGGAGCAAGGTATGATCCCTGATCAACACCTG 1024  
QY 544 TCCGATGAGACACCATGTGAGTGGCCCAAGCGCTGCTGCTGCTGCTGCTGCTGCTG 603  
Db 1025 CTTATGTCACCTGTGTCAAGGCGGAGATGATCATCCGATCAAGCCGCAACTGGCGA 1084  
QY 604 GGCATGGAGCGCTGGCATCCAACTGC 630  
Db 1085 CCATGCGGACCTGTGCGCCACGTTTC 1111

RESULT 8  
US-09-252-991A-5270/c  
; Sequence 5270, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; NUMBER OF SEQ ID NOS: 33142  
; LENGTH: 1458  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa



TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 350..14002  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 14046..20036  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 20110..31284  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 31329..36071  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 36155..41830  
US-08-804-198-1

Query Match 2.5%; Score 41.6; DB 2; Length 44377;  
Best Local Similarity 49.5%; Pred. No. 0.86;  
Matches 107; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 332 CCCTGTCTGGGCACTGGTGAACACCGTCTGAGACATCTGGCTGAAGGTCAAT 391  
DB 43661 CCTCAACACGCGGCGCGCGCGCGGATCAACCGCGAGCAGACGTCGTGTCTGGCGCGCG 43720  
QY 332 CACACATCAACATCTCCAGCTGAGTGAAGCCCTCGGCATGACAGAGACTGTACT 451  
DB 43721 CGGACGGGAGATCCCGGGCGGACCGCTCGGGGGCGCGGACGAGACCGCATCTGGCGCT 43780  
QY 452 CAAGATCCCGCTGACATGTGTGTGATTCACACAGCCCGCTGTCAAGACCATCTGTGA 511  
DB 43781 CGCCCTCCCGGTGATCCGCTGTGGCGGACACCGGGGTCCAGGTCCAGCGCGCGCGCT 43840  
QY 512 GTTCCACATGACGACTGAGGCCCAAGCCACCATCCG 547  
DB 43841 GCCCGGCTGCGGGCGGAGGACCGCCCTGACCCG 43876

## RESULT 11

US-08-937-067-18  
Sequence 18, Application US/08937067  
Patent No. 6433155  
GENERAL INFORMATION:  
APPLICANT: Umanaky, Samuil  
TITLE OF INVENTION: A FAMILY OF GENES ENCODING  
TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND  
TITLE OF INVENTION: METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/937,067  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnhardt, Susan K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 23647-20018.00

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1308 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-937-067-18

Query Match 2.5%; Score 41.2; DB 4; Length 1308;  
Best Local Similarity 44.1%; Pred. No. 0.2;  
Matches 172; Conservative 0; Mismatches 218; Indels 0; Gaps 0;

QY 357 ACCGTCTGAGACATCATCTGGCTGAGATCATACAGTAACTATCTCCAGCTGAG 416  
DB 413 AGCTTCAGTCCGATCGGCGCCGTAACAGAGCGGCGCTTCTACACCAAGCAGCTGAG 472  
QY 417 GTGAAGCCCTGGCCATGACAGAGAGCTGCTAGTCAAGATCCCTGGACATGTGCT 476  
DB 473 TCGGTGAGACATCCCGCGGACCTGCGCTGTCCACAAAGTGGGCTACAAAGATGGTG 532  
QY 477 GATTCACACGCGCCCTGTGTAAGACATCGTGAATTCACATGACGACTGAGGCCCA 536  
DB 533 CTGCCAACCTCTGTGAGAGACGAGACATGGGAGGTGAACACAGGCCAGAGCTGG 592  
QY 537 GCCACATTCGCGATGACACAGTCAAGTGGCCCAACCGGCTGTCTCAGTACTGT 596  
DB 593 GTGCCCTGTCTCAACAGAACTGCCACGCGGCAACCAAGTCTCTGTGCTGCTTTC 652  
QY 597 GCCACAGCATGGAGCGCTGCAATCCACATGCTGCAATGCTCTCTCTCTCTGAGAC 656  
DB 653 GCCCGCTGTGCTGTGAGACCGGCGCATTCACCGTGTGCTGTGAGGCGCTGCGC 712  
QY 657 GCCTTAGCTAAGCAGATCATGAACCTCCTAGTGCATCCCTGCCCAATCTAGTAAAC 716  
DB 713 GACTGTGAGACCGGATGATGCAATTCCTGCGCTCTACTGCGCGGAGATGTTAAGTGT 772  
QY 717 CAGCTGTGCTCCGATGAGGCTTCTTC 746  
DB 773 GACAAGTTCGCCGAGGGGAGCTGTCAATC 802

## RESULT 12

US-09-724-864-31  
Sequence 31, Application US/09724864  
Patent No. 6380362  
GENERAL INFORMATION:  
APPLICANT: Watson, James D  
TITLE OF INVENTION: Polynucleotides, polypeptides expressed  
TITLE OF INVENTION: by the polynucleotides and methods for their use.  
FILE REFERENCE: 11000.1050U1  
CURRENT APPLICATION NUMBER: US/09/724,864  
CURRENT FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678  
PRIOR FILING DATE: 1999-12-23  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 31  
LENGTH: 1093  
TYPE: DNA  
ORGANISM: Mouse  
US-09-724-864-31

Query Match 2.4%; Score 40.8; DB 4; Length 1093;  
Best Local Similarity 45.4%; Pred. No. 0.23;  
Matches 187; Conservative 0; Mismatches 222; Indels 3; Gaps 1;  
QY 361 TCTGAGACATCATCTGTGCTGAAGGTCAACAGCTAATCCTCCAGTGAGTGA 420  
||||| ||||| || || |||



Db 415 TCCTGAACACATCTCTGACATATAATCATCTGATCCGAGCTGCTAGAACTGCTTGG 474  
QY 421 AGCCCTGGGCCAATGACACGAGCTGCTAGTCAAGATCCCCGAGACATGGTGGAT 480  
Db 475 TGCAGAGTCTGTGATGACATCTCTGATGTACACATCCCTGGGCTTGACACTCAAG 534  
QY 481 TCACACGCCCCGCTGCTCAAGACATGATGATGATTCACATGACGATGAGCCCAAGCA 540  
Db 535 TAAATATGCCCCGAGTGTGGAAGCTTTTGGCAATTTGGCTGGAAGCTGAAATTAATG 594  
QY 541 CCATCCGATGACACAGTGCAGTGAAGTGGCCCAACCCGCTGCTCTGACATGCTGCA 600  
Db 595 AACTCTTACCGCGGAAAGACATCAGGGAGGATTAATCTGCTTCTTGATGATGACACC 654  
QY 601 CCAGCCATGGGAGCTGCGCCATCCAACTGCTGATGAAGTCTCTCCCTGGTGAAGCCCT 660  
Db 655 ACTCCCTGCGACGCGAAATATCAGCTGTGCTCAATGAGATGACATCCGTTCAAAAGCTTT 714  
QY 661 TACCTAAGCAGGCTGATGAACTCTCTAGTGCATCCCTGCCCCAATCTAGTAAAAACGAC 720  
Db 715 TAGACAAAC--TCACAGGGATATTGACTAAAGTCTCTCTGAGCTGATCCAGGGCAGG 771  
QY 721 TGTCTCCCGTATGAGGCTTCTCTCAATGAGCATGTATGAGAGACCTCTGCA 772  
Db 772 TATGCTCTGTGCTCAATGGGATTTCTCAGCGGTTTGATGTCACCTGCTGCA 823

RESULT 13  
US-09-252-991A-4460  
; Sequence 4460, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252.991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 4460  
; LENGTH: 381  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-4460

Query Match 2.4%; Score 40.2; DB 4; Length 381;  
Best Local Similarity 46.6%; Pred. No. 0.2;  
Matches 129; Conservative 0; Mismatches 148; Indels 0; Gaps 0;  
QY 583 TCCTCAGTGTGCTGTCACAGCCAGCTGAGAGCTGCGCATCCAACTGCTGATTAAGCTCT 642  
Db 98 TCCGCGGTGAGCCGCTTCCGCAACTGCTGCTCAACGAGGTCTATCCCGGTGG 157  
QY 643 CCTTCTGTGTAAGCGCTTATGCTAAGCAGGTGATGAACCTCTCTAGTGGCATTCCTGCGCA 702  
Db 158 CCTTCTGTGTAAGCGCTTATGCTAAGCAGGTGATGAACCTCTCTAGTGGCATTCCTGCGCA 702  
QY 703 ATCTAGTGAATAACACAGCTGTGCTGCTGATGAGGCTTCTCTCATATGATGATGAGCAG 762  
Db 218 CGCTGATGCTGAGAGCTGCTCACTCACTGCGGATGACGACGCTGACGCGCTGCTGCGTGG 277  
QY 763 ACCTCGTGAAGCTGTAAGTGGCCATTTCCCTCAGACATGACCGCTGAGAGTTGAC 822  
Db 278 AAGGCCACCCCTGTGTAAGATGACGACGATGGGACGCGCGCAGTTGTGCGCC 337  
QY 823 TTCTGTATCTGCTGATCAAGGCTGACACCATTCAGCT 859  
Db 338 TCACCGTGTATCAGCGTGAACCTGGGCGACATCTCTGCT 374

RESULT 14  
US-09-252-991A-4219/c  
; Sequence 4219, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252.991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 4219  
; LENGTH: 1110  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-4219

Query Match 2.4%; Score 40.2; DB 4; Length 1110;  
Best Local Similarity 46.6%; Pred. No. 0.34;  
Matches 129; Conservative 0; Mismatches 148; Indels 0; Gaps 0;  
QY 583 TCCTCAGTGTGCTGTCACAGCCAGCTGAGAGCTGCGCATCCAACTGCTGATTAAGCTCT 642  
Db 1081 TCCGCGGTGAGCCGCTTCCGCAACTGCTGCTCAACGAGGTCTATCCCGGTGG 1022  
QY 643 CCTTCTGTGTAAGCGCTTATGCTAAGCAGGTGATGAACCTCTCTAGTGGCATTCCTGCGCA 702  
Db 1021 CCTTCTGTGTAAGCGCTTATGCTAAGCAGGTGATGAACCTCTCTAGTGGCATTCCTGCGCA 702  
QY 703 ATCTAGTGAATAACACAGCTGTGCTGCTGATGAGGCTTCTCTCATATGATGATGAGCAG 762  
Db 961 CGCTGATGCTGAGAGCTGCTCACTCACTGCGGATGACGACGCTGACGCGCTGCTGCGTGG 902  
QY 763 ACCTCGTGAAGCTGTAAGTGGCCATTTCCCTCAGACATGACCGCTGAGAGTTGAC 822  
Db 901 AAGGCCACCCCTGTGTAAGATGACGACGATGGGACGCGCGCAGTTGTGCGCC 842  
QY 823 TTCTGTATCTGCTGATCAAGGCTGACACCATTCAGCT 859  
Db 841 TCACCGTGTATCAGCGTGAACCTGGGCGACATCTCTGCT 805

RESULT 15  
US-09-252-991A-12037  
; Sequence 12037, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252.991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 12037  
; LENGTH: 1536  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-12037

Query Match 2.4%; Score 40; DB 4; Length 1536;  
Best Local Similarity 47.7%; Pred. No. 0.46;  
Matches 147; Conservative 0; Mismatches 160; Indels 1; Gaps 1;

```

QY 282 GCAGAGCTGCGGCTGCTCAGTGCATGCGGGAAAAGCCAGCCGAGGATCCCTGTGCTG 341
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 741 GCACCGCTGCGAGTACGCGGCTCCCTCCAGGGGCTGCC -GCGAGAGCATGAGTTGGCG 799
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 342 GGCAGCCCTGCTGTCACCGCTCCTGTAAGACATCATCTGCTGAAGTCTATCACAGCTAAC 401
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 800 GTACAGATGCGCGACCGCTCTCGATGCTGCTGATCAGTAGTATCAGCGCCACCGCGCAGGAAG 859
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 402 ATCTCCAGCTGCGAGGTGAAGCCCTCGGSCAAATGACACAGAGCTGCTAGTCAAGATCCCC 461
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 860 GCCATCCAGTCCGAAGCGAAGCGGCTGCGGCAAGCTGACCGAGCGGCAAGC 919
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 462 CTGGACATGCTGCTGATTCACACAGGCGCCCTGTCAGACCATGCTGAGTTCCACATG 521
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 920 TCGGGCAAGCGCCGCGGACGACAGCGCGGTGCGCCAGGCGCCGCAAGGTTACCCAGCGCC 979
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 522 ACGACTGAGGCCCAAGCCACCATCCGATGACACAGTGCAGAGTGCCGCCACCCGCGCTG 581
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 980 AGGCGGATGACGATGGCGCGCAGGCGCAGCCAGGGCAGCGCGGTTTCAGCAGGACG 1039
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 582 GTCTCTCAG 589
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1040 ATGCTCAG 1047
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Search completed: October 9, 2003, 23:36:15  
 Job time : 114.492 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2003, 12:41:16 ; Search time 495.773 Seconds  
(without alignments)  
9147.448 Million cell updates/sec

Title: US-09-700-770-2

Perfect score: 1680  
Sequence: 1 ggtgtcagcgataaagtt.....tcataaacactgtcgtgt 1680

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

N\_Geneseq\_19jun03:\*

1: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*  
2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*  
3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*  
4: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*  
5: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*  
6: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*  
7: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:\*  
8: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*  
9: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*  
10: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*  
11: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:\*  
12: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:\*  
13: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:\*  
14: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*  
15: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:\*  
16: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:\*  
17: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:\*  
18: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:\*  
19: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*  
20: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:\*  
21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*  
22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*  
23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*  
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*  
25: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
1	1679.6	100.0	1680	21	AAZ29724	Human lung specific	
2	1679.2	100.0	1680	22	AAH77948	Nucleotide sequenc	
3	1667	99.2	1707	21	AAZ87210	Human NTAP cDNA cl	
4	1656.2	98.6	2036	22	AAH77950	Nucleotide sequenc	
5	1617	96.2	1636	21	AAA37057	Human PRO1357 (DNG	
6	1617	96.2	1636	22	AA546064	Human DNA encoding	
7	1617	96.2	1636	22	AA546064	Human DNA encoding	
8	1617	96.2	1636	22	AA546064	Human DNA encoding	

9	1617	96.2	1636	24	AB574416 Human CDNA encodin
10	1617	96.2	1636	25	ACA57822 Human PRO1357 CDNA
11	1617	96.2	1636	25	ACA58848 CDNA encoding huma
12	1617	96.2	1636	25	ACA60401 Novel human secret
13	1617	96.2	1636	25	ACA63411 CDNA encoding huma
14	1617	96.2	1636	25	ABX98292 Human CDNA encodin
15	1617	96.2	1636	25	ABX98794 Novel human secret
16	1617	96.2	1636	25	ACA05839 Human secreted/tra
17	1617	96.2	1636	25	ABX97883 Human PRO polynuc
18	1617	96.2	1636	25	ABX78667 Human PRO polynuc
19	1617	96.2	1636	25	ABX75680 Human CDNA encodin
20	1617	96.2	1636	25	ABX76885 Human PRO polynuc
21	1617	96.2	1636	25	ABX16725 Human CDNA encodin
22	1533	91.2	2121	23	AA572707 DNA encoding novel
23	1367.4	81.4	1392	25	ABX70446 DNA encoding human
24	1367.4	81.4	1392	25	ABX70447 DNA encoding human
25	1367.4	81.4	1392	25	ABX70454 DNA encoding human
26	1365.8	81.3	1392	25	ABX70449 DNA encoding human
27	1365.8	81.3	1392	25	ABX70450 DNA encoding human
28	1365.8	81.3	1392	25	ABX70455 DNA encoding human
29	1364.2	81.2	1392	25	ABX70445 DNA encoding human
30	1364.2	81.2	1392	25	ABX70448 DNA encoding human
31	1364.2	81.2	1392	25	ABX70451 DNA encoding human
32	1364.2	81.2	1392	25	ABX70453 DNA encoding human
33	1362.6	81.1	1392	25	ABX70452 DNA encoding human
34	1359.4	80.9	1392	25	ABX70456 DNA encoding human
35	1305	77.7	1572	25	ABX70444 DNA encoding human
36	931.8	55.5	1023	25	ABX70457 DNA encoding human
37	806	48.0	1035	22	ABA01989 Human NOV6b coding
38	724.2	43.1	963	22	ABA01986 Human NOV6b coding
39	641	38.2	1172	21	AAZ97114 Human secreted pro
40	635.8	37.8	1177	21	AAE18254 Lung cancer associ
41	634.8	37.0	1175	21	AAZ97023 Human secreted pro
42	420	25.0	420	21	AAH30554 Human colon cancer
43	417.4	24.8	455	21	AACT4959 Human ORFX ORF514
44	398.2	23.7	423	22	AA18484 Human breast cance
45	382	22.7	382	24	ABK38912 CDNA encoding lung

#### ALIGNMENTS

RESULT 1  
ID AAZ29724 standard; DNA: 1680 BP.  
XX AAZ29724:  
AC AAZ29724:  
XX 27-MAR-2000 (first entry)  
DT XX  
XX Human lung specific gene-1.  
DE XX  
XX Lung Specific Gene; LSG: human; diagnostic marker;  
KW prognosticate; Lung cancer; diagnosis; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
XX  
PN WO960160-A1.  
PD 25-NOV-1999.  
XX  
XX 12-MAY-1999; 99WO-US10344.  
XX  
XX 21-MAY-1998; 98US-0086212.  
XX  
XX (DIAD-) DIADEXUS LLC.  
XX Yang F, Macina RA, Sun Y;  
XX WPI; 2000-116320/10.  
XX  
XX A new method for diagnosing, monitoring and staging lung cancer -

```

PS Example 1; Pages 33-34; 40pp; English.
XX
CC The present sequence is a lung specific gene (LSG) from human
CC clone ID 2798946. The LSG has high level of tissue specificity for lungs
CC and is overexpressed in cancerous tissues. The sequence serves as a
CC diagnostic marker for detecting, monitoring, staging and prognosticating
CC lung cancer. The diagnosis involves comparing levels of LSG in samples
CC obtained from patient and normal control.
XX
SQ Sequence 1680 BP; 380 A; 503 C; 429 G; 367 T; 1 other:

Query Match      100.0%; Score 1679.6; DB 21; Length 1680;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1680; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGTGAGAGATATATAGGTGGACTTCCAGACCCACTGGCCGGAGAGAGAGAGAGCGGG 60
DB 1 GGTGTGAGAGATATATAGGTGGACTTCCAGACCCACTGGCCGGAGAGAGAGAGAGCGGG 60
QY 61 CCGAGAGACTCCAGCGTCCAGAGGTGCGATCCTGCATCTGCTGCCCTGTGACACCTGGG 120
DB 61 CCGAGAGACTCCAGCGTCCAGAGGTGCGATCCTGCATCTGCTGCCCTGTGACACCTGGG 120
QY 121 AAGATGGCCGCGCCGCTGAGACCTTCAACCTCTCTGTGGTTGCTGGAGACCACTTGAAC 180
DB 121 AAGATGGCCGCGCCGCTGAGACCTTCAACCTCTCTGTGGTTGCTGGAGACCACTTGAAC 180
QY 181 CAAGCCACCCCTAGTCCACTGCACTGTCATCTCTCGGCCAAAAGTCAACAAGAAAG 240
DB 181 CAAGCCACCCCTAGTCCACTGCACTGTCATCTCTCGGCCAAAAGTCAACAAGAAAG 240
QY 241 CTGACACAGAGAGCTGAGAGACCAACAGCCACAGCATCTGACAGAGTGCCTGCTC 300
DB 241 CTGACACAGAGAGCTGAGAGACCAACAGCCACAGCATCTGACAGAGTGCCTGCTC 300
QY 301 AGTGCATGCGGGGAAAGACGAGGAGATCCCTGTGTGGGAGCCCTGTGAAACACCG 360
DB 301 AGTGCATGCGGGGAAAGACGAGGAGATCCCTGTGTGGGAGCCCTGTGAAACACCG 360
QY 361 TCCCTGAGACACATCATCTGTGGTGAAGTCAATCAGAGTAAATCCTCCAGCTGCAAGTGA 420
DB 361 TCCCTGAGACACATCATCTGTGGTGAAGTCAATCAGAGTAAATCCTCCAGCTGCAAGTGA 420
QY 421 AGCCCTGCGCCCAATATACAGAGAGCTGTAAGTAAATCCCTGGACATGCTGGCTGAT 480
DB 421 AGCCCTGCGCCCAATATACAGAGAGCTGTAAGTAAATCCCTGGACATGCTGGCTGAT 480
QY 481 TCAACACGCCCCCTGTGCAAGACATCGTAGAGTGCACATGAGCATGAGGCGCCAAAGCA 540
DB 481 TCAACACGCCCCCTGTGCAAGACATCGTAGAGTGCACATGAGCATGAGGCGCCAAAGCA 540
QY 541 CCATCCGATGAGACACAGTGAAGTGGCCCGCCGCTGTGCTCTGAGTACTGTGCA 600
DB 541 CCATCCGATGAGACACAGTGAAGTGGCCCGCCGCTGTGCTCTGAGTACTGTGCA 600
QY 601 CCAAGCATGGAGAGCTGCGCATCCAGTGTGCAATGAAGTCTCTCTGTGTAAGCGCT 660
DB 601 CCAAGCATGGAGAGCTGCGCATCCAGTGTGCAATGAAGTCTCTCTGTGTAAGCGCT 660
QY 661 TAGCTAACGAGGTCAAGTCAAGTCCAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 661 TAGCTAACGAGGTCAAGTCAAGTCCAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 721 TGTGTCCGCTGATCAGAGCTTCTCTCAATGGAGATATAGCAGACCTCTGACGCTGGTGA 780
DB 721 TGTGTCCGCTGATCAGAGCTTCTCTCAATGGAGATATAGCAGACCTCTGACGCTGGTGA 780
QY 781 AGGTGCCATTTCCCTGAGATGACGCTGAGATTGACCTTGTATCTGTGCATCA 840
DB 781 AGGTGCCATTTCCCTGAGATGACGCTGAGATTGACCTTGTATCTGTGCATCA 840
QY 841 AGGGTGAACCATTCAGCTTACGCGGGGCGCAAGTTGTGGACTCACAGGAAAGGTGA 900
DB 841 AGGGTGAACCATTCAGCTTACGCGGGGCGCAAGTTGTGGACTCACAGGAAAGGTGA 900

```

```

DB 841 AGGGTGAACCATTCAGCTTACGCGGGGCGCAAGTTGTGGACTCACAGGAAAGGTGA 900
QY 901 CCAAGTGGTCAATATACCTGTGAGCTTCCCTGACATATGCCACCTGGAGCAACATCCGT 960
DB 901 CCAAGTGGTCAATATACCTGTGAGCTTCCCTGACATATGCCACCTGGAGCAACATCCGT 960
QY 961 TCAGCCTCATGCTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 961 TCAGCCTCATGCTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1021 AAGAAATTCATGCTCTGTGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
DB 1021 AAGAAATTCATGCTCTGTGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
QY 1081 GCATGGGCTGATCATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
DB 1081 GCATGGGCTGATCATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
QY 1141 TCCCTACTCAGAGACACTCCGAGATTCTTATAGACCAAGGCCATGCCAAGTGGCCAAAC 1200
DB 1141 TCCCTACTCAGAGACACTCCGAGATTCTTATAGACCAAGGCCATGCCAAGTGGCCAAAC 1200
QY 1201 TGATGCTGTGAGAAAGTCTTCCCTCCAGTGAAGCCCTCCGCTTTGTTTCACTGGGCA 1260
DB 1201 TGATGCTGTGAGAAAGTCTTCCCTCCAGTGAAGCCCTCCGCTTTGTTTCACTGGGCA 1260
QY 1261 TCGAAGCCAGCTCGGAGAGCTAGTTTACACCAAGAGTGAACACTTATCAACTTGA 1320
DB 1261 TCGAAGCCAGCTCGGAGAGCTAGTTTACACCAAGAGTGAACACTTATCAACTTGA 1320
QY 1321 ATATACATGAGCTCTGATGAGATCCAGCTGATGAGATCTGGGATGGTGGTTCACAACTG 1380
DB 1321 ATATACATGAGCTCTGATGAGATCCAGCTGATGAGATCTGGGATGGTGGTTCACAACTG 1380
QY 1381 ATGCTCTGAAAAACATCATGAGATCATGATCATCATCTCTGCTGCCGAACGAATG 1440
DB 1381 ATGCTCTGAAAAACATCATGAGATCATGATCATCATCTCTGCTGCCGAACGAATG 1440
QY 1441 GCAAAATTAAGATCTGGGGTCCAGTGTCAATGTTGTAAGGCTTGGGATTCGAGGAGCTG 1500
DB 1441 GCAAAATTAAGATCTGGGGTCCAGTGTCAATGTTGTAAGGCTTGGGATTCGAGGAGCTG 1500
QY 1501 AGTCTCTACAGCAAGAGATGCTTGTGCTTACTACAGCTCTCTGTGGAACCCAGCT 1560
DB 1501 AGTCTCTACAGCAAGAGATGCTTGTGCTTACTACAGCTCTCTGTGGAACCCAGCT 1560
QY 1561 CTCCTGTCTCCAGTGAAGACTTGGATGGACCAATCAGAGGAAAGCTGGTCCAGCTGG 1620
DB 1561 CTCCTGTCTCCAGTGAAGACTTGGATGGACCAATCAGAGGAAAGCTGGTCCAGCTGG 1620
QY 1621 GAGTATGGGTGTGAGCTCTATAGACATCCCTCTGCAATCAATTAACACTTGGCTGTG 1680
DB 1621 GAGTATGGGTGTGAGCTCTATAGACATCCCTCTGCAATCAATTAACACTTGGCTGTG 1680

RESULT 2
AAH77948
ID AAH77948 strand; DNA; 1680 BP.
XX
AC AAH77948;
XX
DT 13-NOV-2001 (first entry)
XX
DE Nucleotide sequence of a human lng103 polypeptide.
XX
KW Human; lung cancer specific gene; LSG; lng103; lung cancer; ss.
XX
OS Homo sapiens.
XX
FH Key 124..1577
FT CDS
FT /tag= a
FT /product= "lng103"

```

```
ET /transl_except= "(pos: 328..329, aa: Gly)"
ET /transl_except= "(pos: 372..374, aa: Val)"
PN W0200161055-A2.
PD 23-AUG-2001.
XX 20-FEB-2001; 2001WO-US05674.
XX 17-FEB-2000; 2000US-0183188.
XX (DIAD-) DIADEXUS INC.
PA Chen S, Sun Y, Macina RA:
XX WPI: 2001-529917/58.
DR P-PSDB; AAG63976.
XX
XX New lung cancer specific gene for the treatment and diagnosis of lung
PT cancer -
XX
XX Claim 1; Page 112-113; 119pp; English.
XX
XX The present sequence represents a human lung cancer specific gene
XX (LSG), and encodes a polypeptide designated Lng103. LSGs are useful
XX in the treatment and diagnosis of lung cancer. The treatment of lung
XX cancer comprises the administration of a molecule which down regulates
XX the expression of an LSG. An immune response can be mounted against a
XX target cell expressing an LSG. Identification of potential therapeutic
XX agents for use in imaging and treating lung cancer which comprises
XX screening molecules for an ability to bind to or decrease expression
XX of an LSG relative to LSG in the absence of the agent where the ability
XX of a molecule to bind to the LSG or decrease expression of the LSG is
XX indicative of the molecule being useful in imaging and treating lung
XX cancer.
XX
XX Sequence 1680 BP; 380 A; 503 C; 429 G; 367 T; 1 other:
SQ
Query Match 100.0%; Score 1679.2; DB 22; Length 1680;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1678; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTGTGCAGATATTAAGTTGGACTTCCAGACCCACTCCCGGGAGAGAGAGCGGG 60
DB 1 GGTGTGCAGATATTAAGTTGGACTTCCAGACCCACTCCCGGGAGAGAGAGCGGG 60
QY 61 CCGAGAGCTCCAGGCTGCCAGGTCTGCGATCTGCACTTGTGCGCTGACACCTGGG 120
DB 61 CCGAGAGCTCCAGGCTGCCAGGTCTGCGATCTGCACTTGTGCGCTGACACCTGGG 120
QY 121 AAGATGGCCGGCCCGTGGAGCTTCACTTCTGTGTGTTGCTGGACGACACTTGATC 180
DB 121 AAGATGGCCGGCCCGTGGAGCTTCACTTCTGTGTGTTGCTGGACGACACTTGATC 180
QY 181 CAAGCCACCTTCATCTCCACTGCTAGTTCTCATCTCTGGCCCAAAAGTATCAAGAAAAG 240
DB 181 CAAGCCACCTTCATCTCCACTGCTAGTTCTCATCTCTGGCCCAAAAGTATCAAGAAAAG 240
QY 241 CTGACACAGAGCTGAAGAGCACAAAGCCACAGCATCTGACAGCACTGCGGTGTC 300
DB 241 CTGACACAGAGCTGAAGAGCACAAAGCCACAGCATCTGACAGCACTGCGGTGTC 300
QY 301 AGTGCATGCGGGAAAAAGCCAGCGGAGATCCCTGTGCTGGGACGCTGGTGAACACCG 360
DB 301 AGTGCATGCGGGAAAAAGCCAGCGGAGATCCCTGTGCTGGGACGCTGGTGAACACCG 360
QY 361 TCCGTAAGACATATCTGCTGTAAGGTGATCAGCTAACAATCTCTCAGCTGACAGTGA 420
DB 361 TCCGTAAGACATATCTGCTGTAAGGTGATCAGCTAACAATCTCTCAGCTGACAGTGA 420
QY 421 AGCCCTGGCCAAATGACAGAGAGCTGTAGTCAAGATCCCTGGAGCATGGTGGCTGAT 480
DB 421 AGCCCTGGCCAAATGACAGAGAGCTGTAGTCAAGATCCCTGGAGCATGGTGGCTGAT 480
```

```
QY 481 TCAACAGCCCCCTGTCTCAAGACCATCTGTGAGTTCCACATGACGACTGAGGCCCAAGCA 540
DB 481 TCAACAGCCCCCTGTCTCAAGACCATCTGTGAGTTCCACATGACGACTGAGGCCCAAGCA 540
QY 541 CCATCCGATGACACACGACGTGAGTGGCCCCCAGCCCTGGTCTCAGTACGTGTGCA 600
DB 541 CCATCCGATGACACACGACGTGAGTGGCCCCCAGCCCTGGTCTCAGTACGTGTGCA 600
QY 601 CCAGCATGGGAGCCTGGCCATCCAAAGCTGACATTAACCTGCTCTGCTGGTGAACGCT 660
DB 601 CCAGCATGGGAGCCTGGCCATCCAAAGCTGACATTAACCTGCTCTGCTGGTGAACGCT 660
QY 661 TAGCTAAGCAGATCATGAGACCTCTAGTCCATCCCTGCCCAATCTAGTAAAAACAGC 720
DB 661 TAGCTAAGCAGATCATGAGACCTCTAGTCCATCCCTGCCCAATCTAGTAAAAACAGC 720
QY 721 TGTGTCCCGTGTATGAGGCTTCTTCAATGAGATGATGACAGACCTCTGACGTGTGA 780
DB 721 TGTGTCCCGTGTATGAGGCTTCTTCAATGAGATGATGACAGACCTCTGACGTGTGA 780
QY 781 AGGTGCCATTTCCCTCAGCAATGACGCTGGAGTTGACCTCTGTATCCTGCAATCA 840
DB 781 AGGTGCCATTTCCCTCAGCAATGACGCTGGAGTTGACCTCTGTATCCTGCAATCA 840
QY 841 AGGGTACACCAATTCAGCTTACCTGAGGGGCCAAAGTTGTGAGTACACAGGAAAAAGTGA 900
DB 841 AGGGTACACCAATTCAGCTTACCTGAGGGGCCAAAGTTGTGAGTACACAGGAAAAAGTGA 900
QY 901 CCAAGTGTCAATATACCTGCTGAGCTTCCCTGACAAATCCACCTGGACAAATCCGCT 960
DB 901 CCAAGTGTCAATATACCTGCTGAGCTTCCCTGACAAATCCACCTGGACAAATCCGCT 960
QY 961 TCAGCCTATGCTGTAGTACGAGACGTGTAAGGAGTGAAGCTGCACTGCTGTCTGCTCAG 1020
DB 961 TCAGCCTATGCTGTAGTACGAGACGTGTAAGGAGTGAAGCTGCACTGCTGTCTGCTCAG 1020
QY 1021 AAGATTCATGCTCTGTGAGACTCTGCTCTGAGAGTGGCCATCGGCTGAAGTCAA 1080
DB 1021 AAGATTCATGCTCTGTGAGACTCTGCTCTGAGAGTGGCCATCGGCTGAAGTCAA 1080
QY 1081 GCATCGGCTGATCATATTAAGGCTGCAAGTAACTGAGTCTACCCAGATCTGTAAGA 1140
DB 1081 GCATCGGCTGATCATATTAAGGCTGCAAGTAACTGAGTCTACCCAGATCTGTAAGA 1140
QY 1141 TCTTACACAGAGACATCCCGAGTTTATAGACCAAGGCCATGCCAAGGTGCCCAAC 1200
DB 1141 TCTTACACAGAGACATCCCGAGTTTATAGACCAAGGCCATGCCAAGGTGCCCAAC 1200
QY 1201 TGATGCTGCTGGAAGTGTTCCTCCATCAGTGAAGCCCTCGGCTTTGTTCAACCTGGGCA 1260
DB 1201 TGATGCTGCTGGAAGTGTTCCTCCATCAGTGAAGCCCTCGGCTTTGTTCAACCTGGGCA 1260
QY 1261 TCGAAGCCAGCTCGGAAGCTCAGTTTATACCAAAAGTGAACCACTTATCTCAACTGA 1320
DB 1261 TCGAAGCCAGCTCGGAAGCTCAGTTTATACCAAAAGTGAACCACTTATCTCAACTGA 1320
QY 1321 ATAAATCATAGCTGTATGAGATCCAGCTGATGAATCTGGGATGGCTGCTCAACTG 1380
DB 1321 ATAAATCATAGCTGTATGAGATCCAGCTGATGAATCTGGGATGGCTGCTCAACTG 1380
QY 1381 ATGTCTGAAAAACATCATCATAGATGATCATCATCTCATCTGCTGCGAAGCAAGATG 1440
DB 1381 ATGTCTGAAAAACATCATCATAGATGATCATCATCTCATCTGCTGCGAAGCAAGATG 1440
QY 1441 GCAATTTAAGATCTGGGGTCCAGTGTATTGTGTGAAGCCCTGGGATTCGAGGCACTG 1500
DB 1441 GCAATTTAAGATCTGGGGTCCAGTGTATTGTGTGAAGCCCTGGGATTCGAGGCACTG 1500
QY 1501 AGTCTCACTAGACCAAGGATGCCCTGTGCTTACTCCAGCCCTCTGTGGAACCAACCT 1560
DB 1501 AGTCTCACTAGACCAAGGATGCCCTGTGCTTACTCCAGCCCTCTGTGGAACCAACCT 1560
```

QY	1561	CTCCTGTCCTCCCATGGAAGACTTGGATGGAGCCATCGAAGGAAGCGTGGGCCAGCTGG	1620
Db	1561		1620
QY	1621	GAGTATGGGAGTGTAGCTCTATATAGACCAATCCCTCTCTGTCATCATCAATTAACACTTGCCTGTG	1680
Db	1621		1680
Db	1621	GAGTATGGGAGTGTAGCTCTATATAGACCAATCCCTCTCTGTCATCATCAATTAACACTTGCCTGTG	1680
RESULT 3			
AAZ87210			
AAZ87210	standard; cDNA; 1707 BP.		
AAZ87210:			
AC			
XX	08-MAY-2000 (first entry)		
DT			
XX			
XX	Human NTAP cDNA clone 2799056.		
DE			
XX			
KW	Neurotransmission-associated protein; NTAP; odorant-binding protein;		
KW	neurological disease; Alzheimer's disease; Parkinson's disease;		
KW	Huntington's disease; cerebral neoplasm; multiple sclerosis;		
KW	drug screening; gene therapy; antagonist; cancer; AIDS; asthma;		
KW	Crohn's disease; osteoporosis; ss.		
XX			
OS	Homo sapiens.		
XX			
XX			
XX	Key	location/Qualifiers	
FT	CDS	124..1578	
FT		/*tag= a	
FT		/product= "Human neurotransmission-associated protein	
FT		(NTAP) 2799056"	
XX			
PN	MO200001821-A2.		
PD			
PD	13-JAN-2000.		
XX			
PF	02-JUL-1999; 99WO-US15121.		
XX			
PR	02-JUL-1998; 98US-0091677.		
XX			
PA	(INCY-) INCYTE PHARM INC.		
XX			
PI	Lal P, Tang YT, Yue H, Corley NC, Guegler KJ, Gorgone GA;		
PI	Baughn MR, Patterson C;		
PT			
PT	New human neurotransmission associated proteins, useful for treatment,		
PT	prevention and diagnosis of neurological disease, e.g. Alzheimer's		
PT	disease, and antagonists for treating cancer or immune disorders		
XX			
PS			
XX	Claim 7; Page 67; 67P; English.		
CC			
CC	Sequences AAZ87205-87210 represent cDNAs encoding six human		
CC	neurotransmission-associated proteins (NTAPs, AAY77121-777126). The		
CC	present sequence, clone 2799056, encodes a putative odorant-binding		
CC	protein, and was produced by extension of cDNA fragments isolated from a		
CC	human nasal polyp tissue cDNA library. The NTAPs are used for treatment		
CC	or prevention of neurological diseases (e.g., Alzheimer's, Parkinson's		
CC	or Huntington's diseases, cerebral neoplasms, or multiple sclerosis).		
CC	They can also be used to raise specific antibodies and to screen for		
CC	specific binding agents (potential agonists and antagonists).		
CC	NTAPs encoding nucleic acids are useful for recombinant production of		
CC	NTAPs, and as a source of therapeutic antagonists (antibense,		
CC	triplex-forming or ribozyme molecules). The nucleic acids may also be		
CC	used as a source of probes and primers for diagnosis or monitoring of		
CC	NTAP expression in hybridisation/amplification tests, for chromosome		
CC	mapping and for identifying related sequences, and for gene therapy. NTAP		
CC	antagonists are used to treat and prevent a wide range of cancers and		
CC	immune disorders (e.g. AIDS, asthma, Crohn's disease, osteoporosis, viral		
CC	or other infections). NTAP antibodies are used to detect NTAPs, for		

CC	diagnosis or monitoring, as therapeutic antagonists, in competitive drug
CC	screens, and for affinity purification of NTAPs from natural sources.
xx	
SQ	Sequence 1707 BP; 406 A; 503 C; 429 G; 369 T; 0 other;
Query Match	99.2%; Score 1667; DB 21; Length 1707;
Best Local Similarity	Pred. 99.8%;
Matches 1678; Conservative	1; Mismatches 1; Gaps 1;

Query Match		99.2%:	Score 1667:	DB 21:	Length 1707:	
Best Local Similarity		99.8%:	Pred. No. 0:			
Matches 1678:		Conservative	1:	Mismatches	1:	Indels
					1:	Gaps
QY	1	GGTGTGCAGATATTAAGTTTGACTTCACAGCCACCTGACCCGAGGAGAGRGAGCGGG	60			
DB	1	GGTGTGCAGATATTAAGTTTGACTTCACAGCCACCTGACCCGAGGAGAGRGAGCGGG	60			
QY	61	CCGAGGATCCAGGGGTGGCCAGGTCTGGCATCCGCACTTGCTGTCGCCCTCTGACACCTGGG	120			
DB	61	CCGAGGATCCAGGGGTGGCCAGGTCTGGCATCCGCACTTGCTGTCGCCCTCTGACACCTGGG	120			
QY	121	AAGATGCGCGGCCCGGTGGACCTTACACCTTCTCTGTGGTTGTCGGCAGCCACCTTGATC	180			
DB	121	AAGATGCGCGGCCCGGTGGACCTTACACCTTCTCTGTGGTTGTCGGCAGCCACCTTGATC	180			
QY	181	CAAGCCACCCCTCATGTCCTCCACCTGCAGTTCATCTCTGGGCCCAAAAGTCATCAAGAAAG	240			
DB	181	CAAGCCACCCCTCATGTCCTCCACCTGCAGTTCATCTCTGGGCCCAAAAGTCATCAAGAAAG	240			
QY	241	CTGACACAGAGAGCTGGAAGGACCAACAGCCACAGACATCTCTGACAGAGTCCCTGCTC	300			
DB	241	CTGACACAGAGAGCTGGAAGGACCAACAGCCACAGACATCTCTGACAGAGTCCCTGCTC	300			
QY	301	AGTGCATGCGGGGAAAAAGCCGCGGAGG - ATCCCTGTGTGCTGGGCAAGCTGTGTAAACAC	359			
DB	301	AGTGCATGCGGGGAAAAAGCCGCGGAGGATCCCTGTGTGCTGGGCAAGCTGTGTAAACAC	360			
QY	360	GTGCTGAAGACATCATCTGCTGAGGTCTATCAGAGTCAACAGTCAACCTCTCAAGCTCAGATG	419			
DB	361	GTGCTGAAGACATCATCTGCTGAGGTCTATCAGAGTCAACAGTCAACCTCTCAAGCTCAGATG	420			
QY	420	AAGCCCTGCGGCATGATGACAGAGGTGTTACTCAAGATCCCCCGGACATGCTGGTGGGGA	479			
DB	421	AAGCCCTGCGGCATGATGACAGAGGTGTTACTCAAGATCCCCCGGACATGCTGGTGGGGA	480			
QY	480	TTCAACACGCCCCGTGTCAAGACCATGCTGGAGTTCCATGACAGACTGAGAGCCCAAGCC	539			
DB	481	TTCAACACGCCCCGTGTCAAGACCATGCTGGAGTTCCATGACAGACTGAGAGCCCAAGCC	540			
QY	540	AACATGCGCATGAGACACAGTGCAGATGAGGCCCCACCGCCGTGTCACAGTACGATGAGCC	599			
DB	541	AACATGCGCATGAGACACAGTGCAGATGAGGCCCCACCGCCGTGTCACAGTACGATGAGCC	600			
QY	600	ACCAAGCATGAGGAGCTCGCATCCACATGCTGTGATAAAGCTCTCTCTGTTGTAAGCGCC	659			
DB	601	ACCAAGCATGAGGAGCTCGCATCCACATGCTGTGATAAAGCTCTCTCTGTTGTAAGCGCC	660			
QY	660	TTAGCTAAGCAGGTATGATACCTCTGTAGTGCATCCCTGCGCCATCTAGTAAAAAACAG	719			
DB	661	TTAGCTAAGCAGGTATGATACCTCTGTAGTGCATCCCTGCGCCATCTAGTAAAAAACAG	720			
QY	720	CTGTGTCCCGTGATGAGAGCTTCTCTCAATGGCATGTATGACAGACTCTGTCAGACTGGTG	779			
DB	721	CTGTGTCCCGTGATGAGAGCTTCTCTCAATGGCATGTATGACAGACTCTGTCAGACTGGTG	780			
QY	780	AAGGTGCCCATTTCCCTAGATGATGACCTGTGGAGTTTGAACCTTCTGTATCTCTGCATC	839			
DB	781	AAGGTGCCCATTTCCCTAGATGATGACCTGTGGAGTTTGAACCTTCTGTATCTCTGCATC	840			
QY	840	AAGGTGCACACATTCAGCTTACTCTGGGGGCCAAGTTGTTGAGATCCACAGGAAAGGTG	899			
DB	841	AAGGTGCACACATTCAGCTTACTCTGGGGGCCAAGTTGTTGAGATCCACAGGAAAGGTG	900			
QY	900	ACCAAGTGTTCATTAATCTGTGACGTTCCCTGACATGATGCCACCTGTGACATATCCG	959			
DB	901	ACCAAGTGTTCATTAATCTGTGACGTTCCCTGACATGATGCCACCTGTGACATATCCG	960			





QY	1618	TGGAGATGATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCATATAACACTGGCT	1677
Db	1658	TGGAGATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCATATAACACTGGCT	1717
QY	1678	GTG 1680	
Db	1718	GTG 1720	
RESULT 5			
AA37057			
ID	AAA37057	standard; cDNA; 1636 BP.	
AC	AAA37057;		
DT	08-AUG-2000	(first entry)	
XX			
DE	Human PRO1357 (UNQ706)	cDNA sequence SEQ ID NO:127.	
XX			
KW	Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;		
KM	transmembrane; secretion; immunoadhesion; pharmaceutical; screening;		
OS	ss.		
XX	Homo sapiens.		
PN	WO200012708-A2.		
PD	09-MAR-2000.		
PF	01-SEP-1999;	99WO-US20111.	
XX			
PR	01-SEP-1998;	98US-0098716.	
PR	01-SEP-1998;	98US-0098749.	
PR	01-SEP-1998;	98US-0098750.	
PR	02-SEP-1998;	98US-0098803.	
PR	02-SEP-1998;	98US-0098821.	
PR	02-SEP-1998;	98US-0098843.	
PR	09-SEP-1998;	98US-0099536.	
PR	09-SEP-1998;	98US-0099596.	
PR	09-SEP-1998;	98US-0099598.	
PR	09-SEP-1998;	98US-0099602.	
PR	09-SEP-1998;	98US-0099642.	
PR	10-SEP-1998;	98US-0099741.	
PR	10-SEP-1998;	98US-0099754.	
PR	10-SEP-1998;	98US-0099763.	
PR	10-SEP-1998;	98US-0099792.	
PR	10-SEP-1998;	98US-0099808.	
PR	10-SEP-1998;	98US-0099812.	
PR	10-SEP-1998;	98US-0099815.	
PR	10-SEP-1998;	98US-0099816.	
PR	15-SEP-1998;	98US-0100385.	
PR	15-SEP-1998;	98US-0100388.	
PR	15-SEP-1998;	98US-0100390.	
PR	16-SEP-1998;	98US-0100584.	
PR	16-SEP-1998;	98US-0100627.	
PR	16-SEP-1998;	98US-0100661.	
PR	16-SEP-1998;	98US-0100662.	
PR	16-SEP-1998;	98US-0100664.	
PR	17-SEP-1998;	98US-0100683.	
PR	17-SEP-1998;	98US-0100684.	
PR	17-SEP-1998;	98US-0100710.	
PR	17-SEP-1998;	98US-0100711.	
PR	17-SEP-1998;	98US-0100919.	
PR	17-SEP-1998;	98US-0100930.	
PR	18-SEP-1998;	98US-0100848.	
PR	18-SEP-1998;	98US-0100849.	
PR	18-SEP-1998;	98US-0101014.	
PR	18-SEP-1998;	98US-0101068.	
PR	18-SEP-1998;	98US-0101071.	
PR	22-SEP-1998;	98US-0101279.	
PR	23-SEP-1998;	98US-0101471.	
PR	23-SEP-1998;	98US-0101472.	

PR 23-SEP-1998; 98US-0101474.  
 PR 23-SEP-1998; 98US-0101475.  
 PR 23-SEP-1998; 98US-0101476.  
 PR 23-SEP-1998; 98US-0101477.  
 PR 23-SEP-1998; 98US-0101479.  
 PR 24-SEP-1998; 98US-0101738.  
 PR 24-SEP-1998; 98US-0101741.  
 PR 24-SEP-1998; 98US-0101743.  
 PR 24-SEP-1998; 98US-0101915.  
 PR 24-SEP-1998; 98US-0101916.  
 PR 29-SEP-1998; 98US-0102207.  
 PR 29-SEP-1998; 98US-0102240.  
 PR 29-SEP-1998; 98US-0102307.  
 PR 29-SEP-1998; 98US-0102330.  
 PR 30-SEP-1998; 98US-0102331.  
 PR 30-SEP-1998; 98US-0102484.  
 PR 30-SEP-1998; 98US-0102487.  
 PR 30-SEP-1998; 98US-0102570.  
 PR 30-SEP-1998; 98US-0102571.  
 PR 01-OCT-1998; 98US-0102684.  
 PR 01-OCT-1998; 98US-0102687.  
 PR 02-OCT-1998; 98US-0102965.  
 PR 06-OCT-1998; 98US-0103258.  
 PR 06-OCT-1998; 98US-0103349.  
 PR 07-OCT-1998; 98US-0103314.  
 PR 07-OCT-1998; 98US-0103315.  
 PR 07-OCT-1998; 98US-0103328.  
 PR 07-OCT-1998; 98US-0103395.  
 PR 07-OCT-1998; 98US-0103396.  
 PR 07-OCT-1998; 98US-0103401.  
 PR 08-OCT-1998; 98US-0103633.  
 PR 08-OCT-1998; 98US-0103678.  
 PR 08-OCT-1998; 98US-0103679.  
 PR 08-OCT-1998; 98US-0103711.  
 PR 14-OCT-1998; 98US-0104257.  
 PR 20-OCT-1998; 98US-0104987.  
 PR 20-OCT-1998; 98US-0105000.  
 PR 20-OCT-1998; 98US-0105002.  
 PR 21-OCT-1998; 98US-0105104.  
 PR 22-OCT-1998; 98US-0105169.  
 PR 22-OCT-1998; 98US-0105266.  
 PR 26-OCT-1998; 98US-0105693.  
 PR 26-OCT-1998; 98US-0105694.  
 PR 27-OCT-1998; 98US-0105807.  
 PR 27-OCT-1998; 98US-0105881.  
 PR 27-OCT-1998; 98US-0105882.  
 PR 28-OCT-1998; 98US-0106023.  
 PR 28-OCT-1998; 98US-0106023.  
 PR 28-OCT-1998; 98US-0106029.  
 PR 28-OCT-1998; 98US-0106030.  
 PR 28-OCT-1998; 98US-0106032.  
 PR 28-OCT-1998; 98US-0106033.  
 PR 28-OCT-1998; 98US-0106178.  
 PR 29-OCT-1998; 98US-0106248.  
 PR 29-OCT-1998; 98US-0106384.  
 PR 29-OCT-1998; 98US-0106500.  
 PR 30-OCT-1998; 98US-0106464.  
 PR 30-OCT-1998; 98US-0106856.  
 PR 30-OCT-1998; 98US-0106856.  
 PR 03-NOV-1998; 98US-0106902.  
 PR 03-NOV-1998; 98US-0106905.  
 PR 03-NOV-1998; 98US-0106919.  
 PR 03-NOV-1998; 98US-0106932.  
 PR 03-NOV-1998; 98US-0106934.  
 PR 10-NOV-1998; 98US-0107783.  
 PR 17-NOV-1998; 98US-0108775.  
 PR 17-NOV-1998; 98US-0108779.  
 PR 17-NOV-1998; 98US-0108787.  
 PR 17-NOV-1998; 98US-0108788.  
 PR 17-NOV-1998; 98US-0108801.  
 PR 17-NOV-1998; 98US-0108802.  
 PR 17-NOV-1998; 98US-0108806.  
 PR 17-NOV-1998; 98US-0108807.  
 PR 17-NOV-1998; 98US-0108867.

PR 17-NOV-1998; 98US-0108925.  
 PR 18-NOV-1998; 98US-0108848.  
 PR 18-NOV-1998; 98US-0108849.  
 PR 18-NOV-1998; 98US-0108850.  
 PR 18-NOV-1998; 98US-0108851.  
 PR 18-NOV-1998; 98US-0108852.  
 PR 18-NOV-1998; 98US-0108858.  
 PR 18-NOV-1998; 98US-0108858.  
 PR 18-NOV-1998; 98US-0108904.  
 XX  
 PA (GENTECH ) GENENTECH INC.  
 XX  
 PI Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;  
 XX WPI; 2000-237871/20.  
 DR P-PSDB; AAY99375.  
 XX  
 XX  
 PT New mammalian DNA sequences encoding transmembrane, receptor or  
 PT secreted PRO polypeptides, useful for screening of potential peptide or  
 PT small molecule inhibitors of the relevant receptor/ligand interactions  
 XX  
 XX Claim 2; Fig 71; 773pp; English.  
 XX  
 CC AAA37022 to AAA37144 encode the new isolated human transmembrane,  
 CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The  
 CC transmembrane and receptor PRO proteins can be used for screening of  
 CC potential peptide or small molecule inhibitors of the relevant  
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences  
 CC encoding them have various industrial applications, including uses as  
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent  
 CC PCR primers and hybridisation probes used in the isolation of the PRO  
 CC polypeptides from the present invention.  
 XX  
 SO Sequence 1636 BP; 374 A; 492 C; 411 G; 359 T; 0 other;  
 Query Match 96.2%; Score 1617; DB 21; Length 1636;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1628; Conservative 1; Mismatches 1; Indels 1; gaps 1;  
 QY 51 GREGAGCGGGCGAGAGCTGCAAGCTGCGCCAGGTCTGGATCTGACCTTGCAGCCCTCT 110  
 DB 1 GAGGAGCGGGCGAGAGCTGCAAGCTGCGCCAGGTCTGGATCTGACCTTGCAGCCCTCT 60  
 QY 111 GACACCTGGGAAAGATGCGCGGCGCTGACCTTGCAGCTTCTGTGTTGCTGGCAGC 170  
 DB 61 GACACCTGGGAAAGATGCGCGGCGCTGACCTTGCAGCTTCTGTGTTGCTGGCAGC 120  
 QY 171 CACCTTGATCCAAAGCCACCTCAATGTCCTGCACTGCACTGCACTGCACTGCACTGCA 230  
 DB 121 CACCTTGATCCAAAGCCACCTCAATGTCCTGCACTGCACTGCACTGCACTGCACTGCA 180  
 QY 231 CAAAGAAAGCTGACACAGAGCTGAAGGACCAACGACACAGATCTGAGAGCT 290  
 DB 181 CAAAGAAAGCTGACACAGAGCTGAAGGACCAACGACACAGATCTGAGAGCT 240  
 QY 291 GCGCTGCTCAGTGCATGCGGAGGAAAGGACGCGGAGG-ATCGCTGCTGGGAGCCT 349  
 DB 241 GCGCTGCTCAGTGCATGCGGAGGAAAGGACGCGGAGGATCGCTGCTGGGAGCCT 300  
 QY 350 GGTGAACACCGTCTGTAAGCAATCATCTGCTGAAGGTGATCAAGTCAATCTCTCA 409  
 DB 301 GGTGAACACCGTCTGTAAGCAATCATCTGCTGAAGGTGATCAAGTCAATCTCTCA 360  
 QY 410 GGTGACAGTGAAGCCCTGCGGCAATGACAGAGCTGCTGATCAATATCCCTGGACAT 469  
 DB 361 GGTGACAGTGAAGCCCTGCGGCAATGACAGAGCTGCTGATCAATATCCCTGGACAT 420  
 QY 470 GGTGCTGATTCACACGCGCTGCTCAAGACATCTGAGATTCACATGACGACTGA 529  
 DB 421 GGTGCTGATTCACACGCGCTGCTCAAGACATCTGAGATTCACATGACGACTGA 480  
 QY 530 GGCCTAAGCCACCATCCGATGAGACACAGTGAAGTGGCCACCGCTGGTCTCAG 589  
 DB 481 GGCCTAAGCCACCATCCGATGAGACACAGTGAAGTGGCCACCGCTGGTCTCAG 540

```

OY 550 TGACTGTGCACACACAGCCATGGGAGCCCTGCGATCCACACTGCTGCAATTAAGCTCTCCCTTCT
    |||||||
DB 541 TGACTGTGCACACACAGCCATGGGAGCCCTGCGATCCACACTGCTGCAATTAAGCTCTCCCTTCT
    |||||||
OY 650 GGTGAGAGCCCTTACGTAAGCAGAGTCATGACCTCTTAAGTCCATCCCTGCCCATACTAGT
    |||||||
DB 601 GGTGAGAGCCCTTACGTAAGCAGAGTCATGACCTCTTAAGTCCATCCCTGCCCATACTAGT
    |||||||
OY 710 GAAAAACAGAGCTGTGTCCTGATGAGAGCTTCCCTCAATGGCATGTATGACAGCTCTCT
    |||||||
DB 661 GAAAAACAGAGCTGTGTCCTGATGAGAGCTTCCCTCAATGGCATGTATGACAGCTCTCT
    |||||||
OY 770 GCAGCTGTGTAAGGTGCCCCATTTCCCTCAGCATTGACCGCTGTGAGTTTGAACCTTCTGTA
    |||||||
DB 721 GCAGCTGTGTAAGGTGCCCCATTTCCCTCAGCATTGACCGCTGTGAGTTTGAACCTTCTGTA
    |||||||
OY 830 TCCCTGCCATCAAGGCTGACACCATTCACCTCTACTGGGGCCCAAGTTTGTGGACTCACA
    |||||||
DB 781 TCCCTGCCATCAAGGCTGACACCATTCACCTCTACTGGGGCCCAAGTTTGTGGACTCACA
    |||||||
OY 890 GGGAAAGGTGACCAAGTGGTTCATTAATCACTGACAGCTTCCCTGACATGCCCCACCTGGA
    |||||||
DB 841 GGGAAAGGTGACCAAGTGGTTCATTAATCACTGACAGCTTCCCTGACATGCCCCACCTGGA
    |||||||
OY 950 CAACATCCCGTTCAAGCTCATGCTGATGATCAGAGACGTGGTGAAGGCTGACGTGCTGTGT
    |||||||
DB 901 CAACATCCCGTTCAAGCTCATGCTGATGATCAGAGACGTGGTGAAGGCTGACGTGCTGTGT
    |||||||
OY 1010 GCTCTCCACAAAGAAATTCATGTCGTCCTGTTGACCTCTGCTCTCTGAGAGTGGCCATACG
    |||||||
DB 961 GCTCTCTCCACAAAGAAATTCATGTCGTCCTGTTGACCTCTGCTCTCTGAGAGTGGCCATACG
    |||||||
OY 1070 GCTGAAGTCAAGCATTCGGGCTGATCATATGAAGGCTCAGATAAGTGGGATTAACCA
    |||||||
DB 1021 GCTGAAGTCAAGCATTCGGGCTGATCATATGAAGGCTCAGATAAGTGGGATTAACCA
    |||||||
OY 1130 GATGTGTAAGTCTTAATCACTCAGACACTCCGAGTTTATATAGCAAGGCCATGCCAA
    |||||||
DB 1081 GATGTGTAAGTCTTAATCACTCAGACACTCCGAGTTTATATAGCAAGGCCATGCCAA
    |||||||
OY 1190 GGTGGCCCAACTGANTCGTGTGGAAGTGTTCCTCCGCAAGGCCCTCCCTCTTGT
    |||||||
DB 1141 GGTGGCCCAACTGANTCGTGTGGAAGTGTTCCTCCGCAAGGCCCTCCCTCTTGT
    |||||||
OY 1250 CACCTGTGGCATTCGAAGCCAGCTCGAAGCTCAGTTTATACCAAGGCTGACCACTTAT
    |||||||
DB 1201 CACCTGTGGCATTCGAAGCCAGCTCGAAGCTCAGTTTATACCAAGGCTGACCACTTAT
    |||||||
OY 1310 ACTCAACTTGAATTAACATCAGCTCTGATCGATCCAGCTGATGAACCTGTGGGATTGGCTG
    |||||||
DB 1261 ACTCAACTTGAATTAACATCAGCTCTGATCGATCCAGCTGATGAACCTGTGGGATTGGCTG
    |||||||
OY 1370 GTTCCACCTGATGTTGTCGAAAAACATCATGATGAGATGATCAATCCATCCCTGCTGCC
    |||||||
DB 1321 GTTCCACCTGATGTTGTCGAAAAACATCATGATGAGATGATCAATCCATCCCTGCTGCC
    |||||||
OY 1430 GAACCAAGATGGCAAAATTAAGATCTGGGGTCCAGTGTCAATGGTGAAGGCTTGGGAT
    |||||||
DB 1381 GAACCAAGATGGCAAAATTAAGATCTGGGGTCCAGTGTCAATGGTGAAGGCTTGGGAT
    |||||||
OY 1490 CGAGGCAAGCTGAGTCTCAGCTGACCAAGAGATGCCCTGTGCTTACTGCCAGCTCTCTG
    |||||||
DB 1441 CGAGGCAAGCTGAGTCTCAGCTGACCAAGAGATGCCCTGTGCTTACTGCCAGCTCTCTG
    |||||||
OY 1550 GAAACCCAGGCTGTCCTGTCCTCCAGTAAGACTTGAAGGAGGAGGAGGAGGCTGG
    |||||||
DB 1501 GAAACCCAGGCTGTCCTGTCCTCCAGTAAGACTTGAAGGAGGAGGAGGAGGCTGG
    |||||||
OY 1610 GTCCAGACTGGAGATATGGGTGAGCTCTATAGACCATCCCTCTGCAATCAATAAAC
    |||||||
DB 1561 GTCCAGACTGGAGATATGGGTGAGCTCTATAGACCATCCCTCTGCAATCAATAAAC
    |||||||

```

```

OY 1670 ACTTGCTGTGTG 1680
    |||||||
DB 1621 ACTTGCTGTGTG 1631

RESULT 6
AAS46064
ID AAS46064 standard; cDNA; 1636 BP.

AAS46064;
18-DEC-2001 (first entry)
XX
XX
DE Human DNA encoding PRO polypeptide sequence #140.
XX
XX
KW PRO polypeptide; mammary tumour; cancer; human; cattle; horse; sheep; ss;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.
XX
OS Homo sapiens.
XX
PN W0200168848-A2.
XX
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US06520.
XX
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 03-MAR-2000; 2000US-187202P.
PR 06-MAR-2000; 2000US-186968P.
PR 14-MAR-2000; 2000US-189320P.
PR 14-MAR-2000; 2000US-189328P.
PR 15-MAR-2000; 2000WO-US06884.
PR 21-MAR-2000; 2000US-190828P.
PR 21-MAR-2000; 2000US-191007P.
PR 21-MAR-2000; 2000US-191048P.
PR 21-MAR-2000; 2000US-191314P.
PR 28-MAR-2000; 2000US-192655P.
PR 29-MAR-2000; 2000US-193032P.
PR 29-MAR-2000; 2000US-193053P.
PR 30-MAR-2000; 2000WO-US08439.
PR 04-APR-2000; 2000US-194449P.
PR 04-APR-2000; 2000US-194447P.
PR 11-APR-2000; 2000US-195975P.
PR 11-APR-2000; 2000US-196000P.
PR 11-APR-2000; 2000US-196187P.
PR 11-APR-2000; 2000US-196690P.
PR 11-APR-2000; 2000US-196820P.
PR 18-APR-2000; 2000US-198121P.
PR 18-APR-2000; 2000US-198585P.
PR 25-APR-2000; 2000US-199397P.
PR 25-APR-2000; 2000US-199550P.
PR 25-APR-2000; 2000US-199554P.
PR 03-MAY-2000; 2000US-201516P.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 05-JUN-2000; 2000US-209832P.
PR 28-JUL-2000; 2000WO-US20710.
PR 22-AUG-2000; 2000US-0644848.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
XX
XX
PA (GENE ) GENENTECH INC.
XX
XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL,
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

```

XX WPI: 2001-602746/68.  
DR P-PSDB: AAU29163.  
XX  
PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
PT presence of tumours, such as prostate and breast tumours, in mammals and  
PT to screen for modulators of the compounds -  
XX  
PS Claim 2: Fig 279: 774bp: English.  
XX  
CC Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR  
CC primers for PRO polypeptides of the invention. The sequences of the  
CC invention can be used to detect the presence of a tumour in a mammal by  
CC comparing the level of expression of a PRO polypeptide in a test sample  
CC of cells from the animal and a control sample of normal cells, whereby a  
CC higher level of expression in the test sample indicates the presence of a  
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,  
CC pigs, goats and rabbits but are preferably human. The polypeptides can be  
CC used to stimulate tumour necrosis factor (TNF) alpha release from human  
CC blood, when contacted with it. A specific polypeptide can be used to  
CC stimulate the proliferation or differentiation of chondrocyte cells. The  
CC PRO proteins can be used to determine the presence of tumours and also  
CC susceptibility to tumour development, particularly adrenal, lung, colon,  
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
CC can be used for genetic analysis of individuals with genetic disorders.  
XX  
SQ Sequence 1636 BP: 374 A; 492 C; 411 G; 359 T; 0 other:  
  
Query Match 96.2%; Score 1617; DB 22; Length 1636;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1628; Conservative 1; Mismatches 1; Indels 1; Gaps 1;  
  
OY 51 GRGAGGCGGGCGAGACTCCAGGTGCGCCAGTGTGGCATCGCACTTCTCCCTCT 110  
|:|||||  
DB 1 GAGAGGCGGGCGAGACTCCAGGTGCGCCAGTGTGGCATCGCACTTCTCCCTCT 60  
|:|||||  
OY 111 GACACGTGGAGATGGCCGGCCGCGTGGACCTTCCTCTGTGTGTGTCGAGC 170  
|:|||||  
DB 61 GACACGTGGAGATGGCCGGCCGCGTGGACCTTCCTCTGTGTGTGTCGAGC 120  
|:|||||  
OY 171 CACCTTATCCAAACCCACCTCATCCACCTGCACTTCTCTCTGGCCCAAAAGTCAT 230  
|:|||||  
DB 121 CACCTTATCCAAACCCACCTCATCCACCTGCACTTCTCTCTGGCCCAAAAGTCAT 180  
|:|||||  
OY 231 CAAAGAAAAGCTGACACAGAGCTGAAGGACACACACCCAGCATCTGCGAGCACT 290  
|:|||||  
DB 181 CAAAGAAAAGCTGACACAGAGCTGAAGGACACACACCCAGCATCTGCGAGCACT 240  
|:|||||  
OY 291 GCCCTGCTCAGTGCATGCGGGAAGAACCCAGCGGAGG-ATCCCTGTGCTGGGCAAGCT 349  
|:|||||  
DB 241 GCCCTGCTCAGTGCATGCGGGAAGAACCCAGCGGAGGATCCCTGTGCTGGGCAAGCT 300  
|:|||||  
OY 350 GGTAAACACCTCTCTGAAGACATCATCTGGCTGAAGTCTACAGCTTAACATCTCTCA 409  
|:|||||  
DB 301 GGTAAACACCTCTCTGAAGACATCATCTGGCTGAAGTCTACAGCTTAACATCTCTCA 360  
|:|||||  
OY 410 GCTCAGGTGAAGCCCTCGGCCAATGACAGAGAGTGTAGTCAAGATCCCTCGAGCAT 469  
|:|||||  
DB 361 GCTCAGGTGAAGCCCTCGGCCAATGACAGAGAGTGTAGTCAAGATCCCTCGAGCAT 420  
|:|||||  
OY 470 GGTGGCTGATTTCAACAGCCCTGTGTCMAAGACCATGTGTGAGTTCCACATGAGACTGA 529  
|:|||||  
DB 421 GGTGGCTGATTTCAACAGCCCTGTGTCMAAGACCATGTGTGAGTTCCACATGAGACTGA 480  
|:|||||  
OY 530 GGGCCCAAGCCACCATCCGATGACACAGAGTGAAGTGGCCCAAGCCCTGTGCTAG 589  
|:|||||  
DB 481 GGGCCCAAGCCACCATCCGATGACACAGAGTGAAGTGGCCCAAGCCCTGTGCTAG 540  
|:|||||  
OY 590 TGACGTGACACAGCCATGGAGGCTGGCATCCAACTGCTGCAATAGCTCTCTCTCT 649  
|:|||||  
DB 541 TGACGTGACACAGCCATGGAGGCTGGCATCCAACTGCTGCAATAGCTCTCTCTCT 600  
|:|||||

OY 650 GGTGAAGCCTTTAGCTAAGCAGGTGATGAACCTCTAGTGGCATCCCTGCCCAATCTAGT 709  
|:|||||  
DB 601 GGTGAAGCCTTTAGCTAAGCAGGTGATGAACCTCTAGTGGCATCCCTGCCCAATCTAGT 660  
|:|||||  
OY 710 GAAAACACAGCTGTGTCTCCGATGAGAGCTTCTTCAATGGCATGTATGACACCTCTCT 769  
|:|||||  
DB 661 GAAAACACAGCTGTGTCTCCGATGAGAGCTTCTTCAATGGCATGTATGACACCTCTCT 720  
|:|||||  
OY 770 GCAGCTGGTGAAGGTGCCATTTCCCTCAGCATGAGCGTGTGGAGTTTGACCTTCTGTA 829  
|:|||||  
DB 721 GCAGCTGGTGAAGGTGCCATTTCCCTCAGCATGAGCGTGTGGAGTTTGACCTTCTGTA 780  
|:|||||  
OY 830 TCTGTCATCAAGGGGTGACACCATTCAGCTTACCTGGGGCCCAAGTTGTGACTGACA 889  
|:|||||  
DB 781 TCTGTCATCAAGGGGTGACACCATTCAGCTTACCTGGGGCCCAAGTTGTGACTGACA 840  
|:|||||  
OY 890 GGGAAAGGTGACCAAGTGTGATTAATCTGTGACGCTTCCCTGACATGCCCCACCTTGA 949  
|:|||||  
DB 841 GGGAAAGGTGACCAAGTGTGATTAATCTGTGACGCTTCCCTGACATGCCCCACCTTGA 900  
|:|||||  
OY 950 CAACATCCGTTCAAGCCTCATCTGAGTCAAGAGGTGGTGAAGCTGAGTGGCTGT 1009  
|:|||||  
DB 901 CAACATCCGTTCAAGCCTCATCTGAGTCAAGAGGTGGTGAAGCTGAGTGGCTGT 960  
|:|||||  
OY 1010 GCTCTCTCAGAGAAATTCATGTCCTGTTGACCTGTGCTCTCTGAGAGTGGCCATCG 1069  
|:|||||  
DB 961 GCTCTCTCAGAGAAATTCATGTCCTGTTGACCTGTGCTCTCTGAGAGTGGCCATCG 1020  
|:|||||  
OY 1070 GCTGAAGTCAAGCATGGGGTGTATCATGAAAAGCTGCAATTAAGTGGGATTCACCA 1129  
|:|||||  
DB 1021 GCTGAAGTCAAGCATGGGGTGTATCATGAAAAGCTGCAATTAAGTGGGATTCACCA 1080  
|:|||||  
OY 1130 GATGCTGAAGTCTTAATCTAGAGACATCCGAGTTTCTTATAGCAAGGCCCATGCCAA 1189  
|:|||||  
DB 1081 GATGCTGAAGTCTTAATCTAGAGACATCCGAGTTTCTTATAGCAAGGCCCATGCCAA 1140  
|:|||||  
OY 1190 GGTGGCCCAACTGATGCTGTGGAAGTCTTCCCTCAGTGAAGCCCTCCGCTTGT 1249  
|:|||||  
DB 1141 GGTGGCCCAACTGATGCTGTGGAAGTCTTCCCTCAGTGAAGCCCTCCGCTTGT 1200  
|:|||||  
OY 1250 CACCTGGGCAATGCAAGCCAGCTGGGAAGCTCATGTTTACACCAAGGTGACCAACTAT 1309  
|:|||||  
DB 1201 CACCTGGGCAATGCAAGCCAGCTGGGAAGCTCATGTTTACACCAAGGTGACCAACTAT 1260  
|:|||||  
OY 1310 ACTCAACTGTAATTAACATCAGCTGATCGATCGATGATGAACCTTGGATTGGCTG 1369  
|:|||||  
DB 1261 ACTCAACTGTAATTAACATCAGCTGATCGATCGATGATGAACCTTGGATTGGCTG 1320  
|:|||||  
OY 1370 GTTCCAACTGATGTTGTGAAAACATCATCATGAGATCATGCACTCATCTGTGCC 1429  
|:|||||  
DB 1321 GTTCCAACTGATGTTGTGAAAACATCATCATGAGATCATGCACTCATCTGTGCC 1380  
|:|||||  
OY 1430 GAACCAAGATGGCAAAATTAATCTGGGGTCCAGTGTGATGGAAGGCTTGGGATT 1489  
|:|||||  
DB 1381 GAACCAAGATGGCAAAATTAATCTGGGGTCCAGTGTGATGGAAGGCTTGGGATT 1440  
|:|||||  
OY 1490 CGAGGACCTGAGTCTCAGTACGACCAAGAGATGCCCTTGTGCTTACTCCAGCTCCTTGTG 1549  
|:|||||  
DB 1441 CGAGGACCTGAGTCTCAGTACGACCAAGAGATGCCCTTGTGCTTACTCCAGCTCCTTGTG 1500  
|:|||||  
OY 1550 GAAACCCAGCTCTCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAGGGAAGGCTGG 1609  
|:|||||  
DB 1501 GAAACCCAGCTCTCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAGGGAAGGCTGG 1560  
|:|||||  
OY 1610 GTCCAGTGGGAGATATGGGTGTAGCTCTTATAGCAATCCCTCTCTGCAATCAATTAAC 1669  
|:|||||  
DB 1561 GTCCAGTGGGAGATATGGGTGTAGCTCTTATAGCAATCCCTCTCTGCAATCAATTAAC 1620  
|:|||||  
OY 1670 ACTTGCTGTG 1680  
|:|||||  
DB 1621 ACTTGCTGTG 1631  
|:|||||





QY 890 GGGAAAGTACCAAGTGGTTCATTAATCTGACGCTTCCGACATGCCACCTGGA 949  
 |||||  
 DB 841 GGGAAAGTACCAAGTGGTTCATTAATCTGACGCTTCCGACATGCCACCTGGA 900  
 |||||  
 QY 950 CAACATCCCGTTCAGGCTCATGCTGAGTACAGACGCTGGTGAAGCTGCAGTGGCTCTGT 1009  
 |||||  
 DB 901 CAACATCCCGTTCAGGCTCATGCTGAGTACAGACGCTGGTGAAGCTGCAGTGGCTCTGT 960  
 |||||  
 QY 1010 GCTCTCTCCAGAAATTCATGCTGCTGTTGACCTGTGCTCTGCTCTGAGAGTGGCCATG 1069  
 |||||  
 DB 961 GCTCTCTCCAGAAATTCATGCTGCTGTTGACCTGTGCTCTGAGAGTGGCCATG 1020  
 |||||  
 QY 1070 GCTGAAGTCAAGCAGTGGGCTGATCAATGAAAAAGCTGAGATAGCTGGATCTACCA 1129  
 |||||  
 DB 1021 GCTGAAGTCAAGCAGTGGGCTGATCAATGAAAAAGCTGAGATAGCTGGATCTACCA 1080  
 |||||  
 QY 1130 GATCGTGAAGTCTTAATCTACGAGACACTCCGAGTTTATAGACCAAGGCTATGCCAA 1189  
 |||||  
 DB 1081 GATCGTGAAGTCTTAATCTACGAGACACTCCGAGTTTATAGACCAAGGCTATGCCAA 1140  
 |||||  
 QY 1190 GGTGGCCCACTGATGCTGCTGGAAGTGTTCCTCCAGTGAAGCCCTCGCCCTTGTAT 1249  
 |||||  
 DB 1141 GGTGGCCCACTGATGCTGCTGGAAGTGTTCCTCCAGTGAAGCCCTCGCCCTTGTAT 1200  
 |||||  
 QY 1250 CACCCGCGGCATCGAAAGCCAGCTCGGAAGCTGATTTACACCAAGGTGACCACTTAT 1309  
 |||||  
 DB 1201 CACCCGCGGCATCGAAAGCCAGCTCGGAAGCTGATTTACACCAAGGTGACCACTTAT 1260  
 |||||  
 QY 1310 ACTCAACTGGAATTAATCAAGCTCTGATGGATCCAGCTGATCAATCTGGATTTGGCTG 1369  
 |||||  
 DB 1261 ACTCAACTGGAATTAATCAAGCTCTGATGGATCCAGCTGATCAATCTGGATTTGGCTG 1320  
 |||||  
 QY 1370 GTTCAACCTGATGTTCTGAAAAAATCAATCACTGAGATCATCTCCATCTGCTGCC 1429  
 |||||  
 DB 1321 GTTCAACCTGATGTTCTGAAAAAATCAATCACTGAGATCATCTCCATCTGCTGCC 1380  
 |||||  
 QY 1430 GAACCAAGATGCAAAATTAAGATCTGGGCTCCAGTGTCAATGGTGAAGGCTTTGGGAT 1489  
 |||||  
 DB 1381 GAACCAAGATGCAAAATTAAGATCTGGGCTCCAGTGTCAATGGTGAAGGCTTTGGGAT 1440  
 |||||  
 QY 1490 CGAGGAGCTGAGTCTCTCACTGACCAAGGATGCCCTTGCTTACATCCAGGCTCTGTG 1549  
 |||||  
 DB 1441 CGAGGAGCTGAGTCTCTCACTGACCAAGGATGCCCTTGCTTACATCCAGGCTCTGTG 1500  
 |||||  
 QY 1550 GAACCCAGCTCTCTGCTCTCCAGTGAAGACTTGGATGGACCAATCAAGGAAGGCTGG 1609  
 |||||  
 DB 1501 GAACCCAGCTCTCTGCTCTCCAGTGAAGACTTGGATGGACCAATCAAGGAAGGCTGG 1560  
 |||||  
 QY 1610 GTCCCAAGCTGGAGTATGGGTGAGCTCTATAGACCAATCCCTCTGCAATCAATTAAC 1669  
 |||||  
 DB 1561 GTCCCAAGCTGGAGTATGGGTGAGCTCTATAGACCAATCCCTCTGCAATCAATTAAC 1620  
 |||||  
 QY 1670 ACTTGCCTGTG 1680  
 |||||  
 DB 1621 ACTTGCCTGTG 1631  
 |||||

XX US200219130-A1.  
 PN 29-OCT-1997; 97US-063435P.  
 XX 29-OCT-1997; 97US-064215P.  
 PD 29-APR-1998; 98US-082797P.  
 XX 29-APR-1998; 98US-083495P.  
 PE 06-DEC-2001; 2001US-0006867.  
 XX 29-OCT-1997; 97US-063435P.  
 XX 29-OCT-1997; 97US-064215P.  
 PR 22-APR-1998; 98US-082797P.  
 PR 29-APR-1998; 98US-083495P.  
 PR 15-MAY-1998; 98US-085579P.  
 PR 10-JUN-1998; 98US-088811P.  
 PR 10-JUN-1998; 98US-088824P.  
 PR 10-JUN-1998; 98US-088825P.  
 PR 11-JUN-1998; 98US-088863P.  
 PR 12-JUN-1998; 98US-089105P.  
 PR 16-JUN-1998; 98US-089514P.  
 PR 16-SEP-1998; 98WO-US19330.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 14-MAY-1999; 99WO-US10733.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21194.  
 PR 22-DEC-1999; 99WO-US30720.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32378.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 XX (GENTH ) GENENTECH INC.  
 PA Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Matanabe CK, Wood WI;  
 DR WPI: 2002-731348/79.  
 XX P-RSDB; ABG95889.  
 PT New isolated secreted and transmembrane PRO polypeptide useful for  
 PT modulating biological activity of a cell, or for treating  
 PT sports-related joint problems, osteoarthritis or rheumatoid arthritis  
 XX  
 PS Claim 2; Fig 77; 399pp; English.  
 XX The invention relates to an isolated secreted and transmembrane PRO  
 CC polypeptide having 80 or sequence identity to a sequence appearing  
 CC as ABG95851-ABG95934 or their associated signal peptide, or a sequence of  
 CC an extracellular domain of the proteins with their associated signal  
 CC peptide or lacking its associated signal peptide. Also included are  
 CC the nucleic acids encoding the proteins, vectors, host cells,  
 CC fusion proteins and antibodies which specifically bind to the proteins.  
 CC The proteins are useful for detecting a polypeptide designated as A, B, C  
 CC or D in a sample suspected of containing an A, B, C or D polypeptide,  
 CC by contacting the sample with a polypeptide designated as E, F, G, H or  
 CC I (or vice versa) and determining the formation of a A/E, B/F, B/G, C/H  
 CC or D/I polypeptide conjugate in the sample, where the formation of the  
 CC conjugate is indicative of the presence of an A, B, C or D polypeptide  
 CC in the sample, where A is a PRO10272 polypeptide, B is a PRO20110  
 CC polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide,  
 CC E is a PRO5801 polypeptide, F is a PRO1 polypeptide, G is a PRO20040  
 CC polypeptide, H is a PRO20233 polypeptide and I is a PRO1890  
 CC polypeptide. The sample comprises a cell suspected of expressing the A,



B, C or D polypeptide. The E, F, G, H or I polypeptide is labeled with a detectable label or is attached to a solid support. The proteins are useful for linking a bioactive molecule to a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive molecule is a toxin, a radiolabel or an antibody. The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H, or I, or antibodies against them are useful for modulating a biological activity of a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H, or I. The cell is killed. The proteins are useful for identifying agonists or antagonists, for the preparation of a medicament useful in the treatment of a condition which is responsive to the proteins, as molecular weight markers for protein electrophoresis purposes, and as therapeutic agents for treating sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis. Nucleic acids encoding the proteins are useful as hybridisation probes, in chromosome and gene mapping, in the generation of anti-sense RNA and DNA, for the preparation of the proteins, to generate transgenic or knockout animals which are useful in the development and screening of therapeutic useful reagents, for chromosome identification, and in gene therapy. The antibody is useful as a therapeutic agent, in a diagnostic assay and for affinity purification of the protein from recombinant cell culture natural sources. The present sequence encodes a novel secreted or transmembrane protein of the invention.

Sequence 1636 BP; 374 A; 492 C; 411 G; 359 T; 0 other;

Query Match 96.2%; Score 1617; DB 24; Length 1636;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1628; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

51 GRRGACGGGGCCGAGAGATCTCAAGCTGCGCCAGTCTGCACTTGTCCCTCT 110  
1 GAGGACCGGGCCGAGAGATCTCAAGCTGCGCCAGTCTGCACTTGTCCCTCT 60  
111 GACACCTGGGAAAGATGCGCGCCGCTGAGACTTCACTCTGCTGCTTGTGCGAGC 170  
61 GACACCTGGGAAAGATGCGCGCCGCTGAGACTTCACTCTGCTGCTTGTGCGAGC 120  
171 CACCTTGATTCAGCCACCTCTAGTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 230  
121 CACCTTGATTCAGCCACCTCTAGTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
231 CAAGAAGAAAGCTGACACAGAGAGCTGAAGAGACCAAGCAGCAGATCTGACGAGCT 290  
181 CAAGAAGAAAGCTGACACAGAGAGCTGAAGAGACCAAGCAGCAGATCTGACGAGCT 240  
291 GCGGCTGCTGAGTGCATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 349  
241 GCGGCTGCTGAGTGCATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300  
350 GGTGAACACCGTCTGAGACATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 409  
301 GGTGAACACCGTCTGAGACATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
410 GCTGCAAGTGAAGCCCTGCGCCATGACACGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 469  
361 GCTGCAAGTGAAGCCCTGCGCCATGACACGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
470 GGTGCTGCTGATTAACAGCGCCCTGGTCAAGACATGCTGCTGCTGCTGCTGCTGCTGCT 529  
421 GGTGCTGCTGATTAACAGCGCCCTGGTCAAGACATGCTGCTGCTGCTGCTGCTGCTGCT 480  
530 GGTGAACACCGTCTGAGACATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 589  
481 GGTGAACACCGTCTGAGACATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
590 TGACTGTGACACGAGCATGGAAGCTGCGCATCAACTGCTGCTGCTGCTGCTGCTGCT 649  
541 TGACTGTGACACGAGCATGGAAGCTGCGCATCAACTGCTGCTGCTGCTGCTGCTGCT 600  
650 GGTGAACACCGTCTGAGACATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 709  
601 GGTGAACACCGTCTGAGACATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660

710 GAAAAACACCTGTGTCCTGATGAGAGCTTCTTCATGATGATGATGATGATGATGATGAT 769  
661 GAAAAACACCTGTGTCCTGATGAGAGCTTCTTCATGATGATGATGATGATGATGATGAT 720  
770 GCACTGTGTGAGAGTGGCCATTTTCCCTGACATGAGCCGTGCTGAGTTGACCTTCTGTA 829  
721 GCAGCTGTGTGAGAGTGGCCATTTTCCCTGACATGAGCCGTGCTGAGTTGACCTTCTGTA 780  
830 TCTGTCATCAAGGTGACACCATTCATGCTCTACCTGAGGAGGAGGAGGAGGAGGAGGAG 889  
781 TCTGTCATCAAGGTGACACCATTCATGCTCTACCTGAGGAGGAGGAGGAGGAGGAGGAG 840  
890 GGGAAAGTGAACCAAGGTGTTCAATACTGCAAGTCTGCTGCAATGCGCCACCTGGA 949  
841 GGGAAAGTGAACCAAGGTGTTCAATACTGCAAGTCTGCTGCAATGCGCCACCTGGA 900  
950 CAACATCCGTTGACCTTCATGCTGAGTCAAGAGCTGTGTAAGAGCTGAGTGTGCTGT 1009  
901 CAACATCCGTTGACCTTCATGCTGAGTCAAGAGCTGTGTAAGAGCTGAGTGTGCTGT 960  
1010 GCTGTCGCAAGAAATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1069  
961 GCTGTCGCAAGAAATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
1070 GCTGAAGTCAAGCATCGGCTGATCAATGAAAAAGCTGCAATTAAGCTGGGATCAACCA 1129  
1021 GCTGAAGTCAAGCATCGGCTGATCAATGAAAAAGCTGCAATTAAGCTGGGATCAACCA 1080  
1130 GATGCTGAAGATCTTAATCACTGAGACACTCCGAGTTTATATAGACCAAGGCCATGCA 1189  
1081 GATGCTGAAGATCTTAATCACTGAGACACTCCGAGTTTATATAGACCAAGGCCATGCA 1140  
1190 GGTGGCCCACTGATGCTGTGAGAGTTTCCCTCAGGAAGCCCTCCGCCCTTGT 1249  
1141 GGTGGCCCACTGATGCTGTGAGAGTTTCCCTCAGGAAGCCCTCCGCCCTTGT 1200  
1250 CACCTGGGATGAGAACCCAGCTCGAGAGCTGAGTTTAAACCAAAAGTGAACCAACTTAT 1309  
1201 CACCTGGGATGAGAACCCAGCTCGAGAGCTGAGTTTAAACCAAAAGTGAACCAACTTAT 1260  
1310 ACTCACTTAATTAATCACTGCTGCTGATGAGATCCAGCTGATGATGATGATGATGATG 1369  
1261 ACTCACTTAATTAATCACTGCTGCTGATGAGATCCAGCTGATGATGATGATGATGATG 1320  
1370 GTTCCAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1429  
1321 GTTCCAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380  
1430 GAACCAAGATGGAATTAATGATCTGGGCTGCCAGTCAATGGTGAAGCCTTGGGAT 1489  
1381 GAACCAAGATGGAATTAATGATCTGGGCTGCCAGTCAATGGTGAAGCCTTGGGAT 1440  
1490 CGAGGAGCTGAGTCTCACTGACCAAGAGTGCCTTGTCTTAATCTGACCTCTTGTG 1549  
1441 CGAGGAGCTGAGTCTCACTGACCAAGAGTGCCTTGTCTTAATCTGACCTCTTGTG 1500  
1550 GAAACCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1609  
1501 GAAACCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560  
1610 GTCCAGCTGAGATGAGTGTGAGTCTATAGAACATCCCTCTGCAATCAATTAAC 1669  
1561 GTCCAGCTGAGATGAGTGTGAGTCTATAGAACATCCCTCTGCAATCAATTAAC 1620  
1670 ACTTGCCTGTG 1680  
1621 ACTTGCCTGTG 1631

RESULT 10  
ACAS7822  
ID ACAS7822 standard; cdna; 1636 BP.

```
XX AC ACAA57822;
XX XX
XX 10-JUN-2003 (first entry)
XX DE Human PRO1357 cDNA.
XX XX
XX Human; PRO; secreted; transmembrane; cytosolic; TNF-alpha; blood; gene;
KW tumour necrosis factor alpha release; chondrocyte cell; proliferation;
KW differentiation; tumour; gene therapy; ss.
XX OS Homo sapiens.
XX PM US2003036143-A1.
XX PD
XX 20-FEB-2003.
XX PF
XX 02-JUL-2002; 2002US-0187600.
XX XX
XX 16-SEP-1998; 98WO-US19330.
XX PR 07-OCT-1998; 98WO-US21141.
XX PR 01-DEC-1998; 98WO-US25108.
XX PR 08-MAR-1999; 99WO-US05028.
XX PR 14-MAY-1999; 99WO-US10733.
XX PR 02-JUN-1999; 99WO-US12252.
XX PR 01-SEP-1999; 99WO-US20111.
XX PR 15-SEP-1999; 99WO-US21090.
XX PR 01-DEC-1999; 99WO-US28301.
XX PR 02-DEC-1999; 99WO-US28551.
XX PR 30-DEC-1999; 99WO-US31274.
XX PR 05-JAN-2000; 2000WO-US00219.
XX PR 18-FEB-2000; 2000WO-US04341.
XX PR 18-FEB-2000; 2000WO-US04342.
XX PR 22-FEB-2000; 2000WO-US04414.
XX PR 24-FEB-2000; 2000WO-US05004.
XX PR 01-MAR-2000; 2000WO-US05601.
XX PR 02-MAR-2000; 2000WO-US05841.
XX PR 15-MAR-2000; 2000WO-US06884.
XX PR 30-MAR-2000; 2000WO-US08439.
XX PR 17-MAY-2000; 2000WO-US13705.
XX PR 22-MAY-2000; 2000WO-US14042.
XX PR 30-MAY-2000; 2000WO-US14941.
XX PR 02-JUN-2000; 2000WO-US15264.
XX PR 28-JUL-2000; 2000WO-US20710.
XX PR 24-AUG-2000; 2000WO-US23328.
XX PR 08-NOV-2000; 2000WO-US30952.
XX PR 01-DEC-2000; 2000WO-US32678.
XX PR 20-DEC-2000; 2000WO-US34956.
XX PR 28-FEB-2001; 2001WO-US06520.
XX PR 01-JUN-2001; 2001WO-US17800.
XX PR 20-JUN-2001; 2001WO-US19692.
XX PR 29-JUN-2001; 2001WO-US21066.
XX PR 09-JUL-2001; 2001WO-US21735.
XX PR 29-AUG-2001; 2001WO-US27099.
XX PR 18-SEP-1997; 97US-0592639.
XX PR 18-SEP-1997; 97US-059266P.
XX PR 17-OCT-1997; 97US-062250P.
XX PR 21-OCT-1997; 97US-063486P.
XX PR 24-OCT-1997; 97US-063120P.
XX PR 28-OCT-1997; 97US-063121P.
XX PR 28-OCT-1997; 97US-063540P.
XX PR 28-OCT-1997; 97US-063541P.
XX PR 28-OCT-1997; 97US-063544P.
XX PR 28-OCT-1997; 97US-063564P.
XX PR 29-OCT-1997; 97US-063734P.
XX PR 31-OCT-1997; 97US-063870P.
XX PR 31-OCT-1997; 97US-064103P.
XX PR 13-NOV-1997; 97US-065311P.
XX PR 21-NOV-1997; 97US-066120P.
XX PR 24-NOV-1997; 97US-066466P.
XX PR 11-DEC-1997; 97US-066772P.
XX PR 12-DEC-1997; 97US-069335P.
XX PR 12-DEC-1997; 97US-069425P.

PR 17-DEC-1997; 97US-069870P.
PR 18-DEC-1997; 97US-068017P.
PR 10-MAR-1998; 98US-077450P.
PR 11-MAR-1998; 98US-077632P.
PR 11-MAR-1998; 98US-077649P.
PR 20-MAR-1998; 98US-078886P.
PR 20-MAR-1998; 98US-078939P.
PR 27-MAR-1998; 98US-079664P.
PR 27-MAR-1998; 98US-079786P.
PR 31-MAR-1998; 98US-080107P.
PR 31-MAR-1998; 98US-080194P.
PR 01-APR-1998; 98US-080327P.
PR 01-APR-1998; 98US-080333P.
PR 08-APR-1998; 98US-081049P.
PR 08-APR-1998; 98US-081070P.
PR 09-APR-1998; 98US-081195P.
PR 15-APR-1998; 98US-081838P.
PR 21-APR-1998; 98US-082568P.
PR 21-APR-1998; 98US-082569P.
PR 22-APR-1998; 98US-082704P.
PR 22-APR-1998; 98US-082797P.
PR 28-APR-1998; 98US-083322P.
PR 29-APR-1998; 98US-083495P.
PR 29-APR-1998; 98US-083496P.
PR 29-APR-1998; 98US-083499P.
PR 29-APR-1998; 98US-083559P.
PR 05-MAY-1998; 98US-083566P.
PR 06-MAY-1998; 98US-084414P.
PR 07-MAY-1998; 98US-084639P.
PR 07-MAY-1998; 98US-084640P.
PR 07-MAY-1998; 98US-084643P.
PR 15-MAY-1998; 98US-085579P.
PR 15-MAY-1998; 98US-085580P.
PR 15-MAY-1998; 98US-085582P.
PR 15-MAY-1998; 98US-085700P.
PR 18-MAY-1998; 98US-086023P.
PR 22-MAY-1998; 98US-086392P.
PR 22-MAY-1998; 98US-086486P.
PR 28-MAY-1998; 98US-087098P.
PR 28-MAY-1998; 98US-087208P.
PR 02-JUN-1998; 98US-087609P.
PR 02-JUN-1998; 98US-087759P.
PR 03-JUN-1998; 98US-087827P.
PR 04-JUN-1998; 98US-088025P.
PR 04-JUN-1998; 98US-088028P.
PR 04-JUN-1998; 98US-088029P.
PR 04-JUN-1998; 98US-088033P.
PR 04-JUN-1998; 98US-088326P.
PR 05-JUN-1998; 98US-088167P.
PR 05-JUN-1998; 98US-088202P.
PR 05-JUN-1998; 98US-088212P.
PR 05-JUN-1998; 98US-088217P.
PR 09-JUN-1998; 98US-088655P.
PR 10-JUN-1998; 98US-088722P.
PR 10-JUN-1998; 98US-088738P.
PR 10-JUN-1998; 98US-088740P.
PR 10-JUN-1998; 98US-088811P.
PR 10-JUN-1998; 98US-088824P.
PR 10-JUN-1998; 98US-088825P.
PR 10-JUN-1998; 98US-088826P.
PR 11-JUN-1998; 98US-088861P.
PR 11-JUN-1998; 98US-088863P.
PR 11-JUN-1998; 98US-088866P.
PR 12-JUN-1998; 98US-089090P.
PR 12-JUN-1998; 98US-089105P.
PR 16-JUN-1998; 98US-089512P.
PR 16-JUN-1998; 98US-089514P.
PR 17-JUN-1998; 98US-089538P.
PR 17-JUN-1998; 98US-089598P.
PR 17-JUN-1998; 98US-089653P.
PR 18-JUN-1998; 98US-089908P.
PR 19-JUN-1998; 98US-089952P.
PR 22-JUN-1998; 98US-090246P.
```

PR 22-JUN-1998; 98US-090252P.  
PR 22-JUN-1998; 98US-090234P.  
PR 24-JUN-1998; 98US-090429P.  
PR 24-JUN-1998; 98US-090435P.  
PR 24-JUN-1998; 98US-090444P.  
PR 24-JUN-1998; 98US-090461P.  
PR 24-JUN-1998; 98US-090535P.  
PR 24-JUN-1998; 98US-090540P.  
PR 25-JUN-1998; 98US-090678P.  
PR 25-JUN-1998; 98US-090688P.  
PR 25-JUN-1998; 98US-090690P.  
PR 25-JUN-1998; 98US-090694P.  
PR 25-JUN-1998; 98US-090695P.  
PR 26-JUN-1998; 98US-090696P.  
PR 26-JUN-1998; 98US-090863P.  
PR 26-JUN-1998; 98US-091010P.  
PR 01-JUL-1998; 98US-091359P.  
PR 01-JUL-1998; 98US-091344P.  
PR 02-JUL-1998; 98US-091478P.  
PR 02-JUL-1998; 98US-091486P.  
PR 02-JUL-1998; 98US-091626P.  
PR 02-JUL-1998; 98US-091628P.  
PR 02-JUL-1998; 98US-091632P.  
PR 24-JUL-1998; 98US-094006P.  
PR 04-AUG-1998; 98US-095282P.  
PR 10-AUG-1998; 98US-095998P.  
PR 10-AUG-1998; 98US-096012P.  
PR 17-AUG-1998; 98US-096757P.  
PR 17-AUG-1998; 98US-096766P.  
PR 17-AUG-1998; 98US-096867P.  
PR 17-AUG-1998; 98US-096891P.  
PR 17-AUG-1998; 98US-096897P.  
PR 18-AUG-1998; 98US-096949P.  
PR 18-AUG-1998; 98US-096959P.  
PR 18-AUG-1998; 98US-097022P.  
PR 26-AUG-1998; 98US-097952P.  
PR 26-AUG-1998; 98US-097954P.  
PR 26-AUG-1998; 98US-097955P.  
PR 26-AUG-1998; 98US-097971P.  
PR 26-AUG-1998; 98US-097974P.  
PR 26-AUG-1998; 98US-098014P.  
PR 01-SEP-1998; 98US-098716P.  
PR 01-SEP-1998; 98US-098723P.  
PR 02-SEP-1998; 98US-098803P.  
PR 02-SEP-1998; 98US-098821P.  
PR 09-SEP-1998; 98US-098843P.  
PR 10-SEP-1998; 98US-099602P.  
PR 10-SEP-1998; 98US-099741P.  
PR 10-SEP-1998; 98US-099754P.  
PR 10-SEP-1998; 98US-099763P.  
PR 10-SEP-1998; 98US-099812P.

Query Match 96.2%; Score 1617; DB 25; Length 1636;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1628; Conservative 1; Mismatches 1; Indels 1; Gaps 1;  
QY 51 GRGAGGCGGCGGAGACTCCAGGTGCGCCAGTCTGGACCTCGACCTTGCCCTCT 110  
Db 1 GAGAGGCGGCGGAGACTCCAGGTGCGCCAGTCTGGACCTCGACCTTGCCCTCT 60  
QY 111 GACACCTGGAGAGTGGCCCGCCGTGAGCTTACCTTCTCTGTGTGTTGCTGAGC 170  
Db 61 GACACCTGGAGAGTGGCCCGCCGTGAGCTTACCTTCTCTGTGTGTTGCTGAGC 120  
QY 171 CACCTTGATCCAGCCACCTTCATCCGACCTGCACTGAGTTCTATCTCTCGGCCCAAAAGTCAT 230  
Db 121 CACCTTGATCCAGCCACCTTCATCCGACCTGCACTGAGTTCTATCTCTCGGCCCAAAAGTCAT 180  
QY 231 CAAAGAAAAGCTGACAGAGCTGAAGAGCACACAGCCGACAGCATCTGACGACACT 290  
Db 181 CAAAGAAAAGCTGACAGAGCTGAAGAGCACACAGCCGACAGCATCTGACGACACT 240

QY 291 GCCGCTGCTAGTGCATGCGGGAAAAGCCAGCCGAG-ATCCCTGTGCTGGCAGCT 349  
Db 241 GCCGCTGCTAGTGCATGCGGGAAAAGCCAGCCGAGGAGTATCCCTGTGCTGGCAGCT 300  
QY 350 GGTAAACAGCTCCTGAAAGCATATCTGTGCTGAAAGTATCATCAGCTAAATCTCCA 409  
Db 301 GGTAAACAGCTCCTGAAAGCATATCTGTGCTGAAAGTATCATCAGCTAAATCTCCA 360  
QY 410 GCTCAGGTGAAGCCCTGCGCATGACAGAGAGTGTATCAAGATCCCGGAGCAT 469  
Db 361 GCTCAGGTGAAGCCCTGCGCATGACAGAGAGTGTATCAAGATCCCGGAGCAT 420  
QY 470 GGTGCTGATTAACAAGCCCTGCTGTCAGAGACCATGCTGGAAGTTCCACATGAGACTGA 529  
Db 421 GGTGCTGATTAACAAGCCCTGCTGTCAGAGACCATGCTGGAAGTTCCACATGAGACTGA 480  
QY 530 GGGCCAAAGCCACATCCGATGACACCATGTCAGAAATGCCCCACCGGCTGTCTCAG 589  
Db 481 GGGCCAAAGCCACATCCGATGACACCATGTCAGAAATGCCCCACCGGCTGTCTCAG 540  
QY 590 TGACTGTGCCACAGCCATGGAGCGCGCATCCAACTGCTGATAGAGTCTCTCTCT 649  
Db 541 TGACTGTGCCACAGCCATGGAGCGCGCATCCAACTGCTGATAGAGTCTCTCTCT 600  
QY 650 GGTAAAGCCTTAGCTAAGAGGTATGATGATGATGATGATGATGATGATGATGATGAT 709  
Db 601 GGTAAAGCCTTAGCTAAGAGGTATGATGATGATGATGATGATGATGATGATGATGAT 660  
QY 710 GAAAACAGCTGTGTGCTGCTGATGAGAGGCTCTCTCAATGATGATGATGATGATGAT 769  
Db 661 GAAAACAGCTGTGTGCTGCTGATGAGAGGCTCTCTCAATGATGATGATGATGATGAT 720  
QY 770 GCAGTGTGAAGGAGCCATTCCTCCATGATGATGATGATGATGATGATGATGATGATGAT 829  
Db 721 GCAGTGTGAAGGAGCCATTCCTCCATGATGATGATGATGATGATGATGATGATGATGAT 780  
QY 830 TCCTGCCATCAAGGAGTGCACATTCAGCTTACCTGGGGGCAAGTTGTGACTACA 889  
Db 781 TCCTGCCATCAAGGAGTGCACATTCAGCTTACCTGGGGGCAAGTTGTGACTACA 840  
QY 890 GGGAAAGGTGACCAAGTGTCTCAATGATGAGCTTCCCTGACATGCCACCTCGGA 949  
Db 841 GGGAAAGGTGACCAAGTGTCTCAATGATGAGCTTCCCTGACATGCCACCTCGGA 900  
QY 950 CAACATCCGTTACGCGCTATGAGTGCAGAGAGTGTGAAGTGCAGAGCTGCTCT 1009  
Db 901 CAACATCCGTTACGCGCTATGAGTGCAGAGAGTGTGAAGTGCAGAGCTGCTCT 960  
QY 1010 GCTCTCTCCAGAAAGTATCATGCTGCTGTTGACTGCTGCTGCTGCTGCTGCTGCTGCT 1069  
Db 961 GCTCTCTCCAGAAAGTATCATGCTGCTGTTGACTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
QY 1070 GCTGAAGTCAAGCATGGGCTGATCATGAAAGGCTCAATAGCTGGGATTCACCA 1129  
Db 1021 GCTGAAGTCAAGCATGGGCTGATCATGAAAGGCTCAATAGCTGGGATTCACCA 1080  
QY 1130 GATCGTGAAGTCCATGATGAGACATCCGAGTTTATGACCAAGGCAATGCCAA 1189  
Db 1081 GATCGTGAAGTCCATGATGAGACATCCGAGTTTATGACCAAGGCAATGCCAA 1140  
QY 1190 GGTGGCCCACTGATGCTGGAAGTGTTCCTCCAGTGAAGCCCTCCGCTTGT 1249  
Db 1141 GGTGGCCCACTGATGCTGGAAGTGTTCCTCCAGTGAAGCCCTCCGCTTGT 1200  
QY 1250 CACCTTGAGCATGCAAGGCTGGAAGTCAAGTTTACCAAGGATGACCAATAT 1309  
Db 1201 CACCTTGAGCATGCAAGGCTGGAAGTCAAGTTTACCAAGGATGACCAATAT 1260  
QY 1310 ACTCAACTTGAATTAACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1369  
Db 1261 ACTCAACTTGAATTAACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320

```

QY 1370 GTTCCAACTGATGTTCTGAAAAACATCATCTGATCATCCATCCATCCTGCTGCC 1429
    |||||||
Db 1321 GTTCCAACTGATGTTCTGAAAAACATCATCTGATCATCCATCCATCCTGCTGCC 1380
    |||||||
QY 1430 GAACCAAGATGGCAATTAAATCTGGGGTCCAGTGTCTGTTGGTGAAGGCTTGGATT 1489
    |||||||
Db 1381 GAACCAAGATGGCAATTAAATCTGGGGTCCAGTGTCTGTTGGTGAAGGCTTGGATT 1440
    |||||||
QY 1490 CGAGGAGCTGAGTCTCTACTGACCAAGATGCGCTTGTCTTACTCCAGCCCTCTTGG 1549
    |||||||
Db 1441 CGAGGAGCTGAGTCTCTACTGACCAAGATGCGCTTGTCTTACTCCAGCCCTCTTGG 1500
    |||||||
QY 1550 GAAACCCAGCTCTCTCTCTCCAGTGAAGACTTGGATGGACCCATCAGGAAGGCTGG 1609
    |||||||
Db 1501 GAAACCCAGCTCTCTCTCTCCAGTGAAGACTTGGATGGACCCATCAGGAAGGCTGG 1560
    |||||||
QY 1610 GTCCCACTGGGAGTATGGGTGTGAGCTCTATAGACATCCCTCTCTGCATCAATAAAC 1669
    |||||||
Db 1561 GTCCCACTGGGAGTATGGGTGTGAGCTCTATAGACATCCCTCTCTGCATCAATAAAC 1620
    |||||||
QY 1670 ACTTGCTGTG 1680
    |||||||
Db 1621 ACTTGCTGTG 1631
    |||||||

```

## RESULT 11

ACAS8848  
ID ACAS8848 standard; cDNA; 1636 BP.

ACAS8848;

10-JUN-2003 (first entry)

CDNA encoding human secreted polypeptide PRO1357.

Human; ss; gene; gene therapy; tumour; cancer.

OS Homo sapiens.

PN US2003013855-A1.

PD 16-JAN-2003.

PF 03-MAY-2002; 2002US-0063616.

PR 30-DEC-1998; 98KR-0062142.

PR 08-MAR-1999; 99WO-US05028.

PR 14-MAY-1999; 99WO-US10733.

PR 30-DEC-1999; 99WO-US31274.

PR 18-FEB-2000; 2000WO-US04341.

PR 01-MAR-2000; 2000WO-US05601.

PR 02-MAR-2000; 2000WO-US05841.

PR 21-MAR-2000; 2000WO-US07532.

PR 22-MAY-2000; 2000WO-US14042.

PR 02-JUN-2000; 2000WO-US15264.

PR 24-AUG-2000; 2000WO-US23328.

PR 10-NOV-2000; 2000WO-US30873.

PR 01-DEC-2000; 2000WO-US32678.

PR 20-DEC-2000; 2000WO-US34956.

PR 28-FEB-2001; 2001WO-US06520.

PR 01-JUN-2001; 2001WO-US17800.

PR 14-MAY-1999; 99US-0311832.

PR 25-AUG-1999; 99US-0380137.

PR 25-AUG-1999; 99US-0380138.

PR 25-AUG-1999; 99US-0380139.

PR 25-AUG-1999; 99US-0380142.

PR 15-SEP-1999; 99US-0397342.

PR 18-OCT-1999; 99US-0403297.

PR 12-NOV-1999; 99US-0423844.

PR 22-AUG-2000; 2000US-0644848.

PR 18-SEP-2000; 2000US-0664610.

PR 18-SEP-2000; 2000US-0665350.

PR 08-NOV-2000; 2000US-0709238.

```

PR 20-DEC-2000; 2000US-0747259.
PR 22-MAR-2001; 2001US-0816744.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 30-MAY-2001; 2001US-0870574.
PR 05-JUN-2001; 2001US-0874503.
PR 29-JUN-2001; 2001US-0869599.
PR 18-JUL-2001; 2001US-0908827.
PR 06-DEC-2001; 2001US-0006867.

```

(GENTH) GENENTECH INC.  
Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ,  
Grimaldi JC, Gurney AL, Matanabe CK, Wood WI,  
WPI: 2003-330485/31.  
P-PSDB; AB071544.

New isolated antibody specifically binding a PRO polypeptide, useful for the preparation of a medicament for treating disorders with the aberrant expression or activity of the PRO polypeptide, such as tumor conditions and cancer.

Example 4; Page 145-146; 406pp; English.

The invention relates to an antibody that binds to a polypeptide with a fully defined sequence given in the specification. The methods and compositions (containing antibodies that specifically bind a PRO polypeptide) of the present invention are useful for the preparation of a medicament for the treatment of disorders associated with the aberrant expression or activity of the PRO polypeptide, such as tumour conditions and cancer. They can also be used to generate transgenic or knockout animals useful in the development and screening of therapeutically useful reagents. The PRO polypeptides and encoding nucleic acids can be used as molecular weight markers for protein electrophoresis, chromosome identification and tissue typing. The PRO polypeptides are useful to induce angiogenesis e.g. wound healing; in the treatment of sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis; diabetes; hyperinsulinaemia and hypoinsulinaemia. The CC antibodies may be used in various diagnostic, competitive binding and/or immunoprecipitation assays. The present sequence represents a cDNA encoding a PRO polypeptide of the invention.

Sequence 1636 BP; 374 A; 492 C; 411 G; 359 T; 0 other;

Query Match 96.2%; Score 1617; DB 25; Length 1636;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1628; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

```

QY 51 GRGAGCGGGCGGAGACTCCAGCTGCGGCAATCTGCACTTCTGCTGCTCT 110
    |||||||
Db 1 GAGGAGCGGGCGGAGACTCCAGCTGCGGCAATCTGCACTTCTGCTGCTCT 60
    |||||||
QY 111 GACACCTGGGAAGATGGCGCGCGGAGACCTCACCTCTCTGTTGGTTGGCGAG 170
    |||||||
Db 61 GACACCTGGGAAGATGGCGCGCGGAGACCTCACCTCTCTGTTGGTTGGCGAG 120
    |||||||
QY 171 CACCTTGATCAAGCAGCAGCTCAGTCCACTGCAATCTCATCTCGGCCCAAAAGTCAT 230
    |||||||
Db 121 CACCTTGATCAAGCAGCAGCTCAGTCCACTGCAATCTCATCTCGGCCCAAAAGTCAT 180
    |||||||
QY 231 CAAAGAAAAGCTGACACAGAGCTGAAGAGCACAAGCCAGCAGATCTTGAGCAGCT 290
    |||||||
Db 181 CAAAGAAAAGCTGACACAGAGCTGAAGAGCACAAGCCAGCAGATCTTGAGCAGCT 240
    |||||||
QY 291 GCCGCTGCTCAGTCCATGCGGGAAGAACAGCCAGCGAGG-ATCCGTGCTGGCGAGCT 349
    |||||||
Db 241 GCCGCTGCTCAGTCCATGCGGGAAGAACAGCCAGCGAGGATCCGTGCTGGCGAGCT 300
    |||||||
QY 350 GGTGAACACCGTCTCTGAGCAGATCATCTGCTGAAGAGTATCAGAGCTAATCTCTCA 409
    |||||||
Db 301 GGTGAACACCGTCTCTGAGCAGATCATCTGCTGAAGAGTATCAGAGCTAATCTCTCA 360
    |||||||

```

```

OY 410 GCTGAGGTGAAGCCCTGGCCCAATGACCAGAGCTGCTAGTCAAGATCCCTGGACAT 469
    |||
Db 361 GCTGAGGTGAAGCCCTGGCCCAATGACCAGAGCTGCTAGTCAAGATCCCTGGACAT 420
OY 470 GGTGCTGATTAACAACAGCCCTGGTCAAGACATCGTGGAGTCCACATAGACATGA 529
    |||
Db 421 GGTGCTGATTAACAACAGCCCTGGTCAAGACATCGTGGAGTCCACATAGACATGA 480
OY 530 GGCCCAAGCCACATCCGATGAGACACAGTGAAGTGGCCACCCGCTGGTCTAG 589
    |||
Db 481 GGCCCAAGCCACATCCGATGAGACACAGTGAAGTGGCCACCCGCTGGTCTAG 540
OY 590 TGACTGTCCACACGCCATGGAGGCTCCGATCCACTGCTGATTAAGTCTCTCTCT 649
    |||
Db 541 TGACTGTCCACACGCCATGGAGGCTCCGATCCACTGCTGATTAAGTCTCTCTCT 600
OY 650 GGTGAAGCCTTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 709
    |||
Db 601 GGTGAAGCCTTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 660
OY 710 GAAAAACGAGTGTGTCCGATGATGAGGCTTCTTCAATGAGCATGATGAGACCTCT 769
    |||
Db 661 GAAAAACGAGTGTGTCCGATGATGAGGCTTCTTCAATGAGCATGATGAGACCTCT 720
OY 770 GCAGCTGTTGAAGTGGCCCATTTCCCTCAGACATTGACCTGTGAGCTTCTGTA 829
    |||
Db 721 GCAGCTGTTGAAGTGGCCCATTTCCCTCAGACATTGACCTGTGAGCTTCTGTA 780
OY 830 TCTGTCCATCAAGGGTGAACACATTCAGCTCTACCTGGGGGCAAGTGTGGACTGCA 889
    |||
Db 781 TCTGTCCATCAAGGGTGAACACATTCAGCTCTACCTGGGGGCAAGTGTGGACTGCA 840
OY 890 GGGAAAGGTGAACAAAGTGTCAATMACTGACAGTTCCTTGACATGCCACCTGGA 949
    |||
Db 841 GGGAAAGGTGAACAAAGTGTCAATMACTGACAGTTCCTTGACATGCCACCTGGA 900
OY 950 CAACATCCCGTTCAGCCCTCATCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1009
    |||
Db 901 CAACATCCCGTTCAGCCCTCATCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 960
OY 1010 GCTCTCTCCAGAAAGTTCATGTCCTGTGAGTCTGTGAGTCTGTGAGTCTGTGAGT 1069
    |||
Db 961 GCTCTCTCCAGAAAGTTCATGTCCTGTGAGTCTGTGAGTCTGTGAGTCTGTGAGT 1020
OY 1070 GCTGAAGTCAAGCATCGGGCTGATCAATGAAAAAGGCTCAGATTAAGTGGATCAACCA 1129
    |||
Db 1021 GCTGAAGTCAAGCATCGGGCTGATCAATGAAAAAGGCTCAGATTAAGTGGATCAACCA 1080
OY 1130 GATCGTGAAGTTCCTAATCTAGAGACATCCGAGTCTTTTATAGACCAAGGCCATGCCAA 1189
    |||
Db 1081 GATCGTGAAGTTCCTAATCTAGAGACATCCGAGTCTTTTATAGACCAAGGCCATGCCAA 1140
OY 1190 GGTGGCCCAATGATCGTGTGAAGTGTTCCTCCAGTGAAGCCCTCCGCTTGTGT 1249
    |||
Db 1141 GGTGGCCCAATGATCGTGTGAAGTGTTCCTCCAGTGAAGCCCTCCGCTTGTGT 1200
OY 1250 CACCCTGGGATCGAAGCCAGCTGGAAGCTCAAGTTTACACCAAGGTGACCAATTAT 1309
    |||
Db 1201 CACCCTGGGATCGAAGCCAGCTGGAAGCTCAAGTTTACACCAAGGTGACCAATTAT 1260
OY 1310 ACTCAACTGTAATTAACATCAGCTCTGATCGAGTCCAGTGAAGTGGATGGGTG 1369
    |||
Db 1261 ACTCAACTGTAATTAACATCAGCTCTGATCGAGTCCAGTGAAGTGGATGGGTG 1320
OY 1370 GTTCCAACTGATGTCTGAAAAAATCATCATGATGATGATGATGATGATGATGATGAT 1429
    |||
Db 1321 GTTCCAACTGATGTCTGAAAAAATCATCATGATGATGATGATGATGATGATGATGAT 1380
OY 1430 GAACCCAGATGCAAAATTAAGATCTGGGGTCCCAAGTGTCAATGGTGAAGGCTTGGGAT 1489
    |||
Db 1381 GAACCCAGATGCAAAATTAAGATCTGGGGTCCCAAGTGTCAATGGTGAAGGCTTGGGAT 1440
OY 1490 CGAGGAGCTGAGTCTCTCACTGACCAAGGATGCCCTTGTCTTACTCCAGCCCTCTTGTG 1549

```

```

Db 1441 CGAGCAGCTGAGTCTCTCACTGACCAAGAGTCCCTTGTGTTACTCAGCCTCTGTG 1500
OY 1550 GAAACCCAGCTCTCTGCTCTCCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1609
    |||
Db 1501 GAAACCCAGCTCTCTGCTCTCCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1560
OY 1610 GTCCAGCTGGAGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1669
    |||
Db 1561 GTCCAGCTGGAGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1620
OY 1670 ACTTGCCTGTG 1680
    |||
Db 1621 ACTTGCCTGTG 1631
    |||

RESULT 12
ACA60401
ID ACA60401 standard; cDNA; 1636 BP.
XX
XX ACA60401;
AC
XX
XX
DT 11-JUN-2003 (first entry)
DE
XX
XX Novel human secreted and transmembrane protein PRO1357 cDNA.
KW Human; secreted and transmembrane polypeptide; gene: ss.
KW chromosome mapping; gene mapping; transgenic animal; knockout animal;
KW therapeutic agent screening; chromosome identification; tissue typing;
KW gene therapy.
XX
XX Homo sapiens.
OS
XX
XX US2003018183-A1.
PN
XX
XX 23-JAN-2003.
PD
XX
XX 01-MAY-2002; 2002US-0063512.
PF
XX
XX 06-DEC-2001; 2001US-0006867.
PR
XX
XX (GETH ) GENENTECH INC.
PA
XX
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WJ.
PT WPT: 2003-330984/31.
XX
XX P-PSDB: AB071990.
XX
XX New secreted and transmembrane PRO polypeptides and nucleic acid
PT molecules encoding the polypeptides, useful in gene therapy or
PT preparing a medicament for treating a condition that is responsive to
PT the PRO polypeptide or antibody.
XX
XX Disclosure: Fig 77; 409pp; English.
XX
XX The invention describes novel isolated PRO polypeptides. The PRO
XX polypeptides or anti-PRO antibodies are useful in preparing a medicament
XX for treating a condition that is responsive to the PRO polypeptide or
XX antibody. The PRO nucleotide sequences may be used as hybridisation
XX probes in chromosome and gene mapping, or in generating antisense RNA
XX and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides,
XX in assays to identify other proteins or molecules involved in binding
XX reaction, to generate transgenic animals or knockout animals, which in
XX turn are useful in the development and screening of therapeutically
XX useful reagents, for chromosome identification, and tissue typing. The
XX PRO polypeptides and nucleic acid molecules are also useful in gene
XX therapy, and as molecular weight markers for protein electrophoresis
XX purposes. The anti-PRO antibodies may be used in diagnostic assays for
XX PRO, or for the affinity purification of PRO from recombinant cell
XX culture or natural sources. This sequence encodes a novel human
XX secreted and transmembrane PRO polypeptide.

```

Sequence 1636 BP; 374 A; 492 C; 411 G; 359 T; 0 other;

Query Match 96.28; Score 1617; DB 25; Length 1636;  
 Best Local Similarity 99.88; Pred. No. 0;  
 Matches 1628; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

```

QY 51 GGGAGGCGGCGGAGAGCTCCAGCGTCCAGGCTCTGGCATCTGCACTTGTGCCCTCT 110
   1 GAGAGAGGCGGCGGAGAGCTCCAGCGTCCAGGCTCTGGCATCTGCACTTGTGCCCTCT 60
QY 111 GAAACCTGGGAATAGGCGCGCGCGGTGAGCTTACCCCTCTCTGTGTGTGTGTGTGT 170
   61 GAAACCTGGGAATAGGCGCGCGCGGTGAGCTTACCCCTCTCTGTGTGTGTGTGTGT 120
QY 171 CACCTTGATCAAGCCACCTCAGTCCAGTTCATCTCATCTCTGCGCCCAAAAGTCAT 230
   121 CACCTTGATCAAGCCACCTCAGTTCATCTCATCTCTGCGCCCAAAAGTCAT 180
QY 231 CAAAGAAAAGCTGACACAGAGCTGAAAGACCAACAGCCACAGCATCTGACAGAGT 290
   181 CAAAGAAAAGCTGACACAGAGCTGAAAGACCAACAGCCACAGCATCTGACAGAGT 240
QY 291 GCGGCTGCTAGGCGCATGCGGGGAAAAGCGCCGAGAG - ATCCCTGTGCTGGGACGCT 349
   241 GCGGCTGCTAGGCGCATGCGGGGAAAAGCGCCGAGAGCATCTCTGTGTGTGTGTGT 300
QY 350 GGTGAACACCGCTCCTGAAGACATCATCTGGTGAAGGTATCATCAGCTAAATCTCCA 409
   301 GGTGAACACCGCTCCTGAAGACATCATCTGGTGAAGGTATCATCAGCTAAATCTCCA 360
QY 410 GTTGCAAGTGAAGCCCTGCGCCAAATGACACAGAGCTGTATGTCAMAGATCCCTGACAT 469
   361 GTTGCAAGTGAAGCCCTGCGCCAAATGACACAGAGCTGTATGTCAMAGATCCCTGACAT 420
QY 470 GGTGGCTGATGTAACACGCGCCCGTGTCAAGACCATGTTGAAGTTCACATGACAGATGA 529
   421 GGTGGCTGATGTAACACGCGCCCGTGTCAAGACCATGTTGAAGTTCACATGACAGATGA 480
QY 530 GGGCCAAAGCCACCATCCGATGAGACACAGTGAAGTGGCCCAACCCGCTGTGTCTGAG 589
   481 GGGCCAAAGCCACCATCCGATGAGACACAGTGAAGTGGCCCAACCCGCTGTGTCTGAG 540
QY 590 TGAATGTGCAACACCATGAGGACCTGCGCATCTCAACTGTGATTAAGCTCTCTCTCT 649
   541 TGAATGTGCAACACCATGAGGACCTGCGCATCTCAACTGTGATTAAGCTCTCTCTCT 600
QY 650 GGTGAAGCGCTTGAAGGATGATGAACCTCTGTGCAATCCCTGGCCAAATCTAGT 709
   601 GGTGAAGCGCTTGAAGGATGATGAACCTCTGTGCAATCCCTGGCCAAATCTAGT 660
QY 710 GAAAAACACAGCTGTGTCCTGTATCGAGGCTTCTTCAATGAGATGTATGACAGCTCT 769
   661 GAAAAACACAGCTGTGTCCTGTATCGAGGCTTCTTCAATGAGATGTATGACAGCTCT 720
QY 770 GCAAGCTGTGAAGGTGCGCAATTTCCCTCAGCATTTGAGAGTTTGAACCTTCTGTA 829
   721 GCAAGCTGTGAAGGTGCGCAATTTCCCTCAGCATTTGAGAGTTTGAACCTTCTGTA 780
QY 830 TCCGGCCATCAAGGGTGAACACATTCAGCTCTACCTGCGGGGCGCAAGTTGTGTGACATACA 889
   781 TCCGGCCATCAAGGGTGAACACATTCAGCTCTACCTGCGGGGCGCAAGTTGTGTGACATACA 840
QY 890 GGGAAAGGTGACCAAGTGTTCATAATTAATCTGCAAGTTCCTCTGACATGCCCAACCTTGA 949
   841 GGGAAAGGTGACCAAGTGTTCATAATTAATCTGCAAGTTCCTCTGACATGCCCAACCTTGA 900
QY 950 CAACATCCGCTTACAGCTCATCTGTAGTCAAGAGCTGTGAAGCTGCAAGTGTGCTGTCT 1009
   901 CAACATCCGCTTACAGCTCATCTGTAGTCAAGAGCTGTGAAGCTGCAAGTGTGCTGTCT 960
QY 1010 GCTCTCCAGGAAGATTAATGAGCTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1069
   961 GCTCTCCAGGAAGATTAATGAGCTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020

```

```

QY 1070 GCTGAAGTCAAGCATCGGCGTATCATGAAAGAGCTGCAGATTAAGCTGGGATATACCA 1129
   1021 GCTGAAGTCAAGCATCGGCGTATCATGAAAGAGCTGCAGATTAAGCTGGGATATACCA 1080
QY 1130 GATCGTGAAGATCTTAATCAAGGACACTCCGAGTTTATATAGACCAAGGCCATGCGCA 1189
   1081 GATCGTGAAGATCTTAATCAAGGACACTCCGAGTTTATATAGACCAAGGCCATGCGCA 1140
QY 1190 GGTGGCCCAATCATGCTGTGAGAGTGTTCCTCCAGTGAAGCCCTCCGCCCTTGTGT 1249
   1141 GGTGGCCCAATCATGCTGTGAGAGTGTTCCTCCAGTGAAGCCCTCCGCCCTTGTGT 1200
QY 1250 CACCTGGGATGGAAGCCAGCTCGGAAGCTAGTTTAAACCAAAAGGTAGCAACTTAT 1309
   1201 CACCTGGGATGGAAGCCAGCTCGGAAGCTAGTTTAAACCAAAAGGTAGCAACTTAT 1260
QY 1310 ACTCACTGAATTAATCAATCAAGCTGTATGCGATCCAGCTAGTAAATCTGAGATTGCTG 1369
   1261 ACTCACTGAATTAATCAATCAAGCTGTATGCGATCCAGCTAGTAAATCTGAGATTGCTG 1320
QY 1370 GTTCCAACTGATGTGTGAAAAATCATCATGATGATCATCATCATCATCATCATCATCAT 1429
   1321 GTTCCAACTGATGTGTGAAAAATCATCATGATGATCATCATCATCATCATCATCATCAT 1380
QY 1430 GAACCAAGATGCGAAATTAAGATCTGGGCTCCAGTGTCAATGTGTAAGGCTTGGGAT 1489
   1381 GAACCAAGATGCGAAATTAAGATCTGGGCTCCAGTGTCAATGTGTAAGGCTTGGGAT 1440
QY 1490 CGAGGAGCTGAGTCTCTCACTGACCAAGATGCTTGTGTCTTACTCTCAAGCTCTTGTG 1549
   1441 CGAGGAGCTGAGTCTCTCACTGACCAAGATGCTTGTGTCTTACTCTCAAGCTCTTGTG 1500
QY 1550 GAAACCCAGCTGCTGTCTCCAGTGAAGACTGTGATGAGAGGACATCAGGGAAGGCTGG 1609
   1501 GAAACCCAGCTGCTGTCTCCAGTGAAGACTGTGATGAGAGGACATCAGGGAAGGCTGG 1560
QY 1610 GTCCACAGCTGAGATGAGGTGTGAGCTCTATAGACATCCCTCTGCAATCAATTAAC 1669
   1561 GTCCACAGCTGAGATGAGGTGTGAGCTCTATAGACATCCCTCTGCAATCAATTAAC 1620
QY 1670 ACTTGCTGTG 1680
   1621 ACTTGCTGTG 1631
Db

```

RESULT 13  
 ACA63411  
 ID ACA63411 standard; cDNA; 1636 BP.  
 XX  
 AC ACA63411;  
 XX  
 DT 13-JUN-2003 (first entry)  
 XX  
 DE cDNA encoding human PRO polypeptide #39.  
 XX  
 DE Human; PRO polypeptide; secreted and transmembrane protein;  
 KW anti-PRO antibody; diagnostic assay; gene expression; gene; ss.  
 OS Homo sapiens.  
 XX  
 PN US2003023042-A1.  
 XX  
 PD 30-JAN-2003.  
 XX  
 PF 01-MAY-2002; 2002US-0063502.  
 XX  
 PR 06-DEC-2001; 2001US-0006867.  
 XX  
 PA (GENTECH ) GENENTECH INC.  
 XX  
 PI Eaton DL, Flivaroff E, Gerritsen ME, Goddard A, Godowski PJ;  
 Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

XX WPI: 2003-331484/31.  
DR P-PSDB: AB07147.  
XX Novel monoclonal antibody that binds to secreted and transmembrane  
PT polypeptide, useful for detecting and purifying the polypeptide and  
PT also for treating conditions responsive to the antibody.  
XX Disclosure: Fig 77: 408pp; English.  
XX The present invention relates to the isolation of novel human PRO  
CC polypeptides, and the polynucleotide sequences encoding them. The  
CC PRO polypeptides are secreted and transmembrane proteins. The PRO  
CC polypeptides and polynucleotides are useful for preparing a  
CC medicament useful in the treatment of a condition responsive to  
CC anti-PRO antibody. Anti-PRO antibodies are useful in diagnostic  
CC assays for PRO, by detecting its expression in specific cells,  
CC tissues or serum, and for affinity purification of PRO from  
CC recombinant cell culture or natural sources. ACA63373-ACA63456  
CC represent cDNA sequences encoding the human PRO polypeptides of  
CC the invention.  
XX  
XX Sequence 1636 BP; 374 A; 492 C; 411 G; 359 T; 0 other;  
SQ  
Query Match 96.28; Score 1617; DB 25; Length 1636;  
Best Local Similarity 99.88; Pred. No. 0;  
Matches 1628; Conservative 1; Mismatches 1; Indels 1; Gaps 1;  
51 GRGAGACGGGCGGAGACTCCAGCTGAGCCAGGTGAGTCTGGACTTGGTCCCTCT 110  
1 GAGAGACGGGCGGAGACTCCAGCTGAGCCAGGTGAGTCTGGACTTGGTCCCTCT 60  
111 GACACCTGGGAGAGATGGCGGCGGCGGTGAGCTTACACCTTCTGTGGTTGGTGAGC 170  
61 GACACCTGGGAGAGATGGCGGCGGCGGTGAGCTTACACCTTCTGTGGTTGGTGAGC 120  
171 CACCTTGATCCAGGCCACCTCTAGTCCCACTGCAATTTCTATCTGGGCCCAAAAGTCAT 230  
121 CACCTTGATCCAGGCCACCTCTAGTCCCACTGCAATTTCTATCTGGGCCCAAAAGTCAT 180  
231 CAAGAAGAGCTGACACAGAGAGTGAAGAGCAACAGCCACAGCATCTCTGAGAGCT 290  
181 CAAGAAGAGCTGACACAGAGAGTGAAGAGCAACAGCCACAGCATCTCTGAGAGCT 240  
291 GCCGTGCTCAGTGCATGCGGAGGAAAAAGCCAGCGAGG-ATCCCTGTGCTGGAGACT 349  
241 GCCGTGCTCAGTGCATGCGGAGGAAAAAGCCAGCGAGGATCCCTGTGCTGGAGACT 300  
350 GGTGAACACGCTGCTGAGACATCATCTGCTGGAAGGTGATCAAGCTTAACATCTCCCA 409  
301 GGTGAACACGCTGCTGAGACATCATCTGCTGGAAGGTGATCAAGCTTAACATCTCCCA 360  
410 GCTGACGTGTAACCCCTCGGCCAATGACAGAGAGTCTAGTCAAGTATCCCTGAGCAT 469  
361 GCTGACGTGTAACCCCTCGGCCAATGACAGAGAGTCTAGTCAAGTATCCCTGAGCAT 420  
470 GGTGGCTGATTTAACAAGCCCTGCTCAAGACATGCTGAGATTCCATGAAGAGTGA 529  
421 GGTGGCTGATTTAACAAGCCCTGCTCAAGACATGCTGAGATTCCATGAAGAGTGA 480  
530 GGGCCAGAGCAGCATCGGATGAGACACAGTGAAGTGGGCCACCGGCTGTGCTCCAG 589  
481 GGGCCAGAGCAGCATCGGATGAGACACAGTGAAGTGGGCCACCGGCTGTGCTCCAG 540  
590 TGACCTGTGCACACGACCATGAGAGCTGAGCATCAACTGCTGATAGCTCTCTCTCT 649  
541 TGACCTGTGCACACGACCATGAGAGCTGAGCATCAACTGCTGATAGCTCTCTCTCT 600  
650 GGTGAAGCGCTTATGCTAAGAGGTGTAAGAACTCTGATGCTCAATCCCTGCAATCTAGT 709  
601 GGTGAAGCGCTTATGCTAAGAGGTGTAAGAACTCTGATGCTCAATCCCTGCAATCTAGT 660  
710 GAAAAACACAGCTGTGTCGCGTGAATGAGAGCTTCTTCAATGAGATATGACACCTCTCT 769

DB 661 GAAAAACACAGCTGTGTCGCGTGAATGAGAGCTTCTTCAATGAGATATGACACCTCTCT 720  
OY 770 GCAAGCTGTGAGAGTGGCCATTCCCTCAGCATTTGACAGCTGGAGTTGACCTTCTGTA 829  
DB 721 GCAAGCTGTGAGAGTGGCCATTCCCTCAGCATTTGACAGCTGGAGTTGACCTTCTGTA 780  
OY 830 TCCCTGCATCAAGGAGTGCACCAATTCAGCTCTGAGAGTGGAGTGGAGTGGAGTGCACA 889  
DB 781 TCCCTGCATCAAGGAGTGCACCAATTCAGCTCTGAGAGTGGAGTGGAGTGGAGTGCACA 840  
OY 890 GGGAAAGGTGACCAAGTGTTCATTAATCTGACAGTTCCTGCAATGCGCCACCTGGA 949  
DB 841 GGGAAAGGTGACCAAGTGTTCATTAATCTGACAGTTCCTGCAATGCGCCACCTGGA 900  
OY 950 CAACATCCGTTGACGCTCATCGAGTGCAGAGAGTGGTGAAGTGCAGTGGTGTCT 1009  
DB 901 CAACATCCGTTGACGCTCATCGAGTGCAGAGAGTGGTGAAGTGCAGTGGTGTCT 960  
OY 1010 GCTCTCTCAGAGAAATTCATGCTCTGTTGAGACTGTGCTCTCTGAGAGTGGCCATCG 1069  
DB 961 GCTCTCTCAGAGAAATTCATGCTCTGTTGAGACTGTGCTCTCTGAGAGTGGCCATCG 1020  
OY 1070 GCTGAAGTCAAGCATGCGGCTGATCAATGAAGAGCTGCAAGATGAGTGGATTCACCA 1129  
DB 1021 GCTGAAGTCAAGCATGCGGCTGATCAATGAAGAGCTGCAAGATGAGTGGATTCACCA 1080  
OY 1130 GATCGTAAGATCTTAATCTGAGGACATCCCGAGTTTATATGACCAAGGCCATGCGCA 1189  
DB 1081 GATCGTAAGATCTTAATCTGAGGACATCCCGAGTTTATATGACCAAGGCCATGCGCA 1140  
OY 1190 GGTGGGCCCAATGATGCTGTGAGAGTGTTCCTCCAGTGAAGACCTCCGCCCTTGT 1249  
DB 1141 GGTGGGCCCAATGATGCTGTGAGAGTGTTCCTCCAGTGAAGACCTCCGCCCTTGT 1200  
OY 1250 CACCTTGGGATGTAAGCCAGCTGCGAGTCACTTTTACACCAAGGTGACCAACTTAT 1309  
DB 1201 CACCTTGGGATGTAAGCCAGCTGCGAGTCACTTTTACACCAAGGTGACCAACTTAT 1260  
OY 1310 ACTCAACTGTAATTAATCAATGAGCTGTGATGAGATCCAGTGAATGAACTGGAGTGGCTG 1369  
DB 1261 ACTCAACTGTAATTAATCAATGAGCTGTGATGAGATCCAGTGAATGAACTGGAGTGGCTG 1320  
OY 1370 GTTCCAACTGATGTTCTGAAAAAATCATCACTGAGATATCCATCTGCTGCTGCC 1429  
DB 1321 GTTCCAACTGATGTTCTGAAAAAATCATCACTGAGATATCCATCTGCTGCTGCC 1380  
OY 1430 GAACCAAGAAATGGCAAAATTAAGATCTGGGATCCAGTGTCAATTGGTGAAGGCTTGGGATT 1489  
DB 1381 GAACCAAGAAATGGCAAAATTAAGATCTGGGATCCAGTGTCAATTGGTGAAGGCTTGGGATT 1440  
OY 1490 CGAGGACAGTGAATCTCAGTACAGCAAGATGACCTTGTCTTACTCAGACCTCTCTGTG 1549  
DB 1441 CGAGGACAGTGAATCTCAGTACAGCAAGATGACCTTGTCTTACTCAGACCTCTCTGTG 1500  
OY 1550 GAAACCCAGCTCTCTGCTCTCCAGTGAAGACTTGAAGTGGACGACATCAGGGAAGGCTGG 1609  
DB 1501 GAAACCCAGCTCTCTGCTCTCCAGTGAAGACTTGAAGTGGACGACATCAGGGAAGGCTGG 1560  
OY 1610 GTCCAGCTGGGAGTATGAGTGTGAGCTCTATAGACATATCCCTCTCTGCAATCAATTAAC 1669  
DB 1561 GTCCAGCTGGGAGTATGAGTGTGAGCTCTATAGACATATCCCTCTCTGCAATCAATTAAC 1620  
OY 1670 ACTTGGCTGTG 1680  
DB 1621 ACTTGGCTGTG 1631  
RESULT 14  
ABX98292  
ID ABX98292 standard; cDNA; 1636 BP.  
XX  
AC ABX98292;



XX 19-MAY-2003 (first entry)  
 DT Human cDNA encoding a secreted/transmembrane protein, SEQ ID 279.  
 DE  
 XX Human, ss; gene; PRO; secreted protein; transmembrane protein;  
 XX cytoskeletal; antiarthritic; osteopathic; adrenal tumour; lung tumour;  
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;  
 KW cervical tumour; liver tumour; TNF-alpha release; arthritis;  
 KW tumour necrosis factor alpha; chondrocyte cell; bone disorder;  
 KW cartilage disorder; sports injury.  
 OS Homo sapiens.  
 XX US2003036156-A1.  
 PN  
 XX 20-FEB-2003.  
 PD  
 XX 02-JUL-2002; 2002US-0186767.  
 PF  
 XX 16-SEP-1998; 98WO-US19330.  
 PR 07-OCT-1998; 98WO-US21141.  
 PR 01-DEC-1998; 98WO-US25108.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 14-MAY-1999; 99WO-US10733.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-JUN-2001; 2001WO-US17800.  
 PR 20-JUN-2001; 2001WO-US19692.  
 PR 29-JUN-2001; 2001WO-US21066.  
 PR 09-JUL-2001; 2001WO-US21735.  
 PR 29-AUG-2001; 2001WO-US27099.  
 PR 18-SEP-1997; 97US-059263P.  
 PR 18-SEP-1997; 97US-059266P.  
 PR 17-OCT-1997; 97US-062250P.  
 PR 21-OCT-1997; 97US-063486P.  
 PR 24-OCT-1997; 97US-063120P.  
 PR 24-OCT-1997; 97US-063121P.  
 PR 28-OCT-1997; 97US-063540P.  
 PR 28-OCT-1997; 97US-063541P.  
 PR 28-OCT-1997; 97US-063544P.  
 PR 28-OCT-1997; 97US-063564P.  
 PR 29-OCT-1997; 97US-063734P.  
 PR 31-OCT-1997; 97US-063870P.  
 PR 31-OCT-1997; 97US-064103P.  
 PR 13-NOV-1997; 97US-065311P.  
 PR 21-NOV-1997; 97US-066120P.  
 PR 24-NOV-1997; 97US-066466P.  
 PR 11-DEC-1997; 97US-066772P.  
 PR 97US-069335P.

PR 12-DEC-1997; 97US-069425P.  
 PR 17-DEC-1997; 97US-069870P.  
 PR 18-DEC-1997; 97US-068017P.  
 PR 10-MAR-1998; 98US-077450P.  
 PR 11-MAR-1998; 98US-077632P.  
 PR 11-MAR-1998; 98US-077649P.  
 PR 20-MAR-1998; 98US-078886P.  
 PR 20-MAR-1998; 98US-078939P.  
 PR 27-MAR-1998; 98US-079664P.  
 PR 27-MAR-1998; 98US-079786P.  
 PR 31-MAR-1998; 98US-080107P.  
 PR 31-MAR-1998; 98US-080194P.  
 PR 01-APR-1998; 98US-080327P.  
 PR 01-APR-1998; 98US-080333P.  
 PR 08-APR-1998; 98US-081049P.  
 PR 08-APR-1998; 98US-081070P.  
 PR 09-APR-1998; 98US-081195P.  
 PR 15-APR-1998; 98US-081838P.  
 PR 21-APR-1998; 98US-082569P.  
 PR 21-APR-1998; 98US-082569P.  
 PR 22-APR-1998; 98US-082704P.  
 PR 22-APR-1998; 98US-082704P.  
 PR 28-APR-1998; 98US-083322P.  
 PR 29-APR-1998; 98US-083493P.  
 PR 29-APR-1998; 98US-083496P.  
 PR 29-APR-1998; 98US-083499P.  
 PR 29-APR-1998; 98US-083559P.  
 PR 05-MAY-1998; 98US-084366P.  
 PR 06-MAY-1998; 98US-084414P.  
 PR 07-MAY-1998; 98US-084639P.  
 PR 07-MAY-1998; 98US-084640P.  
 PR 07-MAY-1998; 98US-084643P.  
 PR 15-MAY-1998; 98US-085579P.  
 PR 15-MAY-1998; 98US-085580P.  
 PR 15-MAY-1998; 98US-085582P.  
 PR 15-MAY-1998; 98US-085700P.  
 PR 18-MAY-1998; 98US-086023P.  
 PR 22-MAY-1998; 98US-086392P.  
 PR 22-MAY-1998; 98US-086486P.  
 PR 28-MAY-1998; 98US-087098P.  
 PR 28-MAY-1998; 98US-087208P.  
 PR 02-JUN-1998; 98US-087609P.  
 PR 02-JUN-1998; 98US-087759P.  
 PR 03-JUN-1998; 98US-087827P.  
 PR 04-JUN-1998; 98US-088025P.  
 PR 04-JUN-1998; 98US-088028P.  
 PR 04-JUN-1998; 98US-088029P.  
 PR 04-JUN-1998; 98US-088033P.  
 PR 04-JUN-1998; 98US-088326P.  
 PR 05-JUN-1998; 98US-088167P.  
 PR 05-JUN-1998; 98US-088202P.  
 PR 05-JUN-1998; 98US-088212P.  
 PR 05-JUN-1998; 98US-088217P.  
 PR 09-JUN-1998; 98US-088655P.  
 PR 10-JUN-1998; 98US-088722P.  
 PR 10-JUN-1998; 98US-088738P.  
 PR 10-JUN-1998; 98US-088740P.  
 PR 10-JUN-1998; 98US-088811P.  
 PR 10-JUN-1998; 98US-088824P.  
 PR 10-JUN-1998; 98US-088825P.  
 PR 10-JUN-1998; 98US-088826P.  
 PR 11-JUN-1998; 98US-088861P.  
 PR 11-JUN-1998; 98US-088863P.  
 PR 11-JUN-1998; 98US-088876P.  
 PR 12-JUN-1998; 98US-089090P.  
 PR 12-JUN-1998; 98US-089105P.  
 PR 16-JUN-1998; 98US-089512P.  
 PR 16-JUN-1998; 98US-089512P.  
 PR 17-JUN-1998; 98US-089538P.  
 PR 17-JUN-1998; 98US-089598P.  
 PR 17-JUN-1998; 98US-089653P.  
 PR 18-JUN-1998; 98US-089908P.  
 PR 19-JUN-1998; 98US-089952P.



DB 1321 GTTCCAACTGATGTTCTGAAAAACATCACTGATCATCCATCCATCTGCTGCC 1380  
QY 1430 GAACCAAGATGCAATTAAGATCTGGGGTCCCAAGTATATGGGAAGGCTTGGGAT 1489  
DB 1381 GAACCAAGATGCAATTAAGATCTGGGGTCCCAAGTATATGGGAAGGCTTGGGAT 1440  
QY 1490 CGAGCAGCTGAGTCTCCTCACTACCAAGATGCCCCCTTGTCTACTCAGGCTCTGG 1549  
DB 1441 CGAGCAGCTGAGTCTCCTCACTACCAAGATGCCCCCTTGTCTACTCAGGCTCTGG 1500  
QY 1550 GAAACCCAGCTCTCCTCTGCTCCAGTGAAGACTTGGATGGCAGCCATCAAGGAGCTGG 1609  
DB 1501 GAAACCCAGCTCTCCTCTGCTCCAGTGAAGACTTGGATGGCAGCCATCAAGGAGCTGG 1560  
QY 1610 GTCCCAAGCTGGAGTATGGGTGAGCTCTATAGACCATCCCTCTGCAATCAATTAAC 1669  
DB 1561 GTCCCAAGCTGGAGTATGGGTGAGCTCTATAGACCATCCCTCTGCAATCAATTAAC 1620  
QY 1670 ACTTGCTCTGG 1680  
DB 1621 ACTTGCTCTGG 1631

RESULT 15  
ABX98794  
ID ABX98794 standard; cDNA; 1636 BP.  
XX  
AC ABX98794;  
XX  
DT 20-MAY-2003 (first entry)  
XX  
DE Novel human secreted and transmembrane protein PRO1357 cDNA.  
XX  
KW Human; secreted protein; transmembrane protein; cytosolic;  
KW gene therapy; TNF-Agonist-Alpha; chondrocyte stimulator; tumour;  
KW adrenal tumour; lung tumour; colon tumour; breast tumour;  
KW prostate tumour; rectal tumour; cervical tumour; liver tumour;  
KW gene; ss.  
XX  
XX OS Homo sapiens.  
XX  
PN US2003036157-A1.  
XX  
PD 20-FEB-2003.  
XX  
PF 02-JUL-2002; 2002US-0188769.  
XX

PR 16-SEP-1998; 98WO-US19330.  
PR 07-OCT-1998; 98WO-US21141.  
PR 01-DEC-1998; 98WO-US25108.  
PR 08-MAR-1999; 99WO-US05028.  
PR 14-MAY-1999; 99WO-US10733.  
PR 02-JUN-1999; 99WO-US12252.  
PR 01-SEP-1999; 99WO-US20111.  
PR 15-SEP-1999; 99WO-US21090.  
PR 01-DEC-1999; 99WO-US28301.  
PR 02-DEC-1999; 99WO-US28551.  
PR 30-DEC-1999; 99WO-US31274.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04432.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 01-MAR-2000; 2000WO-US05601.  
PR 02-MAR-2000; 2000WO-US05841.  
PR 15-MAR-2000; 2000WO-US06884.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 28-JUN-2000; 2000WO-US20710.  
PR 24-AUG-2000; 2000WO-US23328.

PR 08-NOV-2000; 2000WO-US09552.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-JUN-2001; 2001WO-US17800.  
PR 20-JUN-2001; 2001WO-US19692.  
PR 29-JUN-2001; 2001WO-US21066.  
PR 09-JUL-2001; 2001WO-US21735.  
PR 29-AUG-2001; 2001WO-US27099.  
PR 18-SEP-1997; 97US-059263P.  
PR 18-SEP-1997; 97US-059266P.  
PR 17-OCT-1997; 97US-062250P.  
PR 21-OCT-1997; 97US-063486P.  
PR 24-OCT-1997; 97US-063120P.  
PR 24-OCT-1997; 97US-063121P.  
PR 28-OCT-1997; 97US-063540P.  
PR 28-OCT-1997; 97US-063541P.  
PR 28-OCT-1997; 97US-063544P.  
PR 28-OCT-1997; 97US-063546P.  
PR 29-OCT-1997; 97US-063734P.  
PR 31-OCT-1997; 97US-063870P.  
PR 31-OCT-1997; 97US-064103P.  
PR 13-NOV-1997; 97US-065311P.  
PR 21-NOV-1997; 97US-066120P.  
PR 24-NOV-1997; 97US-066466P.  
PR 11-DEC-1997; 97US-066772P.  
PR 11-DEC-1997; 97US-069335P.  
PR 12-DEC-1997; 97US-069425P.  
PR 17-DEC-1997; 97US-069870P.  
PR 18-DEC-1997; 97US-068017P.  
PR 10-MAR-1998; 98US-077450P.  
PR 11-MAR-1998; 98US-077632P.  
PR 11-MAR-1998; 98US-077649P.  
PR 20-MAR-1998; 98US-078866P.  
PR 20-MAR-1998; 98US-078939P.  
PR 27-MAR-1998; 98US-079664P.  
PR 27-MAR-1998; 98US-079786P.  
PR 31-MAR-1998; 98US-080107P.  
PR 31-MAR-1998; 98US-080194P.  
PR 01-APR-1998; 98US-080337P.  
PR 01-APR-1998; 98US-080333P.  
PR 08-APR-1998; 98US-081049P.  
PR 08-APR-1998; 98US-081070P.  
PR 09-APR-1998; 98US-081195P.  
PR 15-APR-1998; 98US-081838P.  
PR 21-APR-1998; 98US-082568P.  
PR 21-APR-1998; 98US-082569P.  
PR 22-APR-1998; 98US-082704P.  
PR 22-APR-1998; 98US-082797P.  
PR 28-APR-1998; 98US-083322P.  
PR 29-APR-1998; 98US-083495P.  
PR 29-APR-1998; 98US-083496P.  
PR 29-APR-1998; 98US-083499P.  
PR 29-APR-1998; 98US-083559P.  
PR 05-MAY-1998; 98US-084366P.  
PR 06-MAY-1998; 98US-084414P.  
PR 07-MAY-1998; 98US-084639P.  
PR 07-MAY-1998; 98US-084640P.  
PR 15-MAY-1998; 98US-084643P.  
PR 15-MAY-1998; 98US-085579P.  
PR 15-MAY-1998; 98US-085580P.  
PR 15-MAY-1998; 98US-085582P.  
PR 15-MAY-1998; 98US-085700P.  
PR 18-MAY-1998; 98US-086032P.  
PR 22-MAY-1998; 98US-086032P.  
PR 22-MAY-1998; 98US-086486P.  
PR 28-MAY-1998; 98US-087098P.  
PR 28-MAY-1998; 98US-087208P.  
PR 02-JUN-1998; 98US-087609P.  
PR 02-JUN-1998; 98US-087759P.  
PR 03-JUN-1998; 98US-088025P.  
PR 04-JUN-1998; 98US-088026P.



```
Db      901  CAACATCCCGTTCAGCTCATGCTGATGACGACGTGATGAAGCTGCATGGCTGCTGT  960
QY      1010  GCTCTCTCCAGAAAGATTCATGTCCTGTGGACTCTGTGCTTCTGTGAGTGGCCATCG  1069
Db      961  GCTCTCTCCAGAAAGATTCATGTCCTGTGGACTCTGTGCTTCTGTGAGTGGCCATCG  1020
QY      1070  GCTGAAGTCAAGCATCGGGCTGATCATGAAAGGCTGACATTAAGCTGGATCTACCCA  1129
Db      1021  GCTGAAGTCAAGCATCGGGCTGATCATGAAAGGCTGACATTAAGCTGGATCTACCCA  1080
QY      1130  GATCGTGAAGATCTCTACTACAGACATCCGAGTTTATATAGACCAAGGCCATGCCAA  1189
Db      1081  GATCGTGAAGATCTCTACTACAGACATCCGAGTTTATATAGACCAAGGCCATGCCAA  1140
QY      1190  GGTGGCCCAACATGATCGTGGTGGAGTGTTCCTCCAGTGAAGCCCTCGCCCTTGTGT  1249
Db      1141  GGTGGCCCAACATGATCGTGGTGGAGTGTTCCTCCAGTGAAGCCCTCGCCCTTGTGT  1200
QY      1250  CACCTTGGGACATCGAAGCCAGCTCGAAGCTCAGTTTACACCAAGGTGACCAACTTAT  1309
Db      1201  CACCTTGGGACATCGAAGCCAGCTCGAAGCTCAGTTTACACCAAGGTGACCAACTTAT  1260
QY      1310  ACTCAACTTGAATTAACATCAGCTGTGATCGGATCCAGCTGATGAACCTGGGATTGGCTG  1369
Db      1261  ACTCAACTTGAATTAACATCAGCTGTGATCGGATCCAGCTGATGAACCTGGGATTGGCTG  1320
QY      1370  GTTCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCATCCTGCTGCC  1429
Db      1321  GTTCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCATCCTGCTGCC  1380
QY      1430  GAACCAAGATGCAAAATTAGATCTGGGGTCCAGTGTCAATTGTGAAGCCCTGGGATT  1489
Db      1381  GAACCAAGATGCAAAATTAGATCTGGGGTCCAGTGTCAATTGTGAAGCCCTGGGATT  1440
QY      1490  CGAGGAGCTGAGTCTCTACAGCAAGGATGCCCTTGTACTACCCAGCCCTCTGTG  1549
Db      1441  CGAGGAGCTGAGTCTCTACAGCAAGGATGCCCTTGTACTACCCAGCCCTCTGTG  1500
QY      1550  GAAACCCAGCTCTCCTGTCCTCCAGTGAAGACTTGGATGGCAGCCATCAGGGAAGGCTGG  1609
Db      1501  GAAACCCAGCTCTCCTGTCCTCCAGTGAAGACTTGGATGGCAGCCATCAGGGAAGGCTGG  1560
QY      1610  GTCCACGCTGGGAGATATGGGTGTGAGCTTATAGACCAATCCCTCTGCAATCAATAAAC  1669
Db      1561  GTCCACGCTGGGAGATATGGGTGTGAGCTTATAGACCAATCCCTCTGCAATCAATAAAC  1620
QY      1670  ACTTGGCTGTG  1680
Db      1621  ACTTGGCTGTG  1631
```

Search completed: October 9, 2003, 13:55:21  
Job time : 499.773 secs